

STIC-Biotech/ChemLib

172534

me

From: CR
Sent: Li, Ruixiang
To: Sunday, November 27, 2005 12:15 PM
Subject: STIC-Biotech/ChemLib
Sequence search of Application No. 10/600,645

Please do a standard search on:

- (i). SEQ ID NO: 2 against both commercial and interference amino acid databases;
(ii). SEQ ID NO: 1 and 2 against both commercial and interference nucleic acid databases.

Thank you very much!

Ruixiang Li
GAU 1646
REM 4D75
Mail Box 4C70
(571) 272-0875

2 aa 532

1 na 1813

me

STIC-BIOTECH/ChemLib

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

Date completed: _____
Searcher: Beverly e 2523
Terminal time: _____
Elapsed time: _____
CPU time: _____
Total time: _____
Number of Searches: _____
Number of Databases: _____

Search Site
____ STIC
____ CM-1
____ Pre-S
Type of Search
____ N.A. Sequence
____ A.A. Sequence
____ Structure
____ Bibliographic

Vendors
____ IG
____ STN
____ Dialog
____ APS
____ Geninfo
____ SDC
____ DARC/Questel
____ Other CGN

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STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 172534

TO: Ruixiang Li
Art Unit: 1646
Location: rem/4D75/4C70
Serial Number: 10/600645

Monday, December 12, 2005

From: Beverly Shears
Location: Biotech-Chem Library
REM 1A54
Phone: 571-272-2528
beverly.shears@uspto.gov

Search Notes

Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

Published Applications Database - November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).



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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 12:46:28 / Search time 6240 Seconds
(without alignments)
16515.573 Million cell updates/sec

Title: US-10-600-645-1

Perfect score: 1813
Sequence: 1 CTAGTGGATCCCGGGCTG.....TTCAGGACTCTGCAGAAATGC 1813

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- GenEmbl.*
1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1813	100.0	1813	6	AR169902 Sequence
2	1813	100.0	1813	6	AR382508 Sequence
3	1750.4	96.5	3003	6	CQ986812 Sequence
4	1750.4	96.5	3003	6	CS027157 Sequence
5	1750.4	96.5	3003	9	RATRALK3
6	1750.4	96.5	3167	6	CQ986810 Sequence
7	1750.4	96.5	3167	6	CQ986811 Sequence
8	1750.4	96.5	3167	6	CS027155 Sequence
9	1750.4	96.5	3167	6	CS027156 Sequence
10	1750.4	96.5	3167	9	S75359 bone morpho
11	1595.8	88.0	1599	9	D17667 Rat mRNA fo
12	1584.6	87.4	2292	9	MUSBMPRC
13	1584.6	87.4	5288	9	BC042611 Mus muscu
14	1581.4	87.2	2070	6	A38817 Sequence 13
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ALIGNMENTS

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LOCUS	AR169902					
DEFINITION	Sequence 1 from patent US 6291206.					
ACCESSION	AR169902					
VERSION	AR169902.1	GI:17907859				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 1813)					
AUTHORS	Wozney,J.M., Celeste,A.J., Thies,R.Scott. and Yamaji,N.					
TITLE	BMP receptor proteins					
JOURNAL	Patent: US 6291206-A 1 18-SEP-2001;					
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Db	1	CTAGTGGATCCCGGGCTGCAGGAATTC	CGCGCCGCGCAGGACACGTGCGAATTTGACA	60
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Db	61	ATGACTCAGCTATACACTTACATCAGATTACTCGGAGCCCTGCTGTTTCATCTTCAT	120	
QY	121	GTTCAAGGGCAGAACTTAGATAGTATGCTCCATGCTAGTATGTAATCAGACGTGGAC	180	
Db	121	GTTCAAGGGCAGAACTTAGATAGTATGCTCCATGCTAGTATGTAATCAGACGTGGAC	180	
QY	181	CAGAGAAGCCGAAAATGGAGTGAGCTTAGCACCAGGACACCTTACCTTTCTTAAAA	240	
Db	181	CAGAGAAGCCGAAAATGGAGTGAGCTTAGCACCAGGACACCTTACCTTTCTTAAAA	240	
QY	241	TGCTATTGCTCAGGACACGTGCCCATGACGCTATTAAATAACATGCATACTAATGCG	300	

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AR382508
LOCUS AR382508 1813 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6610513.
ACCESSION AR382508
VERSION AR382508.1 GI:40091231
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1813)
AUTHORS Wozney,J.M., Celeste,A.J., Thies,R.S. and Yamaji,N.
TITLE Receptor proteins
JOURNAL Patent: US 6610513-A 1 26-AUG-2003;
Genetics Institute, LLC.; Cambridge, MA
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/organism="unknown"
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Query Match 100.0%; Score 1813; DB 6; Length 1813;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
LOCUS CQ986812 3003 bp DNA linear PAT 25-JAN-2005
DEFINITION Sequence 121 from Patent WO2005003158.
ACCESSION CQ986812
VERSION CQ986812.1 GI:58194651
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
1 Brunkow,M.E., Galas,D.J., Kovacevich,B., Mulligan,J.T.,
Paepke,B.W., van Ness,J., and Winkler,D.G.
Compositions and methods for increasing bone mineralization
Patent: WO 2005003158-A 121 13-JAN-2005;
Celltech R & D, Inc. (US)
FEATURES
Location/Qualifiers
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/organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"

ORIGIN
Query Match 96.5%; Score 1750.4; DB 6; Length 3003;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 6; Indels 2; Gaps 2;
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DB 52 TGGCCCGGACGAGCACGTCGGAATTTGACAAATGATGATGATGATGATGATGATGATGATGAT 111
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Db 52 TGGCCCGGACAGGACACGTCGGAATTCGCAATGCACTCAGCTATACACTACAGATT 111
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RESULT 5

RATRALK3

LOCUS

DEFINITION

Rat mRNA for bone morphogenetic protein type IA receptor, complete cds.

RATRALK3

Rat mRNA for bone morphogenetic protein type IA receptor, complete cds.

RATRALK3

Rat mRNA for bone morphogenetic protein type IA receptor, complete cds.

RATRALK3

Rat mRNA for bone morphogenetic protein type IA receptor, complete cds.

RATRALK3

Rat mRNA for bone morphogenetic protein type IA receptor, complete cds.

RATRALK3

Rat mRNA for bone morphogenetic protein type IA receptor, complete cds.

RATRALK3

Rat mRNA for bone morphogenetic protein type IA receptor, complete cds.

RATRALK3

Rat mRNA for bone morphogenetic protein type IA receptor, complete cds.

RATRALK3

Rat mRNA for bone morphogenetic protein type IA receptor, complete cds.

RATRALK3

Rat mRNA for bone morphogenetic protein type IA receptor, complete cds.

RATRALK3

Rat mRNA for bone morphogenetic protein type IA receptor, complete cds.

RATRALK3

Rat mRNA for bone morphogenetic protein type IA receptor, complete cds.

RATRALK3

Rat mRNA for bone morphogenetic protein type IA receptor, complete cds.

RATRALK3

3003 bp mRNA linear ROD 08-FEB-1999
RATRALK3
Rat mRNA for bone morphogenetic protein type IA receptor, complete cds.
D38082
D38082.1 GI:1398909
RALK-3; bone morphogenetic protein type IA receptor; bone morphogenetic protein receptor; BMP receptor; serine/threonine kinase; transmembrane protein.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 3003)
Takeda, K., Oida, S., Ichijo, H., Iimura, T., Maruoka, Y., Amagasa, T. and Sasaki, S.
Molecular cloning of rat bone morphogenetic protein (BMP) type IA receptor and its expression during ectopic bone formation induced by BMP
Biochem. Biophys. Res. Commun. 204 (1), 203-209 (1994)
PUBMED 7945360
REFERENCE 2 (bases 1 to 3003)
Oida, S.
Direct Submission
TITLE

JOURNAL	Submitted (26-AUG-1994) Shinichiro Oida, Faculty of Dent., Tokyo Medical and Dental University, Department of Biochemistry; 1-5-45 Yushima, Bunkyo-ku, Tokyo 113, Japan (Tel:03-3813-6111(ex.5126), Fax:03-5684-8047)		
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LOCUS CQ986810 3167 bp DNA linear PAT 25-JAN-2005
DEFINITION Sequence 119 from Patent WO2005003158.
ACCESSION CQ986810
VERSION CQ986810.1 GI:58194649
KEYWORDS
SOURCE
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE
1 Brunkow,M.E., Galas,D.J., Kovacevich,B., Mulligan,J.T.,
Paepel,B.W., van Ness,J. and Winkler,D.G.
Compositions and methods for increasing bone mineralization
Patent: WO 2005003158-A 119 13-JAN-2005;
Celltech R & D, Inc. (US)

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DEFINITION Sequence 120 from Patent WO2005003158.
ACCESSION CQ986811
VERSION CQ986811.1 GI:58194650
KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
1
REFERENCE
AUTHORS Brunkow,M.E., Galas,D.J., Kovacevich,B., Mulligan,J.T.,
Paepker,B.W., van Ness,J. and Winkler,D.G.
TITLE Compositions and methods for increasing bone mineralization
JOURNAL Patent: WO 2005003158-A 120 13-JAN-2005;
Celltech R & D, Inc. (US)
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Matches 1776; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

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S75359
LOCUS 3167 bp mRNA linear ROD 27-MAY-1995
DEFINITION bone morphogenetic protein type IA receptor [rats, mRNA, 3167 nt].
ACCESSION S75359
VERSION S75359.1 GI:834007
KEYWORDS
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 3167)
Takeda,K.
REFERENCE
AUTHORS
TITLE Expression of serine/threonine kinase receptors during ectopic bone
formation induced by bone morphogenetic protein (BMP)
JOURNAL Kokubyo Gakkai Zasshi 61 (4), 512-526 (1994)
PUBMED 7897267
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 160455] from the original journal article.
FEATURES
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Location/Qualifiers
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RESULT 11
RATRB4R1
LOCUS RATRB4R1 1599 bp mRNA linear ROD 04-FEB-1999
DEFINITION Rat mRNA for bone morphogenetic protein 4 receptor, complete cds.
ACCESSION D17667
VERSION D17667.1 GI:684975
KEYWORDS bone morphogenetic protein 4 receptor.
SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE
AUTHORS Ikeda,T. and Takahashi,H.
TITLE Expression pattern of bone morphogenetic protein 4 receptor in
embryo and adult rat
JOURNAL unpublished
REFERENCE
AUTHORS Takahashi,H.
TITLE Direct Submission
JOURNAL Submitted (16-SEP-1993) Hiroshi Takahashi, Tokyo Metropolitan
Institute of Gerontology, Department of Pathology; 35-2 Sakaecho,,
Itabashi-ku, Tokyo 173, Japan (Tel:03-3964-3241(ex.3034),
Fax:03-3579-4776)
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VERSION 1
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SOURCE Mus musculus
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REFERENCE 1 (bases 1 to 2292)
AUTHORS Suzuki, A., Thies, R.S., Yamaji, N., Song, J.J., Wozney, J.M.,
Murakami, K. and Ueno, N.
A truncated bone morphogenetic protein receptor affects
dorsal-ventral patterning in the early xenopus embryo
Proc. Natl. Acad. Sci. U.S.A. 91 (22), 10255-10259 (1994)
7937936
REFERENCE 2 (bases 1 to 2292)
AUTHORS Ueno, N.
Direct Submission
Submitted (13-MAY-1993) Naoto Ueno, Hokkaido University, Faculty of
Pharmaceutical Sciences, Sapporo, Hokkaido 060, Japan
(Tel:81-11-716-8513, Fax:81-11-716-8513)
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Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalhus, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J., and Marz, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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 2 (bases 1 to 5288)
 Strausberg, R.
 Direct Submission
 Submitted (02-JAN-2003) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbe-remail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulsegod, H.,
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
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 This clone was selected for full length sequencing because it
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AUTHORS	Miyazono,K., DiJke,P.T., Franzen,P., Yamashita,H. and Heldin,C.		
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Db	855	CCAAAGCTCTGGAGTGGATCTGGATTGCTTTTATTTGGTTTACGCGNACTATTGCCAAACA	914
QY	759	GATTACAGATGTTTCGGCAGGTTGGTAAAGGCCGGTATGGAGAAGTATGATGGGTAAATG	818

D _b	915	GATTCAGATGGTTCCGACAGTGTGGTAAGAAGCGCGCTATCGGAAGAAGTATCGATGGGTAAATG	974
Q _y	819	CGTGGTGAAAAAGTGGCTGTCAAAAGTATTTTTTACCACCTGAAGAAGCTAGCTGTTTAG	878
D _b	975	CGTGGTGAAAAAGTGGCTGTCAAAAGTGTTTTTTACCACCTGAAGAAGCTAGCTGGTTAG	1034
Q _y	879	AGAACAGAAAATCTACACAGCGGTCTTAATCGGTCATGAAAATATACTTTGGTTTTATAGC	938
D _b	1035	AGAACAGAAAATCTACACAGCGGTGTAAATCGGTCATGAAAATATACTTTGGTTTTATAGC	1094
Q _y	939	TGCAGACATTAAAGGCACCGGTTCTCTGGACTCAGCTGTATTGTGATTACTGATTACCATGA	998
D _b	1095	TGCAGACATTAAAGGCACCTGGTTCTCTGGACTCAGCTGTATTGTGATTACTGATTACCATGA	1154
Q _y	999	GAATGGGTCTCTCTATGACTTCCTGAAATGTGCCACCTGGACACCGAGGCCCTACTCAA	1058
D _b	1155	AAATGGGATCTCTCTATGACTTCCTGAAATGTGCCACACTAGACACCGAGGCCCTACTCAA	1214
Q _y	1059	GTTAGCTTATTCTGCTGCTGTGTCACCTCCACACAGAAATTTATATGACACGCA	1118
D _b	1215	GTTAGCTTATTCTGCTGCTGTGTCACCTCCACACAGAAATTTATATGATCCCCA	1274
Q _y	1119	AGGCAAGCCTGCAATTGCTCATCGAGACCTGAAGACGAAAAACAATCTTATTAAAGAAAA	1178
D _b	1275	AGGCAAGCCTGCAATTGCTCATCGAGACCTGAAGACGAAAAACAATCTTATTAAAGAAAA	1334
Q _y	1179	TGTTAGTTGCTGTTATTCGTGACTGGGGCTAGCTGTTAAATTTCAACAGTGNACACAAATGA	1238
D _b	1335	TGGAAGTTGCTGTTATTCGTGACTGGGGCTAGCTGTTAAATTTCAACAGTGNACACAAATGA	1394
Q _y	1239	AGTTGACATACCTTTGAACACCGGTTGGGACACGAGCGGTACATGCTCCAGAAAGTGCT	1298
D _b	1395	AGTTGACATACCTTTGAATACCAAGGTTGGGACACGAGCGGTACATGCTCCAGAAAGTGCT	1454
Q _y	1299	GGACGAGAGCCTGAGTAAAAACCAATTTCCAGCCCTACATCATGCTGACATCTACAGCTT	1358
D _b	1455	GGATGAAAGCCTGAAATAAAACCAATTTCCAGCCCTACATCATGCTGACATCTATAGCTT	1514
Q _y	1359	TGTTTTCATCATTTTGGGAGATGGCCCGTCCGTGTATTACAGGAGGAATCGTGAGGAATA	1418
D _b	1515	TGTTTTCATCATTTTGGGAAATGGCTCGTGTGTATTACAGGAGGAATCGTGAGGAATA	1574
Q _y	1419	TCAATTACCATATTACAACATGGTGCCTAGTGACCCCATCTTATGAAGACATGCGTGAGGT	1478
D _b	1575	TCAATTACCATATTACAACATGGTGCCTAGTGACCCCATCTTATGAAGACATGCGTGAGGT	1634
Q _y	1479	CGTGCTGTGAACCGCTTGGGCCCAATCGTCTCTAACCGCTGGAAAGTGAATGTCT	1538
D _b	1635	TGTGTGTGTGAACCGCTTGGGCCCAATCGTCTCTAACCGCTGGAAACAGCGATGAATGTCT	1694
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D _b	1695	TCGAGCAGTTTTGNAAGCTAATGTGAGAAATGTTGGGCCCAATANTCCAGCTCCAGACTCAC	1754
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D _b	1755	AGCTTTGAGAAATCAAGAAGACACTTGCAAAAAATGGTTGAAATCCCAGGATGTAAGAATTTG	1814
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D _b	1815	ACAATTAACAAATTTTGAGGAGAAATTTAGACTGCAAGAAATCTCTTCACCCAAGGAATGG	1874
Q _y	1711	GTGGAGTTAGCATGGAATAGGATGTCGGCTTGGTTTTCCAGACTCTCTCTCTCTACCATCTT	1770
D _b	1875	GTGGATTAGCATGGAATAGGATGTSACITGGTTTCCAGACTCCTTCTCTCTA-CATCTT	1933
Q _y	1771	CACAGGCTGCTAACAGTAAACCTTTACGACTCTGAGACTCTGCAAGATGC	1813
D _b	1934	CACAGGCTGCTAACAGTAAACCTTTACCGTACTCTCTACAGAAATAC	1976

LOCUS	AR140650	2070 bp	DNA	linear	PAT 16-JUN-2000
DEFINITION	Sequence 13 from patent US 6207814.				
ACCESSION	AR140650				
VERSION	AR140650.1	GI:14483146			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 2070)				
AUTHORS	Miyazono,K., ten Dijke,P., Franzen,P., Yamashita,H. and Heldin,C.-H.				
TITLE	Activin receptor-like kinases, ALK-3 and ALK-6, and nucleic acids encoding them				
JOURNAL	Patent: US 6207814-A 13 27-MAR-2001;				
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	/organism="unknown"				
	/mol_type="unassigned DNA"				
ORIGIN					
	Query Match	87.2%	Score 1581.4;	DB 6;	Length 2070;
	Best Local Similarity	94.1%	Pred. No. 0;		
	Matches 1678;	Conservative	0;	Mismatches	96;
				Indels	9;
				Gaps	3;
Qy	39	CAGGACACGTGCGAATTGGCAATGACTCAGCTATACACTTACATCAGATTACTGGGAGC	98		
Db	195	CAGGACGCTGGCAATCAGACAATGACTCAGCTATACACTTACATCAGATTACTGGGAGC	254		
Qy	99	CTGCTCTTTCATCATTTTCTCATGTTTCAGGGCAGAATCTAGATAGTATGCTTCATCGTAC	158		
Db	255	CTGCTCTTTCATCATTTTCTCATGTTTCAGGGCAGAATCTAGATAGTATGCTTCATCGTAC	314		
Qy	159	TGGTATGAAATCAGACGTGGACACAGAAGACCGGAAATGGAGTCAGCTTAGCACCCAGA	218		
Db	315	TGGTATGAAATCAGACTTGGACCAAGAAGACCGAATAATGGAGTGACTTTAGCACCCAGA	374		
Qy	219	GGACACCTTACCTTTTCTTAAATGCTATTGCTCAGGACACTGCCAGATGAAGCTATTAA	278		
Db	375	GGATACCTTGCCCTTTCTTAAAGTGCTATTGCTCAGGACACTGCCAGATGATGCTATTAA	434		
Qy	279	TAAACATGATAACTAAATGGCCATTGCTTTGGCCATTATAGAAGAAGATGATCAGGGAGA	338		
Db	435	TAAACATGATAACTAAATGGCCATTGCTTTGGCCATTATAGAAGAAGATGATCAGGGAGA	494		
Qy	339	AACCACGTTAACTTCTGGGTGTATGAAGTATGAAGCTCTGATTTTCAATGCAAGGATTTC	398		
Db	495	AACCACATTAACCTTCTGGGTGTATGAAGTATGAAGCTCTGATTTTCAATGCAAGGATTTC	554		
Qy	399	ACCAAAAGCCACGCTACGACGAGCAATAGAAATGTTGTCGGACCAATTTGTGCAACCAATTA	458		
Db	555	ACCGAAAGCCACGCTACGACGAGCAATAGAAATGTTGTCGGACCAATTTGTGCAACCAATTA	614		
Qy	459	TTTGCAGCTTACACTGCCCGCTGCTGTTATAGGCCCAATTTCTTTGATGGCAGGCTCCGATG	518		
Db	615	TTTGCAGCTTACACTGCCCGCTGCTGTTATAGGCCCAATTTCTTTGATGGCAGGCTCCGATG	674		
Qy	519	GCTGGCTGTGCTCATCTCTATGGCTGTCGTATGTCGCCATGATCGTCTCTCTCCAGCTG	578		
Db	675	GCTGGTGTGCTCATTTCCATGGCTGCTGTATAGTATGCTATGATCATCTTCTCCAGCTG	734		
Qy	579	CTTCTGTTCAAACATTACTGTAAGAGTATCTCAAGCAGAGGTCGTTTACAACCGTACTT	638		
Db	735	CTTTTGTCTATAGCAATTATTGTAAGAGTATCTCAAGCAGGCTCGTTTACAACCGTACTT	794		
Qy	639	GGAAACAGATGAAGCAATTATTCCAGTAGGAGAATCACTGAAAGACCTGATTGACCAAGTC	698		
Db	795	GGAAACAGATGAAGCAATTATTCCAGTAGGAGAATCATTTGAAAGACCTGATTGACCAAGTC	854		
Qy	699	ACAAAGCTCTGGTGTAGTGGATCTGGATTACTTTATTGGTTTACGCAACTATTGGCCAAACA	758		
Db	855	CCAAAGCTCTGGAGTGGATCTGGATTCTTTATTGGTTTACGCAACTATTGGCCAAACA	914		
Qy	759	GATTTCAGATGGTTTCGGCAGGTTGGTAAGCGCCGGTATGGAGAAGTATGGATGGGTAAATG	818		

Job time : 6247 secs

Db 915 GATTGAGATGGTTCGCGAGGTGGTAAAGGCCGCTATGAGAGAGTATGATGGGTHAAATG 974
Oy 819 GCGTGTGAAAAAGTGGCTGTCAAGTAATTTTACCCTGAGAGAGCTAGCTGGTTTAG 878
Db 975 GCGTGTGAAAAAGTGGCTGTCAAGTGTATTTTACCCTGAGAGAGCTAGCTGGTTTAG 1034
Oy 879 AGAAACAGAAATCTACAGACGGTGTAAATGCGTCATGAAATATATATCTTGGTTTATAGC 938
Db 1035 AGAAACAGAAATCTACAGACGGTGTAAATGCGTCATGAAATATATATCTTGGTTTATAGC 1094
Oy 939 TGCAGACATTTAAAGGACACCGGTTCTCGGACTCAGCTGTATTTGATTACTGATTACCATGA 998
Db 1095 TGCAGACATTTAAAGGACATGGTTCTCGGACTCAGCTGTATTTGATTACTGATTACCATGA 1154
Oy 999 GAATGGGTCTCTCTATGACTTCCTGAAATGTGCCACCTGGACACAGAGCCCTACTCAA 1058
Db 1155 AAATGGATCTCTCTATGACTTCCTGAAATGTGCCACCTAGACACCAGAGCCCTACTCAA 1214
Oy 1059 GTTAGCTTATTTGCTGCTGCTGGTCTGTGCCACCTCCACACAGAAATTTATGGCAGCA 1118
Db 1215 GTTAGCTTATTTGCTGCTGCTGGTCTGTGCCACCTCCACACAGAAATTTATGGTACCCA 1274
Oy 1119 AGCAAGCCTGCAATTTGCTCATCGAGACCTGAAAGACAAAACATCCTTTATTAAGAAAA 1178
Db 1275 AGGAAGCCTGCAATTTGCTCATCGAGACCTGAAAGACAAAACATCCTTTATTAAGAAAA 1334
Oy 1179 TGTAGTTGCTGTATTTGCTGACCTGGGCCCTAGCTGTAAATTTCAACAGTGACACAAATGA 1238
Db 1335 TGGAACTTGTGTATTTGCTGACCTGGGCCCTAGCTGTAAATTTCAACAGTGATACAAATGA 1394
Oy 1239 AGTTGACATACCTTTGAAACACAGAGGTGGGCACCGCGGTACATGGCTCCAGAGTGCT 1298
Db 1395 AGTTGACATACCTTTGAAATACCAAGGTGGGCACCAAGCGGTACATGGCTCCAGAGTGCT 1454
Oy 1299 GGACGAGAGCCTGAGTAAACCAATTTCCAGCCCTACATCATGGCTGACATCTACAGCTT 1358
Db 1455 GGATGAAGCCTGAATTAACCAATTTCCAGCCCTACATCATGGCTGACATCTATAGCTT 1514
Oy 1359 TGGTTTGATCATTTGGGAGATGGCCGCTGCTGTATTTACAGGAGGAATCGTGAGGAATA 1418
Db 1515 TGGTTTGATCATTTGGGAAATGGCTCGTGTGTATTTACAGGAGGAATCGTGAGGAATA 1574
Oy 1419 TCAATTTACCATATTAACAACATGGTGGCTAGTGACCCATCTTATGAAGACATGGTGAGGT 1478
Db 1575 TCAATTTACCATATTAACAACATGGTGGCCAGTGACCCATCTTATGAGGACATGGTGAGGT 1634
Oy 1479 CGTGTGTGTGAACGCTTCGGGCCAATCGTCTTAACCGCTGGAACAGTGATGAATGTCT 1538
Db 1635 TGTGTGTGTGAACGCTTCGGGCCAATCGTGTCTAACCGCTGGAACAGCGGATGAATGTCT 1694
Oy 1539 TCAGACCGTTTGAAGCTGATGTCAAGATGCTGGGCCATAATCCAGCATCCAGACTCAC 1598
Db 1695 TCGAGCAGTTTGAAGCTAATGTCAAGATGTTGGGCCATAATCCAGCCTCCAGACTCAC 1754
Oy 1599 AGCTTTGAGAAATCAAGAGACGCTCCGAAAGATGGTTGAATCCAGGATGTAAAGATTG 1658
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Oy 1659 AC---AAACAGTTTGAAGAAAGAAATTTAGACTGCAAGAAATTC---ACCCGAGGAAG 1710
Db 1815 ACAATTAACAATTTTGAAGGAGAAATTTAGACTGCAAGAAATTC---ACCCGAGGAAG 1874
Oy 1711 GTGGAGTTAGCATGAGTATGAGTATGGCTTGGTTTCCAGACTCTCTCTCTACCATCTT 1770
Db 1875 GTGGAGTTAGCATGAGTATGAGTATGGCTTGGTTTCCAGACTCTCTCTCTCTA-CATCTT 1933
Oy 1771 CACAGGCTGTAACAGTAAACCTTTTCCAGACTCTGAGAAATGC 1813
Db 1934 CACAGGCTGTAACAGTAAACCTTTTCCAGACTCTGAGAAATGC 1976

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: December 9, 2005, 05:59:38 ; Search time 767 Seconds
(without alignments)
15753.700 Million cell updates/sec

Title: US-10-600-645-1
Perfect score: 1813
Sequence: 1 CTAGTGGATCCCCGGGCTG.....TTCAGGACTCTGCAGATGC 1813

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 4996997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1813	100.0	1813	2	AAQ83530
2	1750.4	96.5	3003	14	Adw28817 Rat bone
3	1750.4	96.5	3003	14	Adx97430 Rat bone
4	1750.4	96.5	3167	14	Adw28816 Rat bone
5	1750.4	96.5	3167	14	Adw28815 Rat bone
6	1750.4	96.5	3167	14	Adw28815 Rat bone
7	1750.4	96.5	3167	14	Adx97428 Rat bone
8	1581.4	87.2	2070	2	AAZ09847
9	1581.4	87.2	2070	14	Ady51875 Murine AL
10	1579.8	87.1	2070	2	AAQ66640
11	1574.2	86.8	2402	2	AAQ90184
12	1574.2	86.8	2402	2	AAT27228
13	1574.2	86.8	2402	2	AAT28021
14	1574.2	86.8	2402	2	AAV71972
15	1424.4	78.6	2056	2	AAQ90183
16	1387	76.5	2932	2	AAT06031
17	1387	76.5	2932	2	AAZ09843
18	1387	76.5	2932	5	AAS87057
19	1387	76.5	2932	10	ACF05952

20	1387	76.5	2932	14	Adw28812
21	1387	76.5	2932	14	Adx07490 Cyclin-de
22	1387	76.5	2932	14	Adx97425
23	1387	76.5	2932	14	Ady51867 Human ALK
24	1387	76.5	2932	14	AEC02077
25	1385.4	76.4	2932	2	AAQ66636
26	1385.4	76.4	3631	14	Ady81406 Human act
27	1374.6	75.8	2623	8	Ady53821 DNA used
28	1343	74.1	1599	13	Adq89877 Antagonis
29	1343	74.1	1599	13	Adr73164 Human bon
30	1258.8	69.4	2730	5	AAS87064 DNA enco
31	1104	60.9	1743	10	Ade07106 Novel cod
32	1104	60.9	1743	14	Adu40263 Novel hum
33	978.2	54.0	1185	12	ACH87174 Human gen
34	918	50.6	1929	10	Adc07107 Novel cod
35	918	50.6	1929	14	Adu40264 Novel hum
36	810.4	44.7	1695	5	AAS87063 DNA enco
37	773.8	42.7	2659	10	ADC74824
38	716	39.5	1952	2	AAT06032
39	716	39.5	1952	2	AAZ09849
40	716	39.5	1952	14	Ady51879
41	714.4	39.4	1952	2	AAQ66642
42	707.6	39.0	1575	8	ACD13394
43	707.6	39.0	1575	14	Adw28813
44	707.6	39.0	1575	14	Adx97426
45	707.6	39.0	2032	6	ABK92206

ALIGNMENTS

RESULT 1
AAQ83530
ID AAQ83530 standard; DNA; 1813 BP.
XX
AC AAQ83530;
XX
DT 25-MAR-2003 (revised)
DT 26-SEP-1995 (first entry)
XX
DE Sequence encoding bone morphogenic protein receptor CFK1-23a.
XX
KW Bone morphogenic protein; receptor; serine/threonine kinase; BMP; bone;
KW cartilage; injury; treatment; inhibition; ss.
XX
OS Rattus rattus.
XX
FH Key Location/Qualifiers
FT CDS 61..1659
FT /tag= a
FT /product= "Bone morphogenic protein receptor."
XX
PN W09507982-A1.
XX
PD 23-MAR-1995.
XX
PF 07-SEP-1994; 94WO-US010080.
XX
PR 17-SEP-1993; 93US-00123934.
XX
PA (GEM) GENETICS INST INC.
XX
PI Wozney JM, Celeste AJ, Thies RS, Yamaji N;
XX
DR WPI; 1995-131350/17.
XX
DR P-PSDB; AAR70237.
XX
PT Truncated BMP and serine/threonine kinase receptor proteins - used to
XX inhibit the effects of BMP-2 and/or BMP-4.
XX
PS Claim 2; Page 48-50; 83pp; English.
XX
CC Truncated bone morphogenic protein (BMP) receptors and serine/threonine

kinase receptors may be used in compositions to inhibit the effects of BMP's such as BMP 2 and BMP-4. The truncated receptors prefer comprise the ligand binding domain, but not the serine/threonine kinase and transmembrane domains. The truncated proteins are soluble and will be excreted into supernatant by recombinant mammalian cells expressing them. Such cells can be delivered in a medium or matrix which partially impedes their mobility, thereby localising the cells to a site of bone or cartilage injury. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 1813 BP; 506 A; 397 C; 439 G; 471 T; 0 U; 0 Other;

Query Match 100.0%; Score 1813; DB 2; Length 1813;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	ATGACTCAGGTATACACTTACATCAGATTACT	GGGAGCCGTCTGTTTCATCTCAT	120
DB	61	ATGACTCAGGTATACACTTACATCAGATTACT	GGGAGCCGTCTGTTTCATCTCAT	120
QY	121	GTTCAAGGCGAGAACTCTAGATAGTATGCT	CCATGGTACTGGTATGAATCAGACGTGGAC	180
DB	121	GTTCAAGGCGAGAACTCTAGATAGTATGCT	CCATGGTACTGGTATGAATCAGACGTGGAC	180
QY	181	CAGAAGAAGCCGGAAATGGAGTACGTTAG	CACACAGGACACCTTACCTTTTAA	240
DB	181	CAGAAGAAGCCGGAAATGGAGTACGTTAG	CACACAGGACACCTTACCTTTTAA	240
QY	241	TGCTATTGCTCAGGACACTGCCCAGATGAC	CGTATTAAACACATGCAATATGGC	300
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QY	301	CATTGCTTTGCCATTATAGAAGATGATCAG	GGGAGAACACCGTTAACTCTGGGCT	360
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QY	361	ATGAAGTATGAAGGCTCTGATTTTCAATG	CAAGGATTCACCAAGCCAGCTACGCAGG	420
DB	361	ATGAAGTATGAAGGCTCTGATTTTCAATG	CAAGGATTCACCAAGCCAGCTACGCAGG	420
QY	421	ACAAATAGATGTTGTCGGACCAATTTTG	CAACCAATATTTGACGCTTACCTGCCCT	480
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QY	481	GTGCTTATAGGCCCATTTCTTGATGCGAC	GGTCCGATGGCTGTCTCTCTATG	540
DB	481	GTGCTTATAGGCCCATTTCTTGATGCGAC	GGTCCGATGGCTGTCTCTCTATG	540
QY	541	GCTGCTGTATTGTCGCCATGATCGCTTCT	CCAGCTGCTTCTGTTACAAACATTACT	600
DB	541	GCTGCTGTATTGTCGCCATGATCGCTTCT	CCAGCTGCTTCTGTTACAAACATTACT	600
QY	601	AGAGTATCTCAAGCAGAGGTGTTTCAAC	CCGTTGACTTGGAACAGGATGAAGATT	660
DB	601	AGAGTATCTCAAGCAGAGGTGTTTCAAC	CCGTTGACTTGGAACAGGATGAAGATT	660
QY	661	CCAGTAGGAGAACTCACTGAAAGACCTG	ATTGACCACTCAAGCTCTGTAGTGGAT	720
DB	661	CCAGTAGGAGAACTCACTGAAAGACCTG	ATTGACCACTCAAGCTCTGTAGTGGAT	720
QY	721	GGATTACCTTTTATGTTTACAGCGAACT	ATTGCGCAAAACAGATTTCAGATGGT	780
DB	721	GGATTACCTTTTATGTTTACAGCGAACT	ATTGCGCAAAACAGATTTCAGATGGT	780
QY	781	GGTAAGGCGCGGTATCGAGAGATGATG	GGTAAATGGCGGTGAAAGATGGGCTGTC	840
DB	781	GGTAAGGCGCGGTATCGAGAGATGATG	GGTAAATGGCGGTGAAAGATGGGCTGTC	840
QY	841	AAAGTATTTTTTACCACCTCAAGAGCT	AGCTAGCTGTTTAGAGAACACAGAAATCT	900
DB	841	AAAGTATTTTTTACCACCTCAAGAGCT	AGCTAGCTGTTTAGAGAACACAGAAATCT	900

RESULT 2
ADW28817
ID ADW28817 standard; DNA; 3003 BP.
XX
AC ADW28817;
XX

DB	841	AAAGTATTTTTTACCACCTCAAGAGCTAG	CTGTTTAGAGAACACAGAAATCTACCAG	900
QY	901	GTGTTAATGCGTCATGAAATAATATCT	TGGTTTTATAGTGCAGACATTAAGGC	960
DB	901	GTGTTAATGCGTCATGAAATAATATCT	TGGTTTTATAGTGCAGACATTAAGGC	960
QY	961	TCCTGGACTCAGCTGTATTGATTACT	GATTAACCATGAGAAATGGGCTCTCT	1020
DB	961	TCCTGGACTCAGCTGTATTGATTACT	GATTAACCATGAGAAATGGGCTCTCT	1020
QY	1021	CTGAAATGTGCCACCTGGACACCCAG	AGCCCTACTCAAGTTAGCTTATTTCT	1080
DB	1021	CTGAAATGTGCCACCTGGACACCCAG	AGCCCTACTCAAGTTAGCTTATTTCT	1080
QY	1081	GGTCTGTGCCACCTCCACACAGAAAT	TATATGCGACGCAAGCAAGCTGCAAT	1140
DB	1081	GGTCTGTGCCACCTCCACACAGAAAT	TATATGCGACGCAAGCAAGCTGCAAT	1140
QY	1141	CGAGACCTGAAGAGCAAAAACATCT	TATTAGAAAATGGTAGTGTATTTG	1200
DB	1141	CGAGACCTGAAGAGCAAAAACATCT	TATTAGAAAATGGTAGTGTATTTG	1200
QY	1201	CTGGGCTTAGCTGTTAAATTTCAAC	AGTGAACAAATGAATTTGACATAC	1260
DB	1201	CTGGGCTTAGCTGTTAAATTTCAAC	AGTGAACAAATGAATTTGACATAC	1260
QY	1261	AGGGTGGGCAACAGCGGTACATGCT	CCAGAAAGTCTGGAACAGAGCTG	1320
DB	1261	AGGGTGGGCAACAGCGGTACATGCT	CCAGAAAGTCTGGAACAGAGCTG	1320
QY	1321	GATTTCCAGCCCTACATCATGCTG	CATCTACAGCTTTGGTTGATCA	1380
DB	1321	GATTTCCAGCCCTACATCATGCTG	CATCTACAGCTTTGGTTGATCA	1380
QY	1381	GCCCGTGCCTGTTTACAGGAGAA	TCTGAGGAGAAATCAATTTACAT	1440
DB	1381	GCCCGTGCCTGTTTACAGGAGAA	TCTGAGGAGAAATCAATTTACAT	1440
QY	1441	GTGCTTAGTGACCCCATCTTATGA	AGACATGCTGAGGCTGTGTGTGA	1500
DB	1441	GTGCTTAGTGACCCCATCTTATGA	AGACATGCTGAGGCTGTGTGTGA	1500
QY	1501	CCAAATCGTCTTAAACCGCTGGA	ACAGTGAATGCTTCGAGCCGTTT	1560
DB	1501	CCAAATCGTCTTAAACCGCTGGA	ACAGTGAATGCTTCGAGCCGTTT	1560
QY	1561	TCAGAAATGCTGGGCCCATAA	TCCAGCATCCAGCTTTCAGAA	1620
DB	1561	TCAGAAATGCTGGGCCCATAA	TCCAGCATCCAGCTTTCAGAA	1620
QY	1621	CTCGCAAAAGATGGTTGAATCC	CAGGATGTAAAGATTGCAAA	1680
DB	1621	CTCGCAAAAGATGGTTGAATCC	CAGGATGTAAAGATTGCAAA	1680
QY	1681	TTAGACTGCAAGAAATTCACCG	AGGAGGGTGGAGTTAGCATG	1740
DB	1681	TTAGACTGCAAGAAATTCACCG	AGGAGGGTGGAGTTAGCATG	1740
QY	1741	TGTTTTTCAGAGCTCTCTCT	CTTACCATCTTTCAGAGCTG	1800
DB	1741	TGTTTTTCAGAGCTCTCTCT	CTTACCATCTTTCAGAGCTG	1800
QY	1801	CTTCTCAGAAATGC	1813	
DB	1801	CTTCTCAGAAATGC	1813	

DT	XX	07-APR-2005	(first entry)
DE	XX	Rat bone morphogenetic protein (BMP) receptor type 1 DNA Seq 121.	
KW	XX	receptor; bone morphogenetic protein; bone injury; antibody production;	
KW	XX	TGF beta antagonist; BMP-antagonist; osteopathic; osteopenias;	
KX	XX	osteoporosis; gene; ds.	
OS	XX	Rattus norvegicus.	
FH	XX	Key Location/Qualifiers	
FT	XX	CDS 83..1681	
FT	XX	/*tag= a	
FT	XX	/product= "BMP receptor type 1 protein"	
PN	XX	WO2005003158-A2.	
XX	XX		
PD	XX	13-JAN-2005.	
PF	XX	15-JUN-2004; 2004WO-US018910.	
PR	XX	16-JUN-2003; 2003US-00463190.	
PA	XX	(CLLT) CELLTECH R & D INC.	
XX	XX		
PI	XX	Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paepfer BW;	
PI	XX	Van Ness J, Winkler DG;	
DR	XX	WPI; 2005-081936/09.	
DR	XX	P-FSDB; ADW28603.	
PT	XX	New antibody or antigen-binding fragment that binds specifically to	
PT	XX	sclerostin polypeptide and which inhibits binding of sclerostin	
PT	XX	polypeptide to a bone morphogenic protein, useful for increasing bone	
PT	XX	mineral content or density.	
PS	XX	Disclosure; SEQ ID NO 121; 205pp; English.	
CC	XX	This invention relates to a novel antibody or antigen-binding fragment	
CC	XX	that binds specifically to a sclerostin (SOST) polypeptide and impairs	
CC	XX	formation of a sclerostin homodimer. Specifically, it refers to an	
CC	XX	antibody that competitively inhibits binding of the sclerostin	
CC	XX	polypeptide to a bone morphogenic protein (BMP) Type I receptor binding	
CC	XX	site or a BMP Type II receptor binding site. The present invention	
CC	XX	describes a hybridoma cell capable of producing the antibody and a host	
CC	XX	cell for antibody expression. Furthermore, it provides a nucleic acid	
CC	XX	molecule encoding a transforming growth factor-beta (TGF-beta) binding	
CC	XX	protein known as SOST (and also BEER) and methods for detection thereof.	
CC	XX	Accordingly, such antibodies and osteopathic compositions of the	
CC	XX	invention can be used for treating osteopenia, osteoporosis, fractures	
CC	XX	and other disorders related to low bone mineral content and density. As	
CC	XX	such, these compositions improve bone mineralization and can be described	
CC	XX	as TGF-beta antagonists and/or BMP-antagonists. This polynucleotide is a	
CC	XX	bone morphogenetic protein receptor type 1 DNA sequence given in an	
CC	XX	embodiment of the invention.	
SQ	XX	Sequence 3003 BP; 840 A; 626 C; 654 G; 883 T; 0 U; 0 Other;	
		Query Match 96.5%; Score 1750.4; DB 14; Length 3003;	
		Best Local Similarity 99.6%; Pred. No. 0;	
		Matches 1776; Conservative 0; Mismatches 6; Indels 2; Gaps 2;	
QY	30	TGCGGCCCGCCAGGCACGTGGCAATTTGGACAATGACTCAGCTATACACTTACATCAGATT 89	
Dd	52	TGCGCCCGACAGGACACGTGGCAATTTGGACAATGACTCAGCTATACACTTACATCAGATT 111	
QY	90	ACTGGGAGCGCTCTCTGTTTCATCATTTCTCATGTTTCAAGGGCAGAATCTAGATAGTAGTCT 149	
Dd	112	ACTGGGAGCGCTCTCTGTTTCATCATTTCTCATGTTTCAAGGGCAGAATCTAGATAGTAGTCT 171	
QY	150	CCATGGTACTGGTATGAATCATAGACGTGGACAGAAAGACCGGAAAAATGGAGTGACGTT 209	
Dd	172	CCATGGTACTGGTATGAATCATAGACGTGGACAGAAAGACCGGAAAAATGGAGTGACGTT 231	

Db 532 CGTCCGATGGCTGCTGCTCATCTCTATGGCTGTCTGTATTGTGCCATGATCGTCTT 591
Qy 570 CTCAGAGTCTCTGTTTACAAACATTACTGTAGAGTATCTCAAGCAGAGGTGGTTACAA 629
Db 592 CTCAGAGTCTCTGTTTACAAACATTACTGTAGAGTATCTCAAGCAGAGGTGGTTACAA 651
Qy 630 CCGTGACTTGGAAACAGGATGAAGCATTTATTTCCAGTAGGAGATCACTGAAAGACCTGAT 689
Db 652 CCGTGACTTGGAAACAGGATGAAGCATTTATTTCCAGTAGGAGATCACTGAAAGACCTGAT 711
Qy 690 TGACCACTCAAAAGCTCTGGTAGTGTGATCTGGAATACCTTTATTTGGTTTCCAGCAACTAT 749
Db 712 TGACCACTCAAAAGCTCTGGTAGTGTGATCTGGAATACCTTTATTTGGTTTCCAGCAACTAT 771
Qy 750 TGGCAAAACAGATTCCAGATGTTGGCAGAGTTGGTAAGGGCCGGTATGGAGAGTATGGAT 809
Db 772 TGGCAAAACAGATTCCAGATGTTGGCAGAGTTGGTAAGGGCCGGTATGGAGAGTATGGAT 831
Qy 810 GGGTAAATGGCGTGGTGAAGAGTGGCTGTCAAAGTATTTTACCACCTGAAGAGCTAG 869
Db 832 GGGTAAATGGCGTGGTGAAGAGTGGCTGTCAAAGTATTTTACCACCTGAAGAGCTAG 891
Qy 870 CTGGTTTAGAAGAACAGAAATCTACAGACGGTGTAAATGGCTCATGAAATATACCTGG 929
Db 892 CTGGTTTAGAAGAACAGAAATCTACAGACGGTGTAAATGGCTCATGAAATATACCTGG 951
Qy 930 TTTTATAGCTGCAGACATTAAGGCCACCGGTTCTCGACTCAGCTGATTTGATTACTGA 989
Db 952 TTTTATAGCTGCAGACATTAAGGCCACCGGTTCTCGACTCAGCTGATTTGATTACTGA 1011
Qy 990 TTACCATGAGATGGGTCTCTATGACTTCCCTGAAATGTGCCACCTGGACACACAGAGC 1049
Db 1012 TTACCATGAGATGGGTCTCTATGACTTCCCTGAAATGTGCCACCTGGACACACAGAGC 1071
Qy 1050 CTTACTCAAGTTAGCTTATTTCTGCTGCTGTGTGTGCCACCTCCACACAGAAATTTA 1109
Db 1072 CTTACTCAAGTTAGCTTATTTCTGCTGCTGTGTGTGCCACCTCCACACAGAAATTTA 1131
Qy 1110 TGGCAGCAGGCAAGCCTGCAATTTGCTATGACTTCCCTGAAATGTGCCACCTGGACACACAGAGC 1169
Db 1132 TGGCAGCAGGCAAGCCTGCAATTTGCTATGACTTCCCTGAAATGTGCCACCTGGACACACAGAGC 1191
Qy 1170 TAAGAAATATGGTAGTTGCTGATTTGCTGACTGGGCTAGCTGTTAAATTTCAACAGTGA 1229
Db 1192 TAAGAAATATGGTAGTTGCTGATTTGCTGACTGGGCTAGCTGTTAAATTTCAACAGTGA 1251
Qy 1230 CACAAATGAAGTTGACATACCTTTGAACACACAGGGTGGGCAACAGCGGTACATGGCTCC 1289
Db 1252 CACAAATGAAGTTGACATACCTTTGAACACACAGGGTGGGCAACAGCGGTACATGGCTCC 1311
Qy 1290 AGAAGTGGTGGCAGAGCCTGAGTAAGAACCAATTTCCAGCCCTACATCATGCTGACAT 1349
Db 1312 AGAAGTGGTGGCAGAGCCTGAGTAAGAACCAATTTCCAGCCCTACATCATGCTGACAT 1371
Qy 1350 CTACAGCTTTGGTTTGAATCATTTTGGGAGATGGCCCGCTGTATTTACAGGAGCAATCGT 1409
Db 1372 CTACAGCTTTGGTTTGAATCATTTTGGGAGATGGCCCGCTGTATTTACAGGAGCAATCGT 1431
Qy 1410 GGAGGAATATCAATTACCATTATTAACATATGGTGGCTAGTGACCCCATCTTATGAAGACAT 1469
Db 1432 GGAGGAATATCAATTACCATTATTAACATATGGTGGCTAGTGACCCCATCTTATGAAGACAT 1491
Qy 1470 GCGTAGGTCGTGTGTGAAACGCTTGGGCCAATCGTCTTAACCGCTGGAAACAGTGA 1529
Db 1492 GCGTAGGTCGTGTGTGAAACGCTTGGGCCAATCGTCTTAACCGCTGGAAACAGTGA 1551
Qy 1530 TGAATGTCTCGAGCCGTTTGAAGCTGTATGAGATGCTGGGCCCAATTAATCCAGCATC 1589
Db 1552 TGAATGTCTCGAGCCGTTTGAAGCTGTATGAGATGCTGGGCCCAATTAATCCAGCATC 1611
Qy 1590 CAGACTCACAGCTTTGAGAAATCAAGAGACGCTCGCAAGATGGTTGAATCCAGGATGT 1649

Db 1612 CAGACTCACAGCTTTGAGAAATCAAGAAGACGCTCGAAAGATGGTTGAATCCAGGATGT 1671
Qy 1650 AAGATTTGACAAACAGTTTGGAGAAAGATTTAGACTGCAAGAAATTCACCCGAGGAAG 1709
Db 1672 AAGATTTGACAAACAGTTTGGAGAAAGATTTAGACTGCAAGAAATTCACCCGAGGAAG 1731
Qy 1710 GGTGGAGTTAGCATGGATAGGATGTGGCTTGGTTTCCAGACTCTCTCTTACCATCT 1769
Db 1732 GGTGGAGTTAGCATGGATAGGATGTGGCTTGGTTTCCAGACTCTCTCTCTA-CATCT 1790
Qy 1770 TCACAGGCTGCTAACAGTAAACCTTTCCAGACTCTTCAGAAATGC 1813
Db 1791 TCACAGGCTGCTAACAGTAAACCTTTCCAGACTCTTCAGAAATGC 1833

RESULT 4

ADW28816
ID ADW28816 standard; DNA; 3167 BP.

XX AC ADW28816;

XX AC ADW28816;

XX 07-APR-2005 (first entry)

XX Rat bone morphogenetic protein (BMP) receptor type 1 DNA Seq 120.
XX receptor; bone morphogenetic protein; bone injury; antibody production;
XX TGF beta antagonist; BMP-antagonist; osteopathic; osteopenias;
XX osteoporosis; gene; db.

XX Rattus norvegicus.

XX Key Location/Qualifiers
XX CDS 226..1824
XX FT /cag= a

XX FT /product= "BMP receptor type 1 protein"

XX WO2005003158-A2.

XX 13-JAN-2005.

XX 15-JUN-2004; 2004WO-US018910.

XX 16-JUN-2003; 2003US-00463190.

XX (CLLT) CELLTech R & D INC.

XX Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paepers BW;

XX Van Ness J, Winkler DG;

XX WPI; 2005-081936/09.

XX P-PSDB; ADW28802.

XX New antibody or antigen-binding fragment that binds specifically to
XX sclerostin polypeptide and which inhibits binding of sclerostin
XX polypeptide to a bone morphogenic protein, useful for increasing bone
XX mineral content or density.

XX Disclosure; SEQ ID NO 120; 205pp; English.

XX This invention relates to a novel antibody or antigen-binding fragment
XX that binds specifically to a sclerostin (SOST) polypeptide and impairs
XX formation of a sclerostin homodimer. Specifically, it refers to an
XX antibody that competitively inhibits binding of the sclerostin
XX polypeptide to a bone morphogenic protein (BMP) Type I receptor binding
XX site or a BMP Type II receptor binding site. The present invention
XX describes a hybridoma cell capable of producing the antibody and a host
XX cell for antibody expression. Furthermore, it provides a nucleic acid
XX molecule encoding a transforming growth factor-beta (TGF-beta) binding
XX protein known as SOST (and also BBR) and methods for detection thereof.
XX Accordingly, such antibodies and osteopathic compositions of the
XX invention can be used for treating osteoporosis, osteoporosis, fractures
XX and other disorders related to low bone mineral content and density. As
XX such, these compositions improve bone mineralization and can be described

CC as TGF-beta antagonists and/ or BMP-antagonists. This polynucleotide is a
CC bone morphogenetic protein receptor type 1 DNA sequence given in an
CC exemplification of the invention.

XX	Sequence	3167 BP; 908 A; 647 C; 688 G; 924 T; 0 U; 0 Other;	
SQ	Query Match	96.5%; Score 1750.4; DB 14; Length 3167;	
	Best Local Similarity	99.6%; Pred. No. 0;	
	Matches	1776; Conservative 0; Mismatches 6; Indels 2; Gaps 2;	
QY	30	TGCGCGCCGACGACGTCGCAATTTGGAATGACTACAGCTATACACTTACATCAGATT	89
DB	195	TGCGCCGGACAGACACGTCGCAATTTGGAATGACTACAGCTATACACTTACATCAGATT	254
QY	90	ACTGGAGCCTGTCTGTTTCATCATTTCTCATGTTCAAGGGCAGAAATCTAGATAGTATGCT	149
DB	255	ACTGGAGCCTGTCTGTTTCATCATTTCTCATGTTCAAGGGCAGAAATCTAGATAGTATGCT	314
QY	150	CCATGCTACTGTTATGAATCAGCTGACACAGAGAGCGCGGAAATGGAGTACAGTT	209
DB	315	CCATGCTACTGTTATGAATCAGCTGACACAGAGAGCGCGGAAATGGAGTACAGTT	374
QY	210	AGCACAGAGGACACCTTACCTTTCTTAAATGCTATTGCTCAGGACACTGCCCATGATGA	269
DB	375	AGCACAGAGGACACCTTACCTTTCTTAAATGCTATTGCTCAGGACACTGCCCATGATGA	434
QY	270	CGCTATTATAACACATGATCAATTAATGCGCAATTTGCTTGGCCATTATAGAAAGATGA	329
DB	435	CGCTATTATAACACATGATCAATTAATGCGCAATTTGCTTGGCCATTATAGAAAGATGA	494
QY	330	TCAGGAGAGAAACACGTTTAACTTCTGGGTGATGAAGTATGAAGCTCTGATTTTCAATG	389
DB	495	TCAGGAGAGAAACACGTTTAACTTCTGGGTGATGAAGTATGAAGCTCTGATTTTCAATG	554
QY	390	CAAGGATTACCAAAAGCCAGCTACGACGAGCAATAGAAATGTTGCGACCAATTTGTG	449
DB	555	CAAGGATTACCAAAAGCCAGCTACGACGAGCAATAGAAATGTTGCGACCAATTTGTG	514
QY	450	CAACCAATATTTGACGCTTACACCTGCCCCCTGTGTTATAGGCCCAATTTTGTATGGCAG	509
DB	615	CAACCAATATTTGACGCTTACACCTGCCCCCTGTGTTATAGGCCCAATTTTGTATGGCAG	674
QY	510	CGTCCGATGGCTGGCTGCTCATCTCTATGCTGCTGTTATGTCGCGATGATCGTCTT	569
DB	675	CGTCCGATGGCTGGCTGCTCATCTCTATGCTGCTGTTATGTCGCGATGATCGTCTT	734
QY	570	CTCCAGCTCTTCTGTTACAAACATTTACTGTAAAGATATCTCAAGCAGAGGTCGTTACAA	629
DB	735	CTCCAGCTCTTCTGTTACAAACATTTACTGTAAAGATATCTCAAGCAGAGGTCGTTACAA	794
QY	630	CGGTGACTTTGGAACAGGATGAAGCAATTTATTCAGTAGAGAAATCACTGAAAGACTGAT	689
DB	795	CGGTGACTTTGGAACAGGATGAAGCAATTTATTCAGTAGAGAAATCACTGAAAGACTGAT	854
QY	690	TGACAGGTCACAAAGCTCTGGTAGTGGATCTGGATTCATTTTATTTGGTTCAGCGAACTAT	749
DB	855	TGACAGGTCACAAAGCTCTGGTAGTGGATCTGGATTCATTTTATTTGGTTCAGCGAACTAT	914
QY	750	TGCCAAAACAGATTCAGATGGTTTCGGCAGGTCGGTAAGGCGGATGAGAGATGATGAT	809
DB	915	TGCCAAAACAGATTCAGATGGTTTCGGCAGGTCGGTAAGGCGGATGAGAGATGATGAT	974
QY	810	GGGTAAATGGCTGTGTAAGAAAGTGGCTGTCAAAGTATTTTTTACCACTGAAAGAGCTAG	869
DB	975	GGGTAAATGGCTGTGTAAGAAAGTGGCTGTCAAAGTATTTTTTACCACTGAAAGAGCTAG	1034
QY	870	CTGGTTTATAGAGAAACAGAAATCTACACAGCGTGTAAATGCGTATGAATATATCTGG	929
DB	1035	CTGGTTTATAGAGAAACAGAAATCTACACAGCGTGTAAATGCGTATGAATATATCTGG	1094
QY	930	TTTTATAGCTGACGACATTTAAAGGCACCGGTTTCCTGGACTCAGCTGTATTTGATTACTGA	989
DB	1095	TTTTATAGCTGACGACATTTAAAGGCACCGGTTTCCTGGACTCAGCTGTATTTGATTACTGA	1154

DE Rat bone morphogenetic protein (BMP) receptor type 1 DNA Seq 119.
XX receptor; bone morphogenetic protein; bone injury; antibody production;
KW TGF beta antagonist; BMP-antagonist; osteopathic; osteopenias;
KW osteoporosis; gene; ds.
XX
OS Rattus sp.

RESULT 5

ADW28815

ID ADW28815 standard; DNA; 3167 BP.

XX AC ADW28815;

XX DT 07-APR-2005 (first entry)

XX DE Rat bone morphogenetic protein (BMP) receptor type 1 DNA Seq 119.

XX Key Location/Qualifiers
FH 226..1824
FT /*tag= a
FT /product= "BMP receptor type 1 protein"
XX
PN W02005003158-A2.
XX 13-JAN-2005.
XX
XX 15-JUN-2004; 2004WO-US018910.
XX
XX 16-JUN-2003; 2003US-00463190.
XX
XX (CLLT) CELLTech R & D INC.
XX
PI Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paepfer BW;
PI Van Ness J, Winkler DG;
XX WPI; 2005-081936/09.
DR P-PSDB; ADW28801.
XX
XX New antibody or antigen-binding fragment that binds specifically to
PT sclerostin polypeptide and which inhibits binding of sclerostin
PT polypeptide to a bone morphogenic protein, useful for increasing bone
PT mineral content or density.
XX
XX Disclosure; SEQ ID NO 119; 205pp; English.
XX
XX This invention relates to a novel antibody or antigen-binding fragment
CC that binds specifically to a sclerostin (SOST) polypeptide and impairs
CC formation of a sclerostin homodimer. Specifically, it refers to an
CC antibody that competitively inhibits binding of the sclerostin
CC polypeptide to a bone morphogenic protein (BMP) Type I receptor binding
CC site or a BMP type II receptor binding site. The present invention
CC describes a hybridoma cell capable of producing the antibody and a host
CC cell for antibody expression. Furthermore, it provides a nucleic acid
CC molecule encoding a transforming growth factor-beta (TGF-beta) binding
CC protein known as SOST (and also BESE) and methods for detection thereof.
CC Accordingly, such antibodies and osteopathic compositions of the
CC invention can be used for treating osteopenia, osteoporosis, fractures
CC and other disorders related to low bone mineral content and density. As
CC such, these compositions improve bone mineralization and can be described
CC as TGF-beta antagonists and/or BMP-antagonists. This polynucleotide is a
CC bone morphogenetic protein receptor type 1 DNA sequence given in an
CC exemplification of the invention.
XX
SQ Sequence 3167 BP; 908 A; 647 C; 688 G; 924 T; 0 U; 0 Other;

Query Match 96.5%; Score 1750.4; DB 14; Length 3167;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

QY 30 TGCAGGCGCCGAGCAGCGTCGGAATGGACAATGACTCAGCTATACACTTACATCAGATT 89
DB 195 TGGCCCGGACAGCAGCAGCGTCGGAATGGACAATGACTCAGCTATACACTTACATCAGATT 254
QY 90 ACTGGAGCCCTGCTGTTTCATCATTTCTCATGTTCAAGGCGACAATCTAGATAGTATGCT 149
DB 255 ACTGGAGGCGCTGCTGTTTCATCATTTCTCATGTTCAAGGCGACAATCTAGATAGTATGCT 314
QY 150 CCATGGTACTGGTATGAAATCAGACGTGGACACAGAGAGAGCCGGAATGGAGTGACGTT 209
DB 315 CCATGGTACTGGTATGAAATCAGACGTGGACACAGAGAGAGCCGGAATGGAGTGACGTT 374
QY 210 AGCACCAGAGGACACCTTACCTTTCTTAAATGCTATTTGCTCAGGACACTGCCAGATGA 269
DB 375 AGCACCAGAGGACACCTTACCTTTCTTAAATGCTATTTGCTCAGGACACTGCCAGATGA 434
QY 270 CGCTATTATAACACATGCACTAATGAGCCCATTTGCTTTGCCATTTATGAGAGAGATGA 329
DB 435 CGCTATTATAACACATGCACTAATGAGCCCATTTGCTTTGCCATTTATGAGAGAGATGA 494

QY 330 TCAGGGAGAAACCA CGTTAACTTTCTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATG 389
DB 495 TCAGGGAGAAACCA CGTTAACTTTCTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATG 554
QY 390 CAAGGATTCACAAAAGCCAGCTACGCGAGCAATAGAAATGTTGTCGGAACCAATTTGTG 449
DB 555 CAAGGATTCACAAAAGCCAGCTACGCGAGCAATAGAAATGTTGTCGGAACCAATTTGTG 614
QY 450 CAACCAATATTTGCAGCCTACACTGCCCTGCTGCTTATAGGCCCATTTCTTTGATGCGAG 509
DB 615 CAACCAATATTTGCAGCCTACACTGCCCTGCTGCTTATAGGCCCATTTCTTTGATGCGAG 674
QY 510 CGTCCGATGGCTGGCTGCTCATCTATGCGCTGTCTGATTTGTCGCCCATGATGCGCTT 569
DB 675 CGTCCGATGGCTGGCTGCTCATCTATGCGCTGTCTGATTTGTCGCCCATGATGCGCTT 734
QY 570 CTCACAGCTGCTTCTGTTTACAAA CATTTACTGTAAGAGTATCTCAAGCAGAGAGTGGTTACAA 629
DB 735 CTCACAGCTGCTTCTGTTTACAAA CATTTACTGTAAGAGTATCTCAAGCAGAGAGTGGTTACAA 794
QY 630 CGGTGACTTTGGAACAGGATGAAGCATTTATTCAGTAGGAGAAATCACTGAAGACCTGAT 689
DB 795 CGGTGACTTTGGAACAGGATGAAGCATTTATTCAGTAGGAGAAATCACTGAAGACCTGAT 854
QY 690 TGACCAAGTACAAAAGCTCTGGTAGTGGATCTGGATTACCTTTATTTGTTTCCAGGAACTAT 749
DB 855 TGACCAAGTACAAAAGCTCTGGTAGTGGATCTGGATTACCTTTATTTGTTTCCAGGAACTAT 914
QY 750 TGCCAAACAGATTTCAGATGGTTTCGGCAGGTTGGTAAGGGCCGGTATGGAGAACTATGGAT 809
DB 915 TGCCAAACAGATTTCAGATGGTTTCGGCAGGTTGGTAAGGGCCGGTATGGAGAACTATGGAT 974
QY 810 GGGTAAATGGCGTGGTGAAGAAAGTGGCTGCTCAAGATATTTTTCACCACTGAAGAGCTAG 869
DB 975 GGGTAAATGGCGTGGTGAAGAAAGTGGCTGCTCAAGATATTTTTCACCACTGAAGAGCTAG 1034
QY 870 CTGGTTTAGAGAAACAGAAATCTTACCAGACGGTGTAAATGCGTCATGAAATATACTTGG 929
DB 1035 CTGGTTTAGAGAAACAGAAATCTTACCAGACGGTGTAAATGCGTCATGAAATATACTTGG 1094
QY 930 TTTTATAGCTGCAGACATTTAAAGGCAACCGGTTCTCGGACTCAGCTGTATTTGATTTACTGA 989
DB 1095 TTTTATAGCTGCAGACATTTAAAGGCAACCGGTTCTCGGACTCAGCTGTATTTGATTTACTGA 1154
QY 990 TTACCATGAGATGGGTCTCTCTATGACATTTCTGAAATGTCGACCTGACACCCAGAGC 1049
DB 1155 TTACCATGAGATGGGTCTCTCTATGACTTCCCTGAAATGTGCCACCTGACACCCAGAGC 1214
QY 1050 CCTACTCAAGTTAGCTTTATTTCTGCTGCTGTGCTGTGTCACCTCCACACAGAAATTTA 1109
DB 1215 CCTACTCAAGTTAGCTTTATTTCTGCTGCTGTGCTGTGTCACCTCCACACAGAAATTTA 1274
QY 1110 TGGCAGCGAAGCAAGCCCTGCAATTTGCTCATCGAGACCTGAAGAGCAAAACATCCTTAT 1169
DB 1275 TGGCAGCGAAGCAAGCCCTGCAATTTGCTCATCGAGACCTGAAGAGCAAAACATCCTTAT 1334
QY 1170 TAAAGAAATGGTAGTGTGCTGTATTTGCTGACCTGGGCGCTAGCTGTTAAATTCACAGTGA 1229
DB 1335 TAAAGAAATGGTAGTGTGCTGTATTTGCTGACCTGGGCGCTAGCTGTTAAATTCACAGTGA 1394
QY 1230 CACAAATGAAGTTGACATACCTTTGAAACACAGGGTGGGCGGCGGCTACATGCTGCTCC 1289
DB 1395 CACAAATGAAGTTGACATACCTTTGAAACACAGGGTGGGCGGCGGCTACATGCTGCTCC 1454
QY 1290 AGAAGTGTGCGAGAGCCTGAGTAAACCAATTTCCAGCCCTACATCATGGCTGACAT 1349
DB 1455 AGAAGTGTGCGAGAGCCTGAGTAAACCAATTTCCAGCCCTACATCATGGCTGACAT 1514
QY 1350 CTACAGCTTTGGTTTGTATCATTTGGAGATGGCCCGCTCGCTGTATTTACAGGAGGAATCGT 1409
DB 1515 CTACAGCTTTGGTTTGTATCATTTGGAGATGGCCCGCTCGCTGTATTTACAGGAGGAATCGT 1574
QY 1410 GGAGGAAATCAATTACCATAATTACAAATGCTGCTAGTGACCCCATCTTATGAGAGACAT 1469

Db 1575 GGAGGATATCAATACCATATTTACAAATGTTGCTAGTGACCCATCTTATGAACAT 1634
Qy 1470 GCGTGAGGTCGTGTGTGTAACCGTTGCGGCAATCGTCTCTAAACCGCTGGAACAGTGA 1529
Db 1635 GCGTGAGGTCGTGTGTGTAACCGTTGCGGCAATCGTCTCTAAACCGCTGGAACAGTGA 1694
Qy 1530 TGAATGCTCTCGAGCCGTTTGAAGCTGATGTCAGAAATGCTGGGCCCATTAATCCAGCATC 1589
Db 1695 TGAATGCTCTCGAGCCGTTTGAAGCTGATGTCAGAAATGCTGGGCCCATTAATCCAGCATC 1754
Qy 1590 CAGACTCACAGCTTTTCAGAAATCAAGAGAGCGTCGCAAGATGTTGTAATCCAGGATCT 1649
Db 1755 CAGACTCACAGCTTTTCAGAAATCAAGAGAGCGTCGCAAGATGTTGTAATCCAGGATCT 1814
Qy 1650 AAGATTTCGACAAACAGTTTTCAGAAAGAAATTTAGACTGCAAGAAATTCACCCGAGGAAG 1709
Db 1815 AAGATTTCGACAAACAGTTTTCAGAAAGAAATTTAGACTGCAAGAAATTCACCCGAGGAAG 1874
Qy 1710 GGTGGATTAGCATGCACTAGGATGTCGGCTTGGTTTCCAGACTCTCTCTCTACCATCT 1769
Db 1875 GGTGGATTAGCATGCACTAGGATGTCGGCTTGGTTTCCAGACTCTCTCTCTA-CATCT 1933
Qy 1770 TCACAGGCTGCTAACAGTAAACCTTTTCAGGACTCTGCAGAAATGC 1813
Db 1934 TCACAGGCTGCTAACAGTAAA-CTTTCAGGACTCTGCAGAAATGC 1976

RESULT 6
ADX97428
ID ADX97428 standard; DNA; 3167 BP.
XX AC ADX97428;
XX DT 05-MAY-2005 (first entry)
XX DE Rat bone morphogenic protein type I receptor encoding DNA, SEQ ID 88.
XX KW antibody; sclerostin; SOST; bone morphogenic protein receptor;
KW Transforming Growth Factor; osteopathic; gene therapy; bone repair;
KW osteopenia; osteoporosis; bone injury; gene; ds.
XX OS Rattus sp.
XX FH Key Location/Qualifiers
FT CDS 226..1824
FT FT /*tag= a
FT FT /product= "Rat bone morphogenic protein type I receptor"
XX PN WO2005014650-A2.
XX PD 17-FEB-2005.
XX PF 15-JUN-2004; 2004WO-05018912.
XX PR 16-JUN-2003; 2003US-0478977P.
XX PA (CLLT) CELLTech R & D INC.
XX PI Winkler DG, Shi J, Latham J;
XX WPI; 2005-163219/17.
XX ; F:CB, ADX97414.

XX New isolated antibody specific for a sclerostin polypeptide, useful for
PT increasing bone mineralization or for treating or preventing conditions
PT associated with low bone mineral density, e.g. osteoporosis or
PT osteopenia.
XX Disclosure; SEQ ID NO 88; 157pp; English.
XX PS The invention relates to a novel isolated antibody, or its antigen-
XX binding fragment, which binds specifically to a sclerostin (SOST)

CC polypeptide. The SOST polypeptide comprises any of 6 sequences having 190
CC or 213 amino acids, fully defined in the specification (ADX97341,
CC ADX97360, ADX97398, ADX97400, ADX97402 or ADX97408). The antibody
CC competitively inhibits binding of the SOST polypeptide to a bone
CC morphogenic protein (BMP) type I Receptor binding site and a BMP Type II
CC Receptor binding site, where the BMP Type I Receptor binding site is
CC capable of binding to a BMP Type I Receptor polypeptide. The invention
CC further comprises: a hybridoma cell producing the new antibody; a host
CC cell that is capable of expressing the new antibody; a composition
CC comprising the new antibody, or its antigen-binding fragment, and a
CC physiological carrier; an immunogen comprising a peptide comprising 6, 7,
CC 8, 9, 10, 11, 12, or at least 21-50 or 20-75 consecutive amino acids of
CC the SOST polypeptide; methods for producing an antibody that specifically
CC binds to the SOST polypeptide; and methods for identifying an antibody
CC that modulates a Transforming Growth Factor (TGF)-beta signaling pathway,
CC that impairs binding of a BMP to the SOST polypeptide, that impairs SOST
CC homodimer formation, or that increases bone mineral content. The novel
CC antibody and compositions have osteopathic activity. The SOST nucleic
CC acids may be used in gene therapy. The composition and methods are useful
CC for increasing bone mineralization, which may treat or prevent diseases
CC or conditions associated with low bone mineral density, such as
CC osteopenia, osteoporosis or bone fractures. This polynucleotide sequence
CC represents a rat bone morphogenic protein type I receptor encoding DNA of
CC the invention.
XX
SQ Sequence 3167 BP; 908 A; 647 C; 688 G; 924 T; 0 U; 0 Other;

Query Match 96.5%; Score 1750.4; DB 14; Length 3167;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

Qy 30 TCGGCCCGCAGGACACGTGCGAATTGGACAATGACTCAGCTATACACTTACATCAGATT 89
Db 195 TGGCCCGACAGGACACGTGCGAATTGGACAATGACTCAGCTATACACTTACATCAGATT 254

Qy 90 ACTGGAGCGTCTGTTTCATCATTTCTCAAGGCGGAGAAATCTAGATAGTATGCT 149
Db 255 ACTGGAGCGTCTGTTTCATCATTTCTCAAGGCGGAGAAATCTAGATAGTATGCT 314

Qy 150 CCATGGTACTGGTATGAAATCAGCGTGGACAGGACGCGGAAAGCGGAAATGGAGTGACGTT 209
Db 315 CCATGGTACTGGTATGAAATCAGCGTGGACAGGACGCGGAAAGCGGAAATGGAGTGACGTT 374

Qy 210 AGCACAGGACACCTTACCTTTCTTAAATGCTATTGCTCAGGACACTGCCAGATCA 269
Db 375 AGCACAGGACACCTTACCTTTCTTAAATGCTATTGCTCAGGACACTGCCAGATCA 434

Qy 270 CGCTATTAAACACATGCATAAATGCGCCATTTGCGCATTTAGGAAGAGATCA 329
Db 435 CGCTATTAAACACATGCATAAATGCGCCATTTGCGCATTTAGGAAGAGATCA 494

Qy 330 TCAGGGAGAAACACGTTAACTTCTGGGTGATGAAGTATGAAGCTCTGATTTTCAATG 389
Db 495 TCAGGGAGAAACACGTTAACTTCTGGGTGATGAAGTATGAAGCTCTGATTTTCAATG 554

Qy 390 CAGGATTTCACCAAAAGCCGACGTAAGGAGCAATAGAAATGTTGTCGACCAATTTGTG 449
Db 555 CAGGATTTCACCAAAAGCCGACGTAAGGAGCAATAGAAATGTTGTCGACCAATTTGTG 614

Qy 450 CAAACCAATATTTCAGGCGCTACACTGCCCCCTGCTGTTATAGGCCCATTTCTTGTGGCAG 509
Db 615 CAAACCAATATTTCAGGCGCTACACTGCCCCCTGCTGTTATAGGCCCATTTCTTGTGGCAG 674

Qy 510 CGTCCGATGGCTGGCTGCTCATCTCTATGSCCTGCTGTATGTCGCATGATCGTCTT 569
Db 675 CGTCCGATGGCTGGCTGCTCATCTCTATGSCCTGCTGTATGTCGCATGATCGTCTT 734

Qy 570 CTCAGCTGCTTCTGTTACAAACATTACTGTAAGAGTATCTCAAGCAGAGGTCGTTACAA 629
Db 735 CTCAGCTGCTTCTGTTACAAACATTACTGTAAGAGTATCTCAAGCAGAGGTCGTTACAA 794

Qy 630 CGTGACTTTGGAACAGGATGAAGCAATTTATTCAGTAGGAAATCACTGAAAGACCTGAT 689

Db 795 CCGTGAATGGAACAGGATGAAGCAATTTATTCAGTAGGAAATCACTGAAAGACCTGAT 854
Qy 690 TGACCAAGTCAAAAGCTCTGGTAGTGGATCTGGATTACCTTTATTTGGTTTCAGCGAATAT 749
Db 855 TGACCAAGTCAAAAGCTCTGGTAGTGGATCTGGATTACCTTTATTTGGTTTCAGCGAATAT 914
Qy 750 TGCCAAAACAGATTCAGATGGTTTCGCGAGGTTGGTAAGGCGCGGTATGGAGAAGTATGGAT 809
Db 915 TGCCAAAACAGATTCAGATGGTTTCGCGAGGTTGGTAAGGCGCGGTATGGAGAAGTATGGAT 974
Qy 810 GGGTAAATGGCGTGGTGAAGAGTGGCTGTCAAGTATTTTTTACCACTGAAGAGCTAG 869
Db 975 GGGTAAATGGCGTGGTGAAGAGTGGCTGTCAAGTATTTTTTACCACTGAAGAGCTAG 1034
Qy 870 CTGGTTTGAAGAAACAGAAATCTACCAAGCGGTGTTAATGCTCATGAATATATCTGG 929
Db 1035 CTGGTTTGAAGAAACAGAAATCTACCAAGCGGTGTTAATGCTCATGAATATATCTGG 1094
Qy 930 TTTTATAGCTGCAGACATTAAGGCAACCGGTTCTCGGACTCAGCTGTATTTGATTACTGA 989
Db 1095 TTTTATAGCTGCAGACATTAAGGCAACCGGTTCTCGGACTCAGCTGTATTTGATTACTGA 1154
Qy 990 TTACCATGAGATGGGTCTCTATGACTTCCCTGAAGTGTGCCACCTGGACACAGAGC 1049
Db 1155 TTACCATGAGATGGGTCTCTATGACTTCCCTGAAGTGTGCCACCTGGACACAGAGC 1214
Qy 1050 CCTACTCAAGTTAGCTTATCTGCTGCTGTGGTCTGTGCCACCTGCACACAGAAATTA 1109
Db 1215 CCTACTCAAGTTAGCTTATCTGCTGCTGTGGTCTGTGCCACCTGCACACAGAAATTA 1274
Qy 1110 TGGCACGCAAGGCAAGCCTCAATTTGCTCATCGAGACCTGAAGAGCAAAACATCCTTAT 1169
Db 1275 TGGCACGCAAGGCAAGCCTCAATTTGCTCATCGAGACCTGAAGAGCAAAACATCCTTAT 1334
Qy 1170 TAAGAAAATGGTATGCTGTATGCTGACTGGGCTAGCTGTAAATTCACACAGTGA 1229
Db 1335 TAAGAAAATGGTATGCTGTATGCTGACTGGGCTAGCTGTAAATTCACACAGTGA 1394
Qy 1230 CACAAATGAAGTTGACATACCTTTGAACACAGAGGTGGGACCGGTACATGGCTCC 1289
Db 1395 CACAAATGAAGTTGACATACCTTTGAACACAGAGGTGGGACCGGTACATGGCTCC 1454
Qy 1290 AGAAGTCTGGACGAGACCTGAGTAAACCAATTTCCAGCCCTACATCATGCTGACAT 1349
Db 1455 AGAAGTCTGGACGAGACCTGAGTAAACCAATTTCCAGCCCTACATCATGCTGACAT 1514
Qy 1350 CTACAGCTTTGGTTTGAATCTTTGGGAGATGGGCCGCTGCTGTATTACAGGAGGAATCGT 1409
Db 1515 CTACAGCTTTGGTTTGAATCTTTGGGAGATGGGCCGCTGCTGTATTACAGGAGGAATCGT 1574
Qy 1410 GGAGGAATACATTTACCATATTACACATGGTGCCTAGTGACCCATCTTATGAGACAT 1469
Db 1575 GGAGGAATACATTTACCATATTACACATGGTGCCTAGTGACCCATCTTATGAGACAT 1634
Qy 1470 GCGTGAGGTGCTGTGTGAAACCGCTTGGCGCCCAATCTCTTAACCGCTGGAACAGTGA 1529
Db 1635 GCGTGAGGTGCTGTGTGAAACCGCTTGGCGCCCAATCTCTTAACCGCTGGAACAGTGA 1694
Qy 1530 TGAATGTCTCGAGCGCTTTTGAAGCTGTGTGAGATGTGGGCCCATTAATCCAGCATC 1589
Db 1695 TGAATGTCTCGAGCGCTTTTGAAGCTGTGTGAGATGTGGGCCCATTAATCCAGCATC 1754
Qy 1590 CAGACTCACAGCTTTGAGATTCAGAGACGCTCGCAAGATGGTTGAATCCAGGATGT 1649
Db 1755 CAGACTCACAGCTTTGAGATTCAGAGACGCTCGCAAGATGGTTGAATCCAGGATGT 1814
Qy 1650 AAAGATTGACAAACAGCTTTTGAGAAAGAAATTTAGACTGCAAGAAATTCACCCGAGGAG 1709
Db 1815 AAAGATTGACAAACAGCTTTTGAGAAAGAAATTTAGACTGCAAGAAATTCACCCGAGGAG 1874
Qy 1710 GGTGGAGTTAGCATGGACTAGGATGTGGCTTGGTTTCCAGACTCTCTCTTACCATTCT 1769
Db 1875 GGTGGAGTTAGCATGGACTAGGATGTGGCTTGGTTTCCAGACTCTCTCTTACCATTCT 1933

Qy 1770 TCACAGCTCTACAGTAAACCTTTTCAGGACTCTGCAGATGC 1813
Db 1934 TCACAGCTCTACAGTAAACCTTTTCAGGACTCTGCAGATGC 1976

RESULT 7
ADX97429
ID ADX97429 standard; DNA; 3167 BP.
XX AC ADX97429;
XX DT 05-MAY-2005 (first entry)
XX Rat bone morphogenic protein type I receptor encoding DNA, SEQ ID 89.
XX antibody; sclerostin; SOST; bone morphogenic protein receptor;
XX Transforming Growth Factor; osteopathic; gene therapy; bone repair;
XX osteopenia; osteoporosis; bone injury; gene; ds.
XX Rattus norvegicus.
XX Key Location/Qualifiers
FT CDS 226..1824
FT /*tag= a
FT /product= "Rat bone morphogenic protein type I receptor"
XX WO2005014650-A2.
XX 17-FEB-2005.
XX 15-JUN-2004; 2004WO-US018912.
XX 16-JUN-2003; 2003US-0478977P.
XX (CLLT) CELLTECH R & D INC.
XX Winkler DG, Shi J, Latham J;
XX WPI; 2005-163219/17.
XX P-PSDB; ADX97415.
XX New isolated antibody specific for a sclerostin polypeptide, useful for
XX increasing bone mineralization or for treating or preventing conditions
XX associated with low bone mineral density, e.g. osteoporosis or
XX osteopenia.
XX Disclosure; SEQ ID NO 89; 157pp; English.
XX The invention relates to a novel isolated antibody, or its antigen-
XX binding fragment, which binds specifically to a sclerostin (SOST)
XX polypeptide. The SOST polypeptide comprises any of 6 sequences having 190
XX or 213 amino acids, fully defined in the specification (ADX97341,
XX ADX97360, ADX97398, ADX97400, ADX97402 or ADX97408). The antibody
XX competitively inhibits binding of the SOST polypeptide to a bone
XX morphogenic protein (BMP) Type I Receptor binding site and a BMP Type II
XX Receptor binding site, where the BMP type I Receptor binding site is
XX capable of binding to a BMP Type I Receptor polypeptide. The invention
XX further comprises: a hybridoma cell producing the new antibody; a host
XX cell that is capable of expressing the new antibody; a composition
XX comprising the new antibody, or its antigen-binding fragment, and a
XX physiological carrier; an immunogen comprising a peptide comprising 6, 7,
XX 8, 9, 10, 11, 12, or at least 21-50 or 20-75 consecutive amino acids of
XX the SOST polypeptide; methods for producing an antibody that specifically
XX binds to the SOST polypeptide; and methods for identifying an antibody
XX that modulates a Transforming Growth Factor (TGF)-beta signaling pathway,
XX that impairs binding of a BMP to the SOST polypeptide, that impairs SOST
XX homodimer formation, or that increases bone mineral content. The novel
XX antibody and compositions have osteopathic activity. The SOST nucleic
XX acids may be used in gene therapy. The composition and methods are useful
XX for increasing bone mineralization, which may treat or prevent diseases
XX or conditions associated with low bone mineral density, such as
XX osteopenia, osteoporosis or bone fractures. This polynucleotide sequence

CC represents a rat bone morphogenic protein type I receptor encoding DNA of
CC the invention.

XX Sequence 3167 BP; 908 A; 647 C; 688 G; 924 T; 0 U; 0 Other;

SQ Query Match 96.5%; Score 1750.4; DB 14; Length 3167;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

QY	30	TGCGCGCCGACGACACGTCGCAATTTGGCAATGACTCAGCTATACACTTACATCAGATT	89
DB	195	TGCGCCGGAACAGGACACGTCGCAATTTGGCAATGACTCAGCTATACACTTACATCAGATT	254
QY	90	ACTGGAGCGCTGCTGTTCAATCAATTTCTCATGTTCAAGGCGAGAATCTAGATAGTGT	149
DB	255	ACTGGAGCGCTGCTGTTCAATCAATTTCTCATGTTCAAGGCGAGAATCTAGATAGTGT	314
QY	150	CCATGGTACTGGTATGAAATCAGACGTGGACCAAGAGAAGCCGGAATTTGGAGTACGTT	209
DB	315	CCATGGTACTGGTATGAAATCAGACGTGGACCAAGAGAAGCCGGAATTTGGAGTACGTT	374
QY	210	AGCACGAGGACACCTTACCTTTTAAATGCTATTGCTCAGGACACTGCCCGATGA	269
DB	375	AGCACGAGGACACCTTACCTTTTAAATGCTATTGCTCAGGACACTGCCCGATGA	434
QY	270	CGCTATTATAACACATGCATTAATAATGGCCATTCCTTGGCCATTTATAGAGAAGATGA	329
DB	435	CGCTATTATAACACATGCATTAATAATGGCCATTCCTTGGCCATTTATAGAGAAGATGA	494
QY	330	TCAGGAGAGAACACACGTTAACTTCTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATG	389
DB	495	TCAGGAGAGAACACACGTTAACTTCTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATG	554
QY	390	CAAGGATTCACCAAAAGCCAGCTACGACGGAACAATAGAAATGTTGTCGGACCAATTTGTG	449
DB	555	CAAGGATTCACCAAAAGCCAGCTACGACGGAACAATAGAAATGTTGTCGGACCAATTTGTG	614
QY	450	CAACCAATATTGACAGCTACACTGCCCTGTCGTTATAGGCCCATTCCTTTGATGGCAG	509
DB	615	CAACCAATATTGACAGCTACACTGCCCTGTCGTTATAGGCCCATTCCTTTGATGGCAG	674
QY	510	CGTCCGATGGCTGGCTGCTCATCTATGGCTGCTGTTATGTCGCCATGATGCTTT	569
DB	675	CGTCCGATGGCTGGCTGCTCATCTATGGCTGCTGTTATGTCGCCATGATGCTTT	734
QY	570	CTCCAGCTGCTTCTGTTACAAACATTAATCTAAGAGTATCTCAAGCAGAGGTCGTTACAA	629
DB	735	CTCCAGCTGCTTCTGTTACAAACATTAATCTAAGAGTATCTCAAGCAGAGGTCGTTACAA	794
QY	630	CCGTGACTTGGAAACAGATGAAGCATTTATCCAGTAGGAGAAATCACTGAAGACCTGAT	689
DB	795	CCGTGACTTGGAAACAGATGAAGCATTTATCCAGTAGGAGAAATCACTGAAGACCTGAT	854
QY	690	TGACCAAGTACAAAGCTCTGGTAGTGATCTGATTTACCTTTTATGCTTCAGCACTAT	749
DB	855	TGACCAAGTACAAAGCTCTGGTAGTGATCTGATTTACCTTTTATGCTTCAGCACTAT	914
QY	750	TGCCAAACAGATTTCAGATGGTTCCGACAGGTTGGTAAGGCCGGTATGGAGAAATATGGAT	809
DB	915	TGCCAAACAGATTTCAGATGGTTCCGACAGGTTGGTAAGGCCGGTATGGAGAAATATGGAT	974
QY	810	GGGTAATGGCTGGTGAAG	869
DB	975	GGGTAATGGCTGGTGAAG	1034
QY	870	CTGGTTTACGAGAAACAGAAATCTTACACAGAGGTTGTAATGCGCTCATGAAATATCTGG	929
DB	1035	CTGGTTTACGAGAAACAGAAATCTTACACAGAGGTTGTAATGCGCTCATGAAATATCTGG	1094
QY	930	TTTTATAGCTGCAGACATTTAAAGGCCACCGGTTCTGGACTCAGCTGATTTTGAATTA	989
DB	1095	TTTTATAGCTGCAGACATTTAAAGGCCACCGGTTCTGGACTCAGCTGATTTTGAATTA	1154

QY	990	TTACCATGGAATGGGTCTCTCTATGACTTCTCTGAAATGTCGCCACCTCGACACCCAGAGC	1049
DB	1155	TTACCATGGAATGGGTCTCTCTATGACTTCTCTGAAATGTCGCCACCTCGACACCCAGAGC	1214
QY	1050	CCTACTCAAGTTAGCTTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1109
DB	1215	CCTACTCAAGTTAGCTTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1274
QY	1110	TGGCAGCGAAGCAAGCCCTGCAATTTGCTCATCGAGACCTGGAAGAGCAAAAAATCCTTAT	1169
DB	1275	TGGCAGCGAAGCAAGCCCTGCAATTTGCTCATCGAGACCTGGAAGAGCAAAAAATCCTTAT	1334
QY	1170	TAAAGAAAATGCTAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1229
DB	1335	TAAAGAAAATGCTAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1394
QY	1230	CACAAATGAAGTTGACATACCTTCAACACACAGAGGTGGGCACGCGGTACATGGCTCC	1289
DB	1395	CACAAATGAAGTTGACATACCTTCAACACACAGAGGTGGGCACGCGGTACATGGCTCC	1454
QY	1290	AGAAAGTGTGGACGAGAGCTGAGTAAACCATTTTCCAGCCCTACATCATGGCTGACAT	1349
DB	1455	AGAAAGTGTGGACGAGAGCTGAGTAAACCATTTTCCAGCCCTACATCATGGCTGACAT	1514
QY	1350	CTACAGCTTGGTTCATCATTTGGAGATGGCCCGTGGCTGCTGCTGCTGCTGCTGCTGCTG	1409
DB	1515	CTACAGCTTGGTTCATCATTTGGAGATGGCCCGTGGCTGCTGCTGCTGCTGCTGCTGCTG	1574
QY	1410	GGAGAAATATCAATTAACCATATTCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1469
DB	1575	GGAGAAATATCAATTAACCATATTCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1634
QY	1470	CGCTGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1529
DB	1635	CGCTGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1694
QY	1530	TGAATGCTTCGAGCGCTTTTGAAGCTGATGTCAGAAATGCTGGGCGCCATAATCCAGCATC	1589
DB	1695	TGAATGCTTCGAGCGCTTTTGAAGCTGATGTCAGAAATGCTGGGCGCCATAATCCAGCATC	1754
QY	1590	CAGACTCACAGCTTTGAGAAATCAAGAAACGCTCCCAAGATGCTGCTGCTGCTGCTGCTGCTG	1649
DB	1755	CAGACTCACAGCTTTGAGAAATCAAGAAACGCTCCCAAGATGCTGCTGCTGCTGCTGCTGCTG	1814
QY	1650	AAAGATTTGACAAAACAGTTTGGAGAAATTTAGACTGCAAGAAATTTACCCGAGGAAG	1709
DB	1815	AAAGATTTGACAAAACAGTTTGGAGAAATTTAGACTGCAAGAAATTTACCCGAGGAAG	1874
QY	1710	GGTGGAGTTAGCATGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1769
DB	1875	GGTGGAGTTAGCATGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1933
QY	1770	TCACAGGCTGCTTAAACAGTAAACCTTTTCAGGACTCTGCAGAAATGC	1813
DB	1934	TCACAGGCTGCTTAAACAGTAAACCTTTTCAGGACTCTGCAGAAATGC	1976

RESULT 8

AAZ09847

ID AAZ09847 standard; cDNA; 2070 BP.

XX

AC AAZ09847;

XX

DT 26-NOV-1999 (first entry)

XX

XX Human mAUK-3 from clone ME-7 and ME-D cDNA.

DE

KW mAUK-3; activin receptor-like kinase; therapy; activin; TGF-beta; cancer;
fibrosis; liver cirrhosis; pulmonary fibrosis; glomerulonephritis; mouse;
rheumatoid arthritis; detection; diagnosis; drug screening; ds.

XX

OS Mus sp.

XX

Qy	39	CAGGACACGTCGGAATTGGACAATGA	CTCAGCTATACATTACATCAGATTACTTGGGAGC	98
Db	195	CAGGACGCGTGGCAATCAGACAATGA	CTCAGCTATACATTACATCAGATTACTTGGGAGC	254
Qy	99	CTGTCTGTTCAATCATTTTCTCATGTT	CAAGGGCAGAACTAGATAGTATGCTCCATGTTAC	158
Db	255	CTGTCTGTTCAATCATTTTCTCATGTT	CAAGGGCAGAACTAGATAGTATGCTCCATGTTAC	314
Qy	159	TGGTATGAAATCAGACGTTGGACACAG	AGACCGGAAATGSGAGTGCAGTTTAGCACACAGA	218
Db	315	TGGTATGAAATCAGACCTTGGACACAG	AGACCGGAAATGSGAGTGCAGTTTAGCACACAGA	374
Qy	219	GGACACCTTACCTTTTCTTAAATGCT	ATTGCTCAGGACACTGCCCCAGATGACGCTATTAA	278
Db	375	GGATACCTTTGCTTTTCTTAAAGTGCT	ATTGCTCAGGACACTGCCCCAGATGATGCTATTAA	434
Qy	279	TAAACATGCAATACTAATGGCCATTTG	CTTGGCCATTATAGAGAAGATGATCAGGAGAGA	338
Db	435	TAAACATGCAATACTAATGGCCATTTG	CTTGGCCATTATAGAGAAGATGATCAGGAGAGA	494
Qy	339	AACCACGTTTAACTTCTGGGTGTATGA	AGTATGAAGGCTCTGATTTTCAATGCAAGGATTC	398
Db	495	AACCACATTTAACTTCTGGGTGTATGA	AGTATGAAGGCTCTGATTTTCAATGCAAGGATTC	554
Qy	399	ACCAAAAGCCCAGCTACGCGAGCAATA	TGTTGTGCGGACCAATTTGTGCACCAATA	458
Db	555	ACCGAAAGCCCAGCTACGCGAGCAATA	TGTTGTGCGGACCAATTTGTGCACCAAGTA	614
Qy	459	TTTGCAGCCTACATGCGCCCTGCTGTT	ATAGGCCCAATCTTTGATGGCAGCGTCCGATG	518
Db	615	TTTGCAGCCTACATGCGCCCTGCTGTT	ATAGGTCCGTTCTTTGATGGCAGCATCCGATG	674
Qy	519	GCTGCGTGTGCTCATCTATGCGCTGCT	GTATTGTGCGCATGATCTCTTCTCCAGCTG	578
Db	675	GCTGTTGTGCTCATTTCCATGGCTGCT	GTATTGTGCTATGATCATCTTCTCCAGCTG	734
Qy	579	CTTCTGTTTACAAACATTTACTGTAAG	AGTATCTCAAGCAGAGGTCGTTACAACCGTGACTT	638
Db	735	CTTTTGCTATAAGCATTTATTGTAGAG	TATCTCAAGCAGGGTCGTTACAACCGTGATTT	794
Qy	639	GGAAACAGATGAAGCATTTATTCAGTA	GGAGAAATCACTGAAGACCTGATGACCAAGTC	698
Db	795	GGAAACAGATGAAGCATTTATTCAGTA	GGAGAAATCACTGAAGACCTGATGACCAAGTC	854
Qy	699	ACAAAGCTCTGGTAGTGATCTGATTA	CCCTTTATGTTTCAGCGAATCTATGCCAAACA	758
Db	855	CCAAAGCTCTGGGATGGATCTGATTA	TGCTTTATGTTTCAGCGAATCTATGCCAAACA	914
Qy	759	GATTCAGATGGTTCCGGCAGGTTTGT	ATAGGCGCGGTATGGAGAAGTATGGATGGGTAATG	818
Db	915	GATTCAGATGGTTCCGCAGGTTTGT	ATAGGCGCGCTATGGAGAAGTATGGATGGGTAATG	974
Qy	819	CGCTGGTGA AAAAGTGGCTGTCAAAG	TATTTTCACTGAAGAAGCTAGCTGGTTTAG	878
Db	975	CGCTGGTGA AAAAGTGGCTGTCAAAG	TGTTTTTACCACCTGAAGAAGCTAGCTGGTTTAG	1034
Qy	879	AGAAACAGAAATCTAACGACCGGT	TTAATCGCTCATGAAATATATCTTGGTTTTATAGC	938
Db	1035	AGAAACAGAAATCTAACGACCGGT	TTAATCGCTCATGAAATATATCTTGGTTTTATAGC	1094
Qy	939	TGCAGACATTAAGGCACTGGTCTCG	ACTCAGCTGATTTGATTAATCTGATTAACCATGA	998
Db	1095	TGCAGACATTAAGGCACTGGTCTCG	ACTCAGCTGATTTGATTAATCTGATTAACCATGA	1154
Qy	999	GAATGGGTCTCTATGATCTTCTGAA	ATGTCGCAACCTGACACCCAGAGCCCTACTCAA	1058
Db	1155	AAATGGATCTCTATGATCTTCTGAA	ATGTCGCAACCTGACACCCAGAGCCCTACTCAA	1214
Qy	1059	GTTAGCTTATTTCTGCTGCTGTGTG	CCACTCCACACAGAAATTTATGGCAGCGCA	1118
Db	1215	GTTAGCTTATTTCTGCTGCTGTGTG	CCACTCCACACAGAAATTTATGGTACCGCA	1274

[illegible]

```
Mus sp.
Key
CDS
Location/Qualifiers
11..1609
/*tag= a
11..79
/*tag= b
80..1606
/*tag= c
W09514778-A2.
```

[illegible]

Db 1681 TGAATAGGATGTTGACTGGTTTCCAGACTCCTTCCTCTA-CATCTTCACAGGCTGCTA 1739
QY 1783 ACAGTAAACCTTTCAGGACTGTCGAGAATGC 1813
Db 1740 ACAGTAAACCTTACCAGCACTCTACAGAAATAC 1770

RESULT 12
AAT27228
ID AAT27228 standard; cDNA; 2402 BP.
XX
AC AAT27228;
XX
DT 22-AUG-1996 (first entry)
XX
DE Bone morphogenetic protein type-I receptor kinase-1 gene.
XX
KW Mouse; bone morphogenetic protein receptor kinase-1;
KW bone morphogenetic protein receptor kinase-3; antibody; diagnostic;
KW bone disorder; osteogenic; bone morphogenetic protein-agonist;
KW drug screening; reporter gene; bone morphogenetic protein-antagonist;
KW hormone-responsive element; ds.
XX
OS Mus musculus.

XX
FH Key Location/Qualifiers
FT CDS 11..1609
FT /*tag= a
FT /product= "Bone morphogenetic protein receptor kinase-1"
XX
PN W09614412-A2.
XX
PD 17-MAY-1996.
XX
PF 30-OCT-1995; 95WO-US014085.
XX
PR 04-NOV-1994; 94US-00334179.
XX
PA (PROC) PROCTER & GAMBLE CO.
XX
PI Rosenbaum JS, Nohno T;
XX
DR WPI: 1996-251762/25.
DR P-PSDB; AAR96201.

XX
PT Isolated bone morphogenic protein receptor kinase protein - used to
PT determine if a test cpd. is capable of binding to, or is (ant)agonist of
PT BMP receptor kinase protein transcription.
XX
PS Example 4; Page 61-63; 87pp; English.

XX
CC The sequence encodes mouse bone morphogenetic protein (BMP) receptor type
CC -I kinase-1 (BRK-1), which induces cellular differentiation in response
CC to BMP. The gene may be inserted in plasmid pJT4, to form plasmid pJT4-
CC J159F, and co-expressed with a type-II BRK-3 gene to study complex
CC formation between the 2 receptor types. The BRK-3 receptor and antibodies
CC against it may be used in diagnostic assays for BMP disorders, or in
CC therapy to bind or scavenge BMPs. In addition, expression of the BRK-3
CC gene along with a reporter gene under the control of a hormone-
CC responsive element in a cell culture may be used to screen compounds for
CC BRK-agonist or -antagonist activity, by monitoring reporter gene
CC expression
XX

SQ Sequence 2402 BP; 676 A; 482 C; 540 G; 704 T; 0 U; 0 Other;
Query Match 86.8%; Score 1574.2; DB 2; Length 2402;
Best Local Similarity 94.2%; Pred. No. 0; Mismatches 93; Indels 9; Gaps 3;
Matches 1669; Conservative 0

QY 51 GAATGGACAATGACTTCAGCTATACATCTTACAGTACTCGGAGCCTGTCGTTCAT 110
Db 1 GAATCAGACAATGACTTCAGCTATACATCTTACATCAGTACTCGGAGCCTGTCGTTCAT 60

QY 111 CATTTCTCATGTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGCTGCTACTGTTATGAATC 170
Db 61 CATTTCTCATGTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGCTGCTACTGTTATGAATC 120
QY 171 AGACGTGACCAAGAAAGCCGGAATATGGAGTGCACGTTAGCACCAGAGGACACCTTACC 230
Db 121 AGACTTGGACCAGAAAGCCAGAAATGGAGTGCACGTTAGCACCAGAGGATACCTTGCC 180
QY 231 TTTCTTAAATGCTATTGCTCAGGACACTGCCCCAGATGACGCTATTATAACACATGAT 290
Db 181 TTTCTTAAATGCTATTGCTCAGGACACTGCCCCAGATGATGCTATTATAACACATGAT 240
QY 291 AACTAATGGCCATTGCTTTGCCATTATAGAAAGATGATCAGGGAGAAACACGTTAAC 350
Db 241 AACTAATGGCCATTGCTTTGCCATTATAGAAAGATGATCAGGGAGAAACACATTAAC 300
QY 351 TTCTGGGTGATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCAAAAGCCCA 410
Db 301 TTCTGGGTGATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCGAAAGCCCA 360
QY 411 GCTACGCAAGCAATAGAAATGTTGCGACCAATTTGTGCAACCAATATTTGACGCTTAC 470
Db 361 GCTACGCAAGCAATAGAAATGTTGCGACCAATTTGTGCAACCAATATTTGACGCTTAC 420
QY 471 ACTGCCCCCTGCTGTTATAGGCCCAATTTCTTGATGGCAGCGCTCCGATGGCTGGCTGCT 530
Db 421 ACTGCCCCCTGCTGTTATAGGCCCAATTTCTTGATGGCAGCATCCGATGGCTGGCTGCT 480
QY 531 CATCTCATGCTGCTGTTATGTCGCATCATGCTCTCTCCAGCTGCTCTCTGTTTACAA 590
Db 481 CATTTCCATGCTGCTGTTATGTTGCTATGATCATCTTCTCCAGCTGCTTTTGTCTATAA 540
QY 591 ACATTACTGTAAGAGTATCTCAAGCAGAGGTCGTTTACCAACCGTGATTTGGAAACAGATGA 650
Db 541 GCATTATTGTAAGAGTATCTCAAGCAGGGTCGTTTACCAACCGTGATTTGGAAACAGATGA 600
QY 651 AGCATTATTCCAGTAGGAGAAATCACTGAAAGACCTGATTCACCAGTACCAAGGCTCTGG 710
Db 601 AGCATTATTCCAGTAGGAGAAATCACTGAAAGACCTGATTCACCAGTACCAAGGCTCTGG 660
QY 711 TAGTGGATCTGGATTACCTTTATTTGTTTACGCAACTATTGCCAAACAGATTCAGATGCT 770
Db 661 GAGTGGATCTGGATTGCTTTATTTGTTTACGCAACTATTGCCAAACAGATTCAGATGCT 720
QY 771 TCGCAGAGTTGGTAAGGCCCGGTATGGAAGATATGGAATGGGTAAATGGCGTGGTGAATA 830
Db 721 TCGGAGGTTGGTAAAGGCCCGTATGGAAGATATGGAATGGGTAAATGGCGTGGTGAATA 780
QY 831 AGTGGCTGTCAAAGTATTTTATTTTACCACTGAAAGAGCTAGCTGGTTTACGAAACAGAAAT 890
Db 781 AGTGGCTGTCAAAGTATTTTATTTTACCACTGAAAGAGCTAGCTGGTTTACGAAACAGAAAT 840
QY 891 CTACAGACGGTGTAAATGCTCATGAAATATATCTGTTTATAGCTGCAGACATTAA 950
Db 841 CTACAGACGGTGTAAATGCTCATGAAATATATCTGTTTATAGCTGCAGACATTAA 900
QY 951 AGGCACCGGTTCTCGGACTCAGCTGTATTTGATTACTGATTACCAATGGAATGGATCTCT 1010
Db 901 AGGCACCGGTTCTCGGACTCAGCTGTATTTGATTACTGATTACCAATGGAATGGATCTCT 960
QY 1011 CTATGACTTCTGAAATGTGCCACCTTGACACACAGAGCCCTACTCAAGTTAGCTTATTC 1070
Db 961 CTATGACTTCTGAAATGTGCCACCTTGACACACAGAGCCCTACTCAAGTTAGCTTATTC 1020
QY 1071 TGCTGCCCTGCTGCTGTCACCTCCACACAGAAATTTATGGCAGCGCAAGGCAAGCCTGTC 1130
Db 1021 TGCTGCTGCTGCTGTCGTCACCTCCACAGAAATTTATGTCACCCAGGAGGAGCCTGTC 1080
QY 1131 AATTGCTCATCGAGACCTGGAAGAGCAAAACATCTTTATTAAGAAAAATGTTAGTTGCTG 1190
Db 1081 AATTGCTCATCGAGACCTGGAAGAGCAAAACATCTTTATTAAGAAAAATGGAAGTTGCTG 1140
QY 1191 TATTGCTGACCTGGGCTAGCTGTTTAAATTTCAAGTACACAAATGAAGTTGACATACC 1250

Db 1141 TATTGCTGACCTGGGCTAGCTGTTAAATTCACAGTGATACAAATGAAGTTGACATACC 1200
Qy 1251 CTTGAACACAGGCTGGGACACAGCGGTACATGGCTCCAGAGTCTCGAGAGAGCTT 1310
Db 1201 CTTGAATACAGGCTGGGACCAAGCGGTACATGGCTCCAGAGTCTCGAGTGAAGCTT 1260
Qy 1311 GAGTAAAAACCAATTTCCAGCCCTACATCATGGCTGACATCTACAGCTTTGGTTGATCAT 1370
Db 1261 GAATAAAAACCAATTTCCAGCCCTACATCATGGCTGACATCTATAGCTTTGGTTGATCAT 1320
Qy 1371 TTGGAGATAGGCCCGCTGGCTGTATTACAGAGAAATCGTGGAGGAATATCAATTACCATA 1430
Db 1321 TTGGGAATAGGCTGCTGCTGTATTACAGAGGAATCGTGGAGGAATATCAATTACCATA 1380
Qy 1431 TTACAAACATGGTGGCTAGTGACCCATCTTATGAAGACATGCGTGAGTCTGTGTGTGA 1490
Db 1381 TTACAAACATGGTGGCCAGTGACCCATCTTATGAGGACATGCGTGAGTCTGTGTGTGA 1440
Qy 1491 ACGCTTGGCGCCCAATCGTCTCTAAACCGCTCGAACAGTGATGAATGTCTTCGAGCCGTTT 1550
Db 1441 ACGCTTGGCGCCCAATCGTCTCTAAACCGCTGGAACAGGATGAATGTCTTCGAGCAGTTT 1500
Qy 1551 GAAGCTGATGTGAGAAATGCTGGGCCCAATTAATCCAGCATCCAGACTCACAGCTTTGAGAAT 1610
Db 1501 GAAGCTAAATGTGAGAAATGCTGGGCCCAATTAATCCAGCCTCCAGACTCACAGCTTTGAGAAT 1560
Qy 1611 CAAGAAGAGCTCGCAAAAGATGGTGAATCCAGGATGTAAGATTTGAC----AAACAG 1666
Db 1561 CAAGAAGAGCATTGCAAAAGATGGTGAATCCAGGATGTAAGATTTGACAAATTAACAA 1620
Qy 1667 TTTTGAGAAAGATTTAGACTGCAAGAAATTC----ACCGAGGAGGCTGGAGTTAGCA 1722
Db 1621 TTTTGAGGAGAAATTTAGACTGCAAGAAATTCCTTACCCCAAGGAATGGTGGGATTAGCA 1680
Qy 1723 TGGACTAGGATGTGGCTTTGGTTTCAGACTCTCTCTCTCAATCTTCCAGAGCTGCTA 1782
Db 1681 TGGAAATAGGATGTGACTTTGGTTTCAGACTCTCTCTCTCA-CATCTTCACAGGCTGCTA 1739
Qy 1783 ACAGTAAACCTTTCAGGACTCTGCAGAAATGC 1813
Db 1740 ACAGTAAACCTTACCGCACTCTACAGAAATAC 1770

RESULT 13

ID AAT28021 standard; cDNA; 2402 BP.

XX AC AAT28021;

XX AC AAT28021;

XX 31-DEC-1996 (first entry)

XX Mouse BMP type I receptor kinase (BRK-1) cDNA.

DE BMP type II receptor kinase-3; BRK-3; bone morphogenetic protein;

KW BMP type I receptor kinase; BRK-1; BMP receptor; ds.

XX Mus sp.

OS Mus sp.

XX Key

XX Location/Qualifiers

FT 11..1609

FT /*tag= a

XX WO9614579-A1.

XX 17-MAY-1996.

XX 30-OCT-1995; 95WO-US014027.

XX 04-NOV-1994; 94US-003341178.

PR 05-JUN-1995; 95US-00462467.

XX (PROC) PROCTER & GAMBLE CO.

XX Rosenbaum JS;
PI WPI: 1996-251987/25.
XX P-PSDB; AAR95225.
PT Assays for bone morphogenetic protein activities - using complex of BMP
type I receptor kinase protein and BMP receptor kinase protein BRK-3.
XX Claim 5; Page 64-66; 101pp; English.
XX A cDNA clone (AAT28021) codes for full-length mouse bone morphogenetic
protein (BMP) type I receptor kinase protein-1 (BRK-1) (AAR95225), a
CC receptor capable of binding BMP and transducing a signal initiated by the
CC binding. Host cells co-transfected with vectors carrying full-length,
CC incomplete or soluble BMP type I receptor kinase protein cDNA and full-
CC length, incomplete, soluble or truncated BMP type II receptor kinase
CC protein-3 (BRK-3) cDNA (see also AAT28018-20 and AAT28022-30) express a
CC BMP receptor complex useful for screening cpds. for BMP receptor affinity
CC or for determining the concentration of a BMP receptor ligand in a
CC clinical sample
XX Sequence 2402 BP; 676 A; 482 C; 540 G; 704 T; 0 U; 0 Other;
Qy Query Match 86.8%; Score 1574.2; DB 2; Length 2402;
Best Local Similarity 94.2%; Pred. No. 0;
Matches 1669; Conservative 0; Mismatches 93; Indels 9; Gaps 3;
Qy 51 GAATTTGGACAATGACTCAGCTATACACTTACATTCAGATTACTGGGAGCCTGTCTGTTCAT 110
Db 1 GAATCAGACAATGACTCAGCTATACACTTACATTCAGATTACTGGGAGCCTGTCTGTTCAT 60
Qy 111 CATTTCTCATGTTCAAGGCGCAATCTAGATAGTATGCTCCATGTTACTGGTATGAATC 170
Db 61 CATTTCTCATGTTCAAGGCGCAATCTAGATAGTATGCTCCATGTTACTGGTATGAATC 120
Qy 171 AGACCTTGACACCAAGAAAGCCGAAATGGAGTGAGCTTTAGCACAGAGACACCTTACC 230
Db 121 AGACTTTGGACCAAGAAAGCCGCAATGAGTGTACTTTAGCACAGAGATACCTTGC 180
Qy 231 TTTCTTAAATGCTATTGCTCAGGACACTGCCCAGATGACGCTATTAAACACATGCAT 290
Db 181 TTTCTTAAATGCTATTGCTCAGGACACTGCCCAGATGATGCTATTAAACACATGCAT 240
Qy 291 AACTTAATGGCCATTCCTTTGCCATTTATAGAAGAATGATCAGGAGAAACACCGTTAC 350
Db 241 AACTTAATGGCCATTCCTTTGCCATTTATAGAAGAATGATCAGGAGAAACACCATTAAC 300
Qy 351 TTTCTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCAAAAGCCCA 410
Db 301 TTTCTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCGAAAGCCCA 360
Qy 411 GCTACGACAGCAATAGAAATGTTGCGGACCAATTTGTGCAACCAATATTTCGAGCCTAC 470
Db 361 GCTACGACAGCAATAGAAATGTTGCGGACCAATTTGTGCAACCAATATTTCGAGCCTAC 420
Qy 471 ACTGCCCTCTGCTTATAGGCCCATCTTTGATGCGCAGCGTCCGATGGCTGGCTGTGCT 530
Db 421 ACTGCCCTCTGCTTATAGGCCCATCTTTGATGCGCAGCATCCGATGGCTGGCTGTGCT 480
Qy 531 CATCTCTATGGCTGTCTGTTATTTGTCGCATGATTCCTTTCCAGCTGCTCTGTGTACAA 590
Db 481 CATTTCCATGGCTGTCTGTTATAGTTGCTATGATCATCTTCTCCAGCTGCTTTTGTATAA 540
Qy 591 ACATTTACTGTAAGATATCTCAAGCAGAGGCTGTTTACCAACCGTGTCTTGGAAACAGATGA 650
Db 541 GCATTTATTGTAAGATATCTCAAGCAGAGGCTGTTTACCAACCGTGTCTTGGAAACAGATGA 600
Qy 651 AGCATTTATTCCAGTAGGAGAAATCACTGAAGACCTGATTTGACAGTCACAAGCTCTGG 710
Db 601 AGCATTTATTCCAGTAGGAGAAATCACTGAAGACCTGATTTGACAGTCACAAGCTCTGG 660
Qy 711 TAGTGGATCTGGATTACCTTTTATTGTTTTCAGGCAACTATTGCGCAAAACAGATTTCAGATGCT 770

Db 121 AGACTTGGACCAGAGAAGCCAGAAAAATGGAGTGAATCTTTAGCACACAGAGATACCTTGCC 180
Qy 231 TTTCTTAAATGCTATTGCTCAGACACTGCCAGATGAGCTATTAAATAACACATGCAT 230
Db 181 TTTCTTAAAGTGTATTGCTCAGACACTGCCAGATGAGCTATTAAATAACACATGCAT 240
Qy 291 AACTAAATGGCCATTGCTTTGCCATTATAGAGAAGATGATCAGGAGAAACCACTTAAC 350
Db 241 AACTAAATGGCCATTGCTTTGCCATTATAGAGAAGATGATCAGGAGAAACCACTTAAC 300
Qy 351 TTTCTGGGTGATGAAGTATGAAGCTCTGATTTTCAATGCAAGATTCACAAAAGCCCA 410
Db 301 TTTCTGGGTGATGAAGTATGAAGCTCTGATTTTCAATGCAAGATTCACAAAAGCCCA 360
Qy 411 GCTACGAGGACCAATAGAAATGTTGTCGACCAATTTGTGCAACCAATATTGACAGCTAC 470
Db 361 GCTACGAGGACCAATAGAAATGTTGTCGACCAATTTGTGCAACCAATATTGACAGCTAC 420
Qy 471 ACTGCCCCCTGTCGTTATAGCCCAATTTTGTGATGGCAGGCTCCGATGGCTGCTGTCT 530
Db 421 ACTGCCCCCTGTTGTTATAGCTCGTTCCTTGTGATGGCAGCATCCGATGGCTGCTGTCT 480
Qy 531 CATCTCTATGGCTGCTGTATTGTCGCATGATGCTTCTCAGCTGCTTCTGTTACAA 590
Db 481 CATTTCCATGGCTGCTGTATTGTCGCATGATGCTTCTCAGCTGCTTCTGTTACAA 540
Qy 591 ACATTACTGTAAGATGATCTCAAGCAGAGTCTGTACACCGTGACTTGGAAACAGATGA 650
Db 541 GCATTATTGTAAGATGATCTCAAGCAGAGTCTGTACACCGTGACTTGGAAACAGATGA 600
Qy 651 AGCATTTATTCCAGTAGGAGAATCACTGAAAGACCTGATTTGACAGCTCAAAAGCTCTGG 710
Db 601 AGCATTTATTCCAGTAGGAGAATCACTGAAAGACCTGATTTGACAGCTCAAAAGCTCTGG 660
Qy 711 TAGTGATCTGGATTACCTTTTATGTTTACGCAATATTGTCGCAACAGATTCAGATGGT 770
Db 661 GAGTGGATCTGGATTGCTTTTATGTTTACGCAACTATTGTCGCAACAGATTCAGATGGT 720
Qy 771 TCGGAGGTGTTGTAAGGCCGGTATGGAAGATGATGAGTGGTAAATGGCGTCAAAA 830
Db 721 TCGGAGGTGTTGTAAGGCCGGTATGGAAGATGATGAGTGGTAAATGGCGTCAAAA 780
Qy 831 AGTGGCTGTCAAAAGTATTTTACCACCTGAAGAAGCTAGCTGGTTTAGAGAAACAGAAAT 890
Db 781 AGTGGCTGTCAAAAGTATTTTACCACCTGAAGAAGCTAGCTGGTTTAGAGAAACAGAAAT 840
Qy 891 CTACACAGCGGTGTTAATGCGTCATGAAAATATACTTGGTTTATAGCTGCAGACATTAA 950
Db 841 CTACACAGCGGTGTTAATGCGTCATGAAAATATACTTGGTTTATAGCTGCAGACATTAA 900
Qy 951 AGGCACGGTTCCTGGACTCAGCTGATTTGATTACTGATTACCATGAGNAATGGGTCTCT 1010
Db 901 AGGCACGGTTCCTGGACTCAGCTGATTTGATTACTGATTACCATGAGNAATGGGTCTCT 960
Qy 1011 CTATGACTTCTGAAATGTGCCACCTTGGACACACAGAGCCCTACTCAAGTTAGCTTTATTC 1070
Db 961 CTATGACTTCTGAAATGTGCCACCTAGACACACAGAGCCCTACTCAAGTTAGCTTTATTC 1020
Qy 1071 TGTGCTGCTGCTGTGCGCACTCCACACAGAAATTTATGGCACGCAAGGCAAGCCTGC 1130
Db 1021 TGTGCTGCTGCTGTGCGCACTCCACACAGAAATTTATGGTACCCAAAGGGAAGCCTGC 1080
Qy 1131 AATTGCTCATCGAGACTGAAGAGCAAAACATCTTATTAGAAAAATGGTAGTTGCTG 1190
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Qy 1191 TATTGCTGACTGGGCTAGCTGTTAAATTTCAACAGTGCACAAATGAAGTTGACATACC 1250
Db 1141 TATTGCTGACTGGGCTAGCTGTTAAATTTCAACAGTGCACAAATGAAGTTGACATACC 1200
Qy 1251 CTTGAACACAGGGTGGGCAACAGCGGTACATGGCTCCAGAGTGTCTGACAGAGCCT 1310
Db 1201 CTTGAATACAGGGTGGGCAACAGCGGTACATGGCTCCAGAGTGTCTGATGAAGCCT 1260

Qy 1311 GAGTAAAAACATTTTCCAGCCCTACATCATGGCTGACATCTACAGCTTTTGGTTTGATCAT 1370
Db 1261 GAATAAAAACATTTTCCAGCCCTACATCATGGCTGACATCTATAGCTTTTGGTTTGATCAT 1320
Qy 1371 TTGGAGATGGCCCGCTGCTGTATTACAGAGGAATCGTGAGGAATATCAATTAACATA 1430
Db 1321 TTGGGAATGGCTCGTCTGTTGATTATACAGGAGAAATCGTGAGGAATATCAATTAACATA 1380
Qy 1431 TTACAAACATGGTCCCTAGTGAACCCATCTTATGAAGACATGCGTGAGGTCTGTGTGTGAA 1490
Db 1381 TTACAAACATGGTCCCTAGTGAACCCATCTTATGAAGACATGCGTGAGGTCTGTGTGTGAA 1440
Qy 1491 ACGCTTGGCGCCAAATCGTCTCTAAACCGCTGGAAACAGTGAATGCTCTTCGAGCCGTTTT 1550
Db 1441 ACGCTTGGCGCCAAATCGTCTCTAAACCGCTGGAAACAGGATGAATGCTCTTCGAGCAGTTTT 1500
Qy 1551 GAAGCTGATGTGCAATATGCTGGGCCCAATATCCAGCATCCAGACTCACAGCTTTGAGAAT 1610
Db 1501 GAAGCTAAATGTGCAATATGCTGGGCCCAATATCCAGCTCCAGACTCACAGCTTTGAGAAT 1560
Qy 1611 CAAGAAGACGCTCGCAAGATGCTTGAATCCCAAGGATGTAAGATTGAC----AAACAG 1666
Db 1561 CAAGAAGACACTTGCAAAAATGTTGAATCCCAAGGATGTAAGATTGACAAATTAACAA 1620
Qy 1667 TTTTGAGAAAGAAATTTAGACTGCAAGAAATTC---ACCGAGGAAGGTTGGAGTTAGCA 1722
Db 1621 TTTTGAGGAGAAATTTAGACTGCAAGAAATTCCTTACCAGGAATGGGTGGGATAGCA 1680
Qy 1723 TGGACTAGGATGTGGCTTGGTTTCCAGACTCTCTCTCTTACCATCTTCAACAGGCTGCTA 1782
Db 1681 TGGAAATAGGATGTGACTTTGGTTTCCAGACTCTCTCTCTA-CATCTTCCAGGCTGCTA 1739
Qy 1783 ACAGTAAACCTTTACGAGCTCTGCAGATGC 1813
Db 1740 ACAGTAAACCTTTACCGCACTCTACAGAAATAC 1770

RESULT 15

AAQ90183
ID AAQ90183 standard; DNA; 2056 BP.

XX AAQ90183;
AC AC
XX 25-MAR-2003 (revised)
DT 01-NOV-1995 (first entry)
XX
XX Truncated BRK-1.

BRK-1; BMP receptor kinase protein-1; bone morphogenetic protein; ds.

Mus sp.

Key Location/Qualifiers
FH CDS 291..1793
FT sig_peptide /*tag= a
FT mat_peptide /*tag= b
FT /*tag= c

W09514778-A2.

01-JUN-1995.

23-NOV-1994; 94WO-US013534.

24-NOV-1993; 93US-00158735.

(PROC) PROCTER & GAMBLE CO.

Cook JS, Correa PE, Koenig BB, Rosenbaum JS, Ting J;

XX

DR WPI: 1995-206935/27.
DR P-PSDB; AAR74342.
XX New bone morphogenetic protein receptor kinase protein - used for
PT identifying cpds. capable of binding it and for developing therapeutic
PT cpds. and detection system(s).
XX
PS Claim 6; Page 25-28; 49pp; English.
XX
CC PCR primers (given in AAQ90186-89) based on unique sequences present in
CC activin and DaF-1 receptor kinase domain VI were used to amplify cDNA
CC derived from NIH3T3 cells. A 300 bp PCR fragment obtd. was used to screen
CC a cDNA library prepd. from NIH3T3 cells in lambda ZapII to obtain clone
CC J159 containing DNA (AAQ90183) encoding truncated Brk-1 (AAR74342).
CC Vectors including the DNA were used to express recombinant EBRK-1 in CHO
CC and COS-7 hosts. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 2056 BP; 573 A; 436 C; 506 G; 541 T; 0 U; 0 Other;

Query Match 78.6%; Score 1424.4; DB 2; Length 2056;
Best Local Similarity 90.3%; Pred. No. 0;
Matches 1584; Conservative 0; Mismatches 76; Indels 94; Gaps 2;

QY 39 CAGGACACGTGGAAATGGACAATGACCTACAGCTATACACTTACATCAGATTACTGGAGC 98
DB 269 CAGGACGGTGGAAATGACAGCAATGACTCAGCTATACACTTACATCAGATTACTGGAGC 328

QY 99 CTGCTGTTTCATCAITTCCTCATGTTCAAGGGCAGAACTCTAGATAGTAGTCTCCATGGTAC 158
DB 329 CTGCTGTTTCATCAITTCCTCATGTTCAAGGGCAGAACTCTAGATAGTAGTCTCCATGGC 388

QY 159 TGGTATGAATCAGAGCTGGACAGAGAGAGCGGAGAAATGAGTGCAGTGTAGCAACGAGA 218
DB 389 TGGTATGAATCAGAGCTGGACAGAGAGAGCGGAGAAATGAGTGCAGTGTAGCAACGAGA 448

QY 219 GGACACCTTTACCTTTCTTAAATGCTATTGCTCAGACACTGCCAGATGAGCTATTAA 278
DB 449 GGATACCTTGCTTTCTTAAAGTGTATTGCTCAGGACACTGCCAGATGAGTGTATTAA 508

QY 279 TAACACATGCATAAATAATGGCCATTGCTTGGCCATTATAGAAAGAGATGATCAGGAGA 338
DB 509 TAACACATGCATAAATAATGGCCATTGCTTGGCCATTATAGAAAGAGATGATCAGGAGA 568

QY 339 AACCAAGTAACTTCTGGGTATGAAAGTATGAAGGCTCTGATTTCAATGCAAGGATTC 398
DB 569 AACCAAGTAACTTCTGGGTATGAAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTC 628

QY 399 ACCAAAGCCAGCTACCGAGACAAATAGAAATGTTGTCGGACCAATTTGTGCAACCAATA 458
DB 629 ACCAAAGCCAGCTACCGAGACAAATAGAAATGTTGTCGGACCAATTTGTGCAACCAATA 688

QY 459 TTTGAGGCTACACTGCCCTGTCGTTATAGGCCATTCTTTGATGGCAGCGTCCGATG 518
DB 689 TTTGAGGCTACACTGCCCTGTCGTTATAGGTCGGTCTTTGATGGCAGCATCCGATG 748

QY 519 GCTGCTGTCTCATCTCTAGGCTGTCTGTATTTGTCGCCATGATGCTCTCTCCAGCTG 578
DB 749 GCTGCTGTCTCATCTTCCATGGCTGTCTGTATGTTGCTATGATCATCTCTCCAGCTG 808

QY 579 CTTCGTTTACAAACATTAAGTATGATGATCTCAGACAGAGTCTGTTACACCGTGACTT 638
DB 809 CTTCGTTTATAGCAATTAAGTATGATGATCTCAGACAGGCTGTTTACACCGTGATTT 868

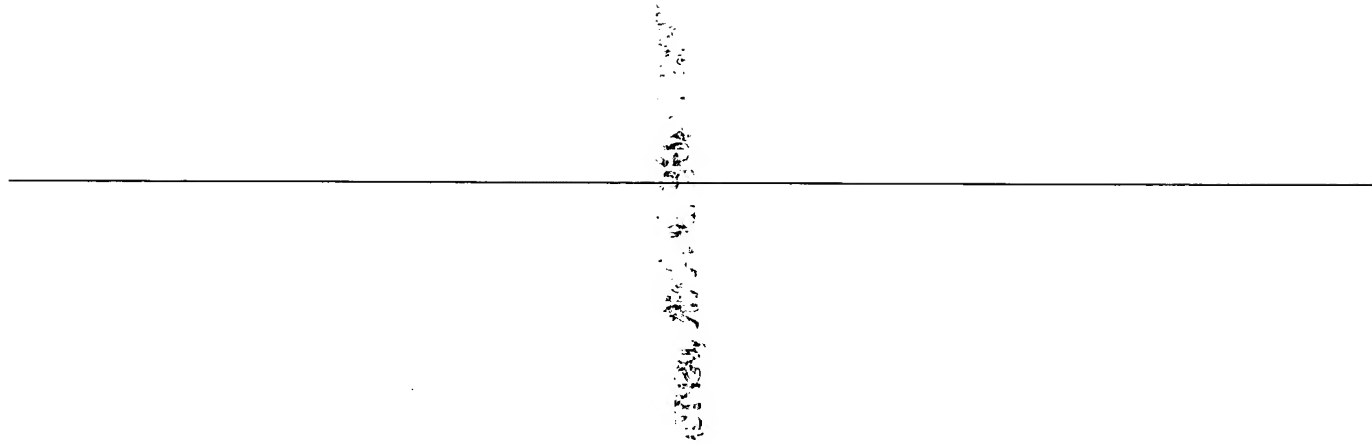
QY 639 GGAAACAGGATGAACATTTATTCAGTAGGAGAATCACTGAAAGACCTGATTTGACCACTC 698
DB 869 GGAAACAGGATGAACATTTATTCAGTAGGAGAATCACTGAAAGACCTGATTTGACCACTC 928

QY 699 ACAAGCTCTGTAGTGAATCTGATTAACCTTTATTTGTTTACGCAACTATTTGCCAACA 758
DB 929 CCAAAGCTCTGGGAGTGGATCTGATTTGCTTTTATTTGTTTACGCGAACTATTTGCCAACA 988

QY 759 GATTTCAGATGTTTCGGCAGGTTGTTAAGGCGGATGAGAGATGATGAGTGGGTAAATG 818
|||||

Search completed: December 9, 2005, 14:08:06
Job time : 775 secs

DB 989 GATTTCAGATGTTTCGGCAGGTTGGTAAAGCGCGCTATCGAGAGATATCGATGGGTAATG 1048
QY 819 CGTGGTGAAGAAAGTGGCTGCTCAAGTATTTTTTACCACTGAGAAAGCTAGCTGGTTTAG 878
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DB 1049 CGTGGTGAAGAAAGTGGCTGCTCAAGTATTTTTTACCACTGAGAAAGCTAGCTGGTTTAG 1108
|||||
QY 879 AGAAACAGAAATCTACACAGACGGTGTAAATGCGTCATGAAAATATATCTGGTTTATAGC 938
|||||
DB 1109 AGAAACAGAAATCTACACAGACGGTGTAAATGCGTCATGAAAATATATCTGGTTTATAGC 1168
|||||
QY 939 TGCACATTTAAAGCACCGGTTCTCGACCTCAGCTGTATTTGATTACTGATTACCATCA 998
DB 1169 TGCACATTTAAAGCACCTGGTTCTCGACCTCAGCTGTATTTGATTACTGATTACCATCA 1228
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QY 999 GAATGGGTCTCTCTATGATCTTCTGAAATGTGCCACCTGGACACACAGAGCCCTACTCAA 1058
DB 1229 AAATGGATCTCTCTATGATCTTCTGAAATGTGCCACCTAGACACACAGAGCCCTACTCAA 1288
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QY 1059 GTTAGCTTATTTCTGCTGCTGTGCTGTGCTGCCACCTCCACACAGAAATTTATGGCAGCA 1118
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DB 1289 GTTAGCTTATTTCTGCTGCTGTGCTGTGCTGCCACCTCCACACAGAAATTTATGGTACCCA 1348
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QY 1119 AGGCAAGCTCGAATTTGCTCATCGAGACCTGAAGAGCAAAACATCTTTATTAAGAAAA 1178
DB 1349 AGGAGAGCTGCAATTTGCTCATCGAGACCTGAAGAGCAAAACATCTTTATTAAGAAAA 1408
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QY 1179 TGGTAGTTGCTGTATTTGCTGACCTGGGCTAGCTGTTAAATTTCAA CAGTGACACAAATGA 1238
DB 1409 TGGAAAGTTGCTGTATTTGCTGACCTGGGCTAGCTGTTAAATTTCAA CAGTGATACAAATGA 1468
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QY 1239 AGTTGACATACCTTTGAACACACAGGCTGGGACACAGGCGGTACATGGCTCCAGAAAGTGT 1298
DB 1469 AGTTGACATACCTTTGAATACACAGGCTGGGACCAAGCGGTACATGGCTCCAGAAAGTGT 1528
|||||
QY 1299 GGACGAGAGCTGAGTAAAAACCAATTTCCAGCCTTACATCATGCTGCTGACATCTACAGCTT 1358
DB 1529 GGATGAAAGCTGAAATAAAAACCAATTTCCAGCCTTACATCATGCTGCTGACATCTATAGCTT 1588
|||||
QY 1359 TGGTTGATCAATTTGGGAGATGGCCGCTGCTGTATTTACAGGAGGAATCGTGGAGGAATA 1418
DB 1589 TGGTTGATCAATTTGGGAAATGGCTGCTGTGTTATTTACAGGAGGAATCGTGGAGGAATA 1648
|||||
QY 1419 TCAATTACCATTTACAAACATGGTGCCTAGTGACCCATCTTTAGAGACATGCGTGAGGT 1478
DB 1649 TCAATTACCATTTACAAACATGGTGCCTAGTGACCCATCTTATGAGGACATGCGTGAGGT 1708
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QY 1479 CGTGTGTGTAAGACGCTTGGCGGCAATCGTCTCTAAACGCTGGAACAGTGATGAA - - - - 1533
DB 1709 TGTGTGTGTAAGACGCTTGGCGGCAATCGTCTCTAAACGCTGGAACAGGATGAAAGTAA 1768
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QY 1534 - - - - - 1533
DB 1769 TTGGAGCAAGTCCCTGTFAAAGTATGATGAGTGGTGGCCGAGTTACTCTGTGCTCACCAC 1828
|||||
QY 1534 - - - - - TGTCTTCGAGCCGTTTTTGAAGCTGATGTCAGAAATG 1568
DB 1829 TCTGTTTGCAITTTATTTCTCTTTAGTGTCTTTTCGAGCAGTTTTTGAAGCTAATGTCAGAAATG 1888
|||||
QY 1569 CTGGGCCCATTAATCCAGCATCCAGACTCAGAGCTTTGAGAATCAAGAGAGACGCTCGCAAA 1628
DB 1889 TTGGGCCCATTAATCCAGCTCCAGACTCAGAGCTTTGAGAATCAAGAGAGACACTTTGCAAA 1948
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QY 1629 GATGTTGTAATCCAGGATGTAAAGATTTGAC - - - - - AAAACAGTTTGTGAGAAAGAAATTTAG 1684
DB 1949 AATGTTGTAATCCAGGATGTAAAGATTTGACAAATTAACCAATTTTGGAGGAGAAATTTAG 2008
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QY 1685 ACTGCAAGAAATTC 1698
|||||
DB 2009 ACTGCAAGAAATTC 2022
|||||



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OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 13:41:38 ; Search time 247 Seconds
(without alignments)
13047.446 Million cell updates/sec

Title: US-10-600-645-1

Perfect score: 1813

Sequence: 1 CTAGTGGATCCCCGGGCTG.....TTCCAGGACTCTGCAGAAATGC 1813

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/8B COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1813	100.0	1813	3	US-08-123-934A-1
2	1813	100.0	1813	3	US-09-874-628-1
3	1813	100.0	1813	6	PCT-US94-10080-1
4	1581.4	87.2	2070	3	US-09-382-256-13
5	1581.4	87.2	2070	3	US-09-395-115-13
6	1581.4	87.2	2070	3	US-08-436-265-13
7	1581.4	87.2	2070	3	US-09-679-187-13
8	1581.4	87.2	2070	3	US-09-267-963D-13
9	1574.2	86.8	2402	3	US-08-462-467B-11
10	1574.2	86.8	2402	3	US-08-158-735A-3
11	1574.2	86.8	2402	3	US-08-334-179A-11
12	1424.4	78.6	2056	3	US-08-158-735A-1
13	1387	76.5	2932	2	US-08-481-337A-5
14	1387	76.5	2932	3	US-09-382-256-5
15	1387	76.5	2932	3	US-09-395-115-5
16	1387	76.5	2932	3	US-08-436-265-5
17	1387	76.5	2932	3	US-09-679-187-5
18	1387	76.5	2932	3	US-08-448-371A-5
19	1387	76.5	2932	3	US-09-267-963D-5
20	1387	76.5	2932	3	US-09-949-016-604
21	1387	76.5	2932	6	PCT-US95-05467-5
22	1385.4	76.4	2892	3	US-09-949-016-1914
C 23	1348	74.4	636591	3	US-09-949-016-11808
C 24	1348	74.4	636591	3	US-09-949-016-13388

25	716	39.5	1952	2	US-08-481-337A-7	Sequence 7, Appli
26	716	39.5	1952	3	US-09-382-256-17	Sequence 17, Appl
27	716	39.5	1952	3	US-09-395-115-17	Sequence 17, Appl
28	716	39.5	1952	3	US-08-436-265-17	Sequence 17, Appl
29	716	39.5	1952	3	US-09-679-187-17	Sequence 17, Appl
30	716	39.5	1952	3	US-08-448-371A-7	Sequence 7, Appli
31	716	39.5	1952	3	US-09-267-963D-17	Sequence 17, Appl
32	716	39.5	1952	6	PCT-US95-05467-7	Sequence 7, Appli
33	697.4	38.5	2076	3	US-08-123-934A-3	Sequence 3, Appli
34	697.4	38.5	2076	3	US-09-874-628-3	Sequence 3, Appli
35	697.4	38.5	2076	6	PCT-US94-10080-3	Sequence 3, Appli
36	690.6	38.1	1765	3	US-09-949-016-4525	Sequence 4525, Ap
37	673	37.1	2252	3	US-08-462-467B-13	Sequence 13, Appl
38	673	37.1	2252	3	US-08-334-179A-13	Sequence 13, Appl
39	647	35.7	706	3	US-08-462-467B-19	Sequence 19, Appl
40	440.8	24.3	469	3	US-08-462-467B-15	Sequence 15, Appl
41	438.8	24.2	466	3	US-08-158-735A-5	Sequence 5, Appli
42	405	22.3	1647	3	US-08-123-934A-7	Sequence 7, Appli
43	405	22.3	1647	3	US-09-874-628-7	Sequence 7, Appli
44	405	22.3	1647	6	PCT-US94-10080-7	Sequence 7, Appli
45	403.4	22.3	2333	3	US-09-382-256-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-123-934A-1
; Sequence 1, Application US/08123934A
; Patent No. 6291206
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, John
; APPLICANT: CELESTE, Anthony J.
; APPLICANT: THIES, R. Scott
; APPLICANT: YAMAJI, No. 6291206oru
; TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute Inc. - Legal Affairs
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,934A
; FILING DATE: 17-SEP-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, Steven R
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 876 1170
; TELEFAX: 617 876 5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1813 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: CFK1-23a
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 61..1656
US-08-123-934A-1

Query Match		100.0%;	Score 1813;	DB 3;	Length 1813;	
Best Local Similarity		100.0%;	Pred. No. 0;			
Matches 1813;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	CTAGTGGATCCCCCGGCTGCAGGAATTC	CGCGCGCCAGGACACGTCGGAATTTGGACA	60		
DB	1	CTAGTGGATCCCCCGGCTGCAGGAATTC	CGCGCGCCAGGACACGTCGGAATTTGGACA	60		
QY	61	ATGACTCAGCTATACACTTTACATCAGATTA	CTGGAGCCCTGCTGTTCATCATTTCTCAT	120		
DB	61	ATGACTCAGCTATACACTTTACATCAGATTA	CTGGAGCCCTGCTGTTCATCATTTCTCAT	120		
QY	121	GTTCAAGGCGAATCTAGATAGTATGCTCCAT	TGCTAGTGTATGAAATCAGACGTGGAC	180		
DB	121	GTTCAAGGCGAATCTAGATAGTATGCTCCAT	TGCTAGTGTATGAAATCAGACGTGGAC	180		
QY	181	CAGAGAAGCCGGAATAGAGTACGTTAGCACC	AGGACACACTTACTCTTTCTTAAA	240		
DB	181	CAGAGAAGCCGGAATAGAGTACGTTAGCACC	AGGACACACTTACTCTTTCTTAAA	240		
QY	241	TGCTATTGCTCAGGACACTGCCAGATGACGCT	ATTAATACACATGCAATAATGGC	300		
DB	241	TGCTATTGCTCAGGACACTGCCAGATGACGCT	ATTAATACACATGCAATAATGGC	300		
QY	301	CATTGCTTTGCCATTTATAGAAGAAGATGAT	CAGGGAGAAACACAGTTAACTTCGGGTG	360		
DB	301	CATTGCTTTGCCATTTATAGAAGAAGATGAT	CAGGGAGAAACACAGTTAACTTCGGGTG	360		
QY	361	ATGAAGTATGAAGGCTCTCATTTTCAATGCA	AGGATTCACAAAAGCCAGCTACGCAGG	420		
DB	361	ATGAAGTATGAAGGCTCTCATTTTCAATGCA	AGGATTCACAAAAGCCAGCTACGCAGG	420		
QY	421	ACAATAGAAATGTTGTCGACCAATTTTGCA	ACCAATATTTGCGCGCTACACTGCCCT	480		
DB	421	ACAATAGAAATGTTGTCGACCAATTTTGCA	ACCAATATTTGCGCGCTACACTGCCCT	480		
QY	481	GTGCTTATAGGCCATTTCTTTGATGGCAGC	GTCCGATGGCTGTGCTCATCTATG	540		
DB	481	GTGCTTATAGGCCATTTCTTTGATGGCAGC	GTCCGATGGCTGTGCTCATCTATG	540		
QY	541	GCTGCTGTATTTGTCGCCATGATCGTCTTC	CCAGCTGCTTGTACAAACATTA	600		
DB	541	GCTGCTGTATTTGTCGCCATGATCGTCTTC	CCAGCTGCTTGTACAAACATTA	600		
QY	601	AAGAGTATCTAAGCAGAGGTGTTTACAA	CCGCTGACTTGGAAACAGGATGAAGCA	660		
DB	601	AAGAGTATCTAAGCAGAGGTGTTTACAA	CCGCTGACTTGGAAACAGGATGAAGCA	660		
QY	661	CCAGTAGGAATCACTGAAGACCTGATTGAC	CAAGCTCAGAGCTCTGGTAGTGATCT	720		
DB	661	CCAGTAGGAATCACTGAAGACCTGATTGAC	CAAGCTCAGAGCTCTGGTAGTGATCT	720		
QY	721	CGATTACCTTTATTTGTTTCAGCGAACTAT	TGCGCAACAGATTGAGTTCGGCAGGTT	780		
DB	721	CGATTACCTTTATTTGTTTCAGCGAACTAT	TGCGCAACAGATTGAGTTCGGCAGGTT	780		
QY	781	GTTAAGGCGCGGTATGGAGAAGTATGGAT	GGGTAAATGGCGGTGGAAGGTGGCTGTC	840		
DB	781	GTTAAGGCGCGGTATGGAGAAGTATGGAT	GGGTAAATGGCGGTGGAAGGTGGCTGTC	840		
QY	841	AAAGTATTTTTCACCTGAAAGCTAGCTGGT	TTAGAGAAACAGAAATCTACACAGC	900		
DB	841	AAAGTATTTTTCACCTGAAAGCTAGCTGGT	TTAGAGAAACAGAAATCTACACAGC	900		
QY	901	GTGTTAATCGCTCATGAAATATACCTGTTT	TATAGCTGCGAGACATTAAGGCCACCGT	960		
DB	901	GTGTTAATCGCTCATGAAATATACCTGTTT	TATAGCTGCGAGACATTAAGGCCACCGT	960		
QY	961	TCCTGGACTCAGCTGTATTTGATTTACTGAT	TACCATGAAATGGGTCTCTTATGACTTC	1020		
DB	961	TCCTGGACTCAGCTGTATTTGATTTACTGAT	TACCATGAAATGGGTCTCTTATGACTTC	1020		

QY	1021	CTGAATCTGCCACCTCGACACAGAGCCCTACT	CAAGTTAGCTTATTTCTGCTGCTCT	1080		
DB	1021	CTGAATCTGCCACCTCGACACAGAGCCCTACT	CAAGTTAGCTTATTTCTGCTGCTCT	1080		
QY	1081	GCTCTGTGCCACCTCCACACAGAAATTTAT	TGGCAGCGCAAGGCAAGCTTGCATTTGCTCAT	1140		
DB	1081	GCTCTGTGCCACCTCCACACAGAAATTTAT	TGGCAGCGCAAGGCAAGCTTGCATTTGCTCAT	1140		
QY	1141	CGAGACCTGGAAGAGCAAAAAATCATCTTAT	TAAAGAAAAATGGTGTGTTGTTGCTGAC	1200		
DB	1141	CGAGACCTGGAAGAGCAAAAAATCATCTTAT	TAAAGAAAAATGGTGTGTTGTTGCTGAC	1200		
QY	1201	CTGGGCTTAGCTGTTAAATTCACAGTGCAC	ACAAATGAAGTTGACATACCTTGAACACC	1260		
DB	1201	CTGGGCTTAGCTGTTAAATTCACAGTGCAC	ACAAATGAAGTTGACATACCTTGAACACC	1260		
QY	1261	AGGTGGGCAACAGGCGGTACATGGCTCCAG	AAAGTCTGGAGAGAGCTGAGTAAAAAC	1320		
DB	1261	AGGTGGGCAACAGGCGGTACATGGCTCCAG	AAAGTCTGGAGAGAGCTGAGTAAAAAC	1320		
QY	1321	CATTTCAGCCCTACATCATGGCTGCATCTAC	AGCTTTGGTTTGCATTTGGGAGATG	1380		
DB	1321	CATTTCAGCCCTACATCATGGCTGCATCTAC	AGCTTTGGTTTGCATTTGGGAGATG	1380		
QY	1381	GCCGCTCGCTGTTTACAGAGGAAATCGTG	AGGAATATCAATTAACCATATTAACACATG	1440		
DB	1381	GCCGCTCGCTGTTTACAGAGGAAATCGTG	AGGAATATCAATTAACCATATTAACACATG	1440		
QY	1441	GTGCTTAGTGACCCATCTTATGAAGACATG	CGTGAGTCTGTTGAAACGCTTTCGG	1500		
DB	1441	GTGCTTAGTGACCCATCTTATGAAGACATG	CGTGAGTCTGTTGAAACGCTTTCGG	1500		
QY	1501	CCAATGCTCTTAACCGCTGGAACAGTGAAT	GTCTTCGAGCGCTTTTGAAGCTGATG	1560		
DB	1501	CCAATGCTCTTAACCGCTGGAACAGTGAAT	GTCTTCGAGCGCTTTTGAAGCTGATG	1560		
QY	1561	TCAGNATCTGGGCGCCATAATCCAGCATCC	AGACTCAAGCTTTTGAAGAAAGAT	1620		
DB	1561	TCAGNATCTGGGCGCCATAATCCAGCATCC	AGACTCAAGCTTTTGAAGAAAGAT	1620		
QY	1621	CTCGCAAGATGTTGAATCCAGGATGTAAGA	TTTGAACAAAGCTTTTGAAGAAAGAT	1680		
DB	1621	CTCGCAAGATGTTGAATCCAGGATGTAAGA	TTTGAACAAAGCTTTTGAAGAAAGAT	1680		
QY	1681	TTAGACTGCAAGAAATTCACCGAGGAAGG	GTGGAGTTAGCATGGAATGTCGGCT	1740		
DB	1681	TTAGACTGCAAGAAATTCACCGAGGAAGG	GTGGAGTTAGCATGGAATGTCGGCT	1740		
QY	1741	TGGTTTCAGACTCTCTCTTACCATCTTCA	CAGGCTTAAACAGTAAACCTTTCAGGA	1800		
DB	1741	TGGTTTCAGACTCTCTCTTACCATCTTCA	CAGGCTTAAACAGTAAACCTTTCAGGA	1800		
QY	1801	CTCTGCAAGATGC	1813			
DB	1801	CTCTGCAAGATGC	1813			

RESULT 2

US-09-874-628-1
; Sequence 1, Application US/09874628
; Patent No. 6610513
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, John
; CELESTE, Anthony J.
; THIES, R. Scott
; YAMAJI, No. 6610513oru
; TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genetics Institute Inc.- Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA

Db	1561	TCGAGATGCTGGGGCCCAATAATCCAGCATCCAGACTCACAGCTTTGAGAAATCAAGAAGACG	1620
Qy	1621	CTCCAAAGATGGTGTGAATCCAGGATGTAAGAATTTGACAAAAGTCTTTTGACAAAAGAAAT	1680
Db	1621	CTCCAAAGATGGTGTGAATCCAGGATGTAAGAATTTGACAAAAGTCTTTTGACAAAAGAAAT	1680
Qy	1681	TTAGACTGCAAGAAATTCACCCGAGGAAGGGTGGAGTTAGCATGGACTAGGATGTCGGCT	1740
Db	1681	TTAGACTGCAAGAAATTCACCCGAGGAAGGGTGGAGTTAGCATGGACTAGGATGTCGGCT	1740
Qy	1741	TGGTTTCCAGACTCTCTCCTCTACCATCTTCCACAGGCTGCTTAACAGTAAACCTTTACAGGA	1800
Db	1741	TGGTTTCCAGACTCTCTCCTCTACCATCTTCCACAGGCTGCTTAACAGTAAACCTTTACAGGA	1800
Qy	1801	CTCTGCAGAAATGC	1813
Db	1801	CTCTGCAGAAATGC	1813

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RESULT 3
PCT-US94-10080-1
; Sequence 1, Application PC/TUS9410080
; GENERAL INFORMATION:
; APPLICANT: GENETICS INSTITUTE, INC.
; TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute Inc.- Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10080
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/123,914
; FILING DATE: 17-SEP-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5203-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8260
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1813 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: CFKL-23a
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 61..1656
PCT-US94-10080-1

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Query Match	100.0%	Score 1813;	DB 6;	Length 1813;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1813;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CTAGTGAATCCCCGGGCTCGAGGAATTCTCGGCCGCCACGACCTGGCAATTGGACA	60	

Db	1	CTAGTGGATCCCGGGCTCGAGAAATTCTGCGGCCGCCAGGACACGTCGGAATTGGACA	60
Qy	61	ATGACTCAGCTATACACTTACATCAGATTACTGGGAGCCGTGTCTGTTTCATCATTTCTCAT	120
Db	61	ATGACTCAGCTATACACTTACATCAGATTACTGGGAGCCGTGTCTGTTTCATCATTTCTCAT	120
Qy	121	GTTCAAGGGCAGAACTPAGATAGTATGCTCCATGGTACTGGTATGAAATCAGACGTGGAC	180
Db	121	GTTCAAGGGCAGAACTPAGATAGTATGCTCCATGGTACTGGTATGAAATCAGACGTGGAC	180
Qy	181	CAGNAGAAGCCGNAATGAGAGTGA CGTTAGCACCGAGGACACCTTACCTTCTTAAAA	240
Db	181	CAGAAGAAGCCGNAATGAGAGTGA CGTTAGCACCGAGGACACCTTACCTTCTTAAAA	240
Qy	241	TGCTATTGCTTCAGGACACTGCCAGATGACGCTATTATTAACAATGCACTAACTAATGGC	300
Db	241	TGCTATTGCTTCAGGACACTGCCAGATGACGCTATTATTAACAATGCACTAATGCACTAATGGC	300
Qy	301	CATTGCTTTGCCATTATPAGAAGATGATCAGGGAGAAACCAAGTTAACTTCTGGGTGT	360
Db	301	CATTGCTTTGCCATTATPAGAAGATGATCAGGGAGAAACCAAGTTAACTTCTGGGTGT	360
Qy	361	ATGAAGTATGAAGCTCTGATTTTCAATGCAAGGATTCACAAAAGCCAGCTACGCAGG	420
Db	361	ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACAAAAGCCAGCTACGCAGG	420
Qy	421	ACAATGAATGTTGTGCGACCAATTTGTGCAACCAATATTTCGACGCTACACATGCCCCCT	480
Db	421	ACAATGAATGTTGTGCGACCAATTTGTGCAACCAATATTTCGACGCTACACATGCCCCCT	480
Qy	481	GTGCTTATAGGCCCATTTCTTTGATGGCAGCGTCCGATGGCTGGCTGTGCTCATCTCTATG	540
Db	481	GTGCTTATAGGCCCATTTCTTTGATGGCAGCGTCCGATGGCTGGCTGTGCTCATCTCTATG	540
Qy	541	GCTGTCTGTATTGTGCGCATGATCGTCTTCACAGTCTGTTCTGTTTCAAAATTAATGTT	600
Db	541	GCTGTCTGTATTGTGCGCATGATCGTCTTCACAGTCTGTTCTGTTTCAAAATTAATGTT	600
Qy	601	AAGAGTATCTCAAGCAGAGGTCGTACACCGTGACTTGGAAACAGATGAAGCATTTATT	660
Db	601	AAGAGTATCTCAAGCAGAGGTCGTACACCGTGACTTGGAAACAGATGAAGCATTTATT	660
Qy	661	CCAGTAGGAAATCACTGAAAGACCTGATTGACCAGTCAAAAGCTCTGTTAGTGATCT	720
Db	661	CCAGTAGGAAATCACTGAAAGACCTGATTGACCAGTCAAAAGCTCTGTTAGTGATCT	720
Qy	721	GGATTACCTTTATTGGTTACAGGAACTATTTGCCAAACAGATTGAGTGGTTCGGCAGGTT	780
Db	721	GGATTACCTTTATTGGTTACAGGAACTATTTGCCAAACAGATTGAGTGGTTCGGCAGGTT	780
Qy	781	GGTAAAGGCGGTATGGAGAAATGAGTGGGTAAATGGCTGGTCAAAAGGTGGCTGTC	840
Db	781	GGTAAAGGCGGTATGGAGAAATGAGTGGGTAAATGGCTGGTCAAAAGGTGGCTGTC	840
Qy	841	AAAGTATTTTTTACCCTGAAGAGCTAGCTGGTTTTAGAGAAACAGAAATCTACACAGCG	900
Db	841	AAAGTATTTTTTACCCTGAAGAGCTAGCTGGTTTTAGAGAAACAGAAATCTACACAGCG	900
Qy	901	GTGTTAATCGGTCAATGAAAAATATCTTGGTTTTATAGTGCAGACATTAAGGCACCGGT	960
Db	901	GTGTTAATCGGTCAATGAAAAATATCTTGGTTTTATAGTGCAGACATTAAGGCACCGGT	960
Qy	961	TCCTGGACTCAGCTGATTTGATTACTGATTACCATGAGAAAGGGTCTCTCTATGACTTC	1020
Db	961	TCCTGGACTCAGCTGATTTGATTACTGATTACCATGAGAAAGGGTCTCTCTATGACTTC	1020
Qy	1021	CTGAAATGTGCCACCTTGGACACAGAGCCCTACTCAAGTTAGCTTTATCTGCTGCTGT	1080
Db	1021	CTGAAATGTGCCACCTTGGACACAGAGCCCTACTCAAGTTAGCTTTATCTGCTGCTGT	1080
Qy	1081	GGTCTGTGCCACCTTCCACACAGAAATTTATGGCACGCAAGGCAAGCTGCAATGCTCAT	1140
Db	1081	GGTCTGTGCCACCTTCCACACAGAAATTTATGGCACGCAAGGCAAGCTGCAATGCTCAT	1140

1141 CGAGACCTGAAGACCAAAACATCTTATTAAAGAAAATGGTAGTTCCTGCTATTGCTGAC 1200
1141 CGAGACCTGAAGACCAAAACATCTTATTAAAGAAAATGGTAGTTCCTGCTATTGCTGAC 1200
1201 CTGGGCTAGCTGTTAAATTAACAGAGTGACACAAATGAAGTTGACATACCTTTGAACACC 1260
1201 CTGGGCTAGCTGTTAAATTAACAGAGTGACACAAATGAAGTTGACATACCTTTGAACACC 1260
1261 AGGTGGGACCAAGCGGTACATGGCTCCAGAAGTGTGACAGAGCCCTGAGTAAAC 1320
1261 AGGTGGGACCAAGCGGTACATGGCTCCAGAAGTGTGACAGAGCCCTGAGTAAAC 1320
1321 CATTTCCAGCCCTACATCATGGCTGACATCTACAGCTTTGCTGTTGATCATTTGGAGATG 1380
1321 CATTTCCAGCCCTACATCATGGCTGACATCTACAGCTTTGCTGTTGATCATTTGGAGATG 1380
1381 GCCCGTCGCTGTTATACAGGAGGAATCGTGGAGGAATATCAATTTACCATATTACAACATG 1440
1381 GCCCGTCGCTGTTATACAGGAGGAATCGTGGAGGAATATCAATTTACCATATTACAACATG 1440
1441 GTGCTAGTACCCATCTTATGAAGACATCGCTGAGTCTGTGTGTGTAACCGCTTGGCGG 1500
1441 GTGCTAGTACCCATCTTATGAAGACATCGCTGAGTCTGTGTGTGTAACCGCTTGGCGG 1500
1501 CCAATGCTCTTAACCGCTGGAACAGTGATGATGCTTCCAGCCGTTTTGAGCTGATG 1560
1501 CCAATGCTCTTAACCGCTGGAACAGTGATGATGCTTCCAGCCGTTTTGAGCTGATG 1560
1561 TCAGATGCTGGGCCCCATATCCAGCATCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCT 1620
1561 TCAGATGCTGGGCCCCATATCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCT 1620
1621 CTGCAAGAGTGTGTAATCCAGGATGTAAGAGTTGACAAACAGTTTGGAGAAAGAT 1680
1621 CTGCAAGAGTGTGTAATCCAGGATGTAAGAGTTGACAAACAGTTTGGAGAAAGAT 1680
1681 TTAGACTGCAAGAAATTCACCCAGGAGGTCGAGTTCAGCTTCCAGCTTCCAGCTTCCAGCT 1740
1681 TTAGACTGCAAGAAATTCACCCAGGAGGTCGAGTTCAGCTTCCAGCTTCCAGCTTCCAGCT 1740
1741 TGCTTTCCAGACTCTCTCTCTACCATCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCT 1800
1741 TGCTTTCCAGACTCTCTCTCTACCATCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCT 1800
1801 CTCTGCAAGATGC 1813
1801 CTCTGCAAGATGC 1813

RESULT 4
US-09-382-256-13
; Sequence 13, Application US/09382256A
; Patent No. 6207814
; GENERAL INFORMATION:
; APPLICANT: MIYAZONO, Kohei
; TEN DUKE, Peter
; FRANZEN, Petra
; YAMASHITA, Hidetoshi
; HELDIN, Carl-Henrik
; TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS
; HAVING SERINE THREONINE KINASE DOMAINS,
; AND THEIR USE
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb

COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/382,256A
FILING DATE: 24-Aug-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: No. 6207814ember 17, 1993
APPLICATION NUMBER: GB 9224057.1
FILING DATE: No. 6207814ember 17, 1992
APPLICATION NUMBER: GB 9304677.9
FILING DATE: March 8, 1993
APPLICATION NUMBER: GB 9304680.3
FILING DATE: March 8, 1993
APPLICATION NUMBER: 9311047.6
FILING DATE: May 28, 1993
APPLICATION NUMBER: 9313763.6
FILING DATE: July 2, 1993
APPLICATION NUMBER: 9316099.2
FILING DATE: August 3, 1993
APPLICATION NUMBER: 321344.5
FILING DATE: October 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 6207814man D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5298.1
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2070 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Mouse
FEATURE:
NAME/KEY: CDS
LOCATION: 217..1812
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-382-256-13

Query Match 87.2%; Score 1581.4; DB 3; Length 2070;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 1678; Conservative 0; Mismatches 96; Indels 9; Gaps 3;
QY 39 CAGGACACCTGCGAATTGGACAATGACTCAGCTATACACTTACATCAGATTACTGGGAGC 98
DB 195 CAGGACGCGTGGCAATCAGCAATGACTCAGCTATACACTTACATCAGATTACTGGGAGC 254
QY 99 CTGCTCTGTTTCATCATTTCTCATGTTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGGTAC 158
DB 255 CTGCTCTGTTTCATCATTTCTCATGTTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGGCAGC 314
QY 159 TGGTATGAATCAGAGCTGGACACAGAGGCGGAAATGGAGTACGCTTAGCACCAGCA 218
DB 315 TGGTATGAATCAGAGCTGGACACAGAGGCGGAAATGGAGTACGCTTAGCACCAGCA 374
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DB 375 GGATACCTTGCCTTTCTTAAATGCTATTGCTCAGGACACTGCCAGATGAGCTATTAA 434
QY 279 TAACACATGCATAACTAATGGCCATTGCTTGGCCATTATAGAGAGATGATCAGGAGCA 338
DB 435 TAACACATGCATAACTAATGGCCATTGCTTGGCCATTATAGAGAGATGATCAGGAGCA 494

;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9136099.2
; FILING DATE: 3-August-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9321344.5
; FILING DATE: 15-October-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohlei, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: LUD 5298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2070 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 217..1812
; US-09-395-115-13

Query Match 87.2%; Score 1581.4; DB 3; Length 2070;

Best Local Similarity 94.1%; Pred. No. 0;

Matches 1678; Conservative 0; Mismatches 96; Indels 9; Gaps 3;

QY	39	CAGGACAGCTGCCAATGGCAATGACTCAGCTATACACTTACATCAGATTACTGGGAGC	98
DB	195	CAGGACGCGTGGCAATCAGACAAATGACTCAGCTATACACTTACATCAGATTACTGGGAGC	254
QY	99	CTGCTGTTTCATCATTTCTCATGCTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGGTAC	158
DB	255	CTGCTGTTTCATCATTTCTCATGCTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGGCAC	314
QY	159	TGCTATGAAATCAGACGTGGACACAGAAAGACGCGGAAATGGAGTACGCTTAGCACCAGA	218
DB	315	TGCTATGAAATCAGACTTGGACACAGAAAGACGCGGAAATGGAGTACCTTAGCACCAGA	374
QY	219	GGACACTTACCTTTCTTAAATGCTATTGCTCAGGACACTGCCCAGATGACGCTATTAA	278
DB	375	GGATACCTTTGCGCTTTCTTAAAGTGTATTGCTCAGGACACTGCCCAGATGATGCTATTAA	434
QY	279	TACACATGCATAACTTAATGGCCATTGCTTTGCCATTATAGAAAGAGATGATCAGGGAGA	338
DB	435	TACACATGCATAACTTAATGGCCATTGCTTTGCCATTATAGAAAGAGATGATCAGGGAGA	494
QY	339	AACACAGCTTAACTTCTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTC	398
DB	495	AACACATTAACCTTCTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTC	554
QY	399	ACCAAAAGCCAGCTACGAGGAGCAATAGAAATGTTGTCGGACCAATTTGTGCAACCAATA	458
DB	555	ACCGAAAGCCAGCTACGAGGAGCAATAGAAATGTTGTCGGACCAATTTGTGCAACCAATA	614
QY	459	TTTGACAGCTTACACTGCCCTGCTGTTATAGGCCATTCTTTGATGGCAGCGTCCGATG	518
DB	615	TTTGACAGCTTACACTGCCCTGCTGTTATAGGCCATTCTTTGATGGCAGCATCCGATG	674
QY	519	GCTGGCTGTGCTCATCTCTATGGCTGCTGTATTTGTCGCCATGATCGTCTTCTCCAGCTG	578
DB	675	GCTGGTGTGCTCATTTCCATGCTGCTGTATAGTATGCTATGATCATCTTCTCCAGCTG	734
QY	579	CTTCTGTTACAAACATTTACTGTAAGAGTATCTCAAGCAGAGGTCGTTTACAAACCGTACTT	638
DB	735	TTTCTGTTACAAACATTTACTGTAAGAGTATCTCAAGCAGGCGTCTTCTTACAAACCGTACTT	794

QY	639	GGAAACAGGATGAAGCATTTATTCAGTAGGAGAATCACTGAAAGACCTGATTGACCAGTC	698
DB	795	GGAAACAGGATGAAGCATTTATTCAGTAGGAGAATCACTGAAAGACCTGATTGACCAGTC	854
QY	699	ACAAAGCTCTGGTAGTGGATCTGGATTAACCTTTATTTGGTTTCAGCGAACTATTGCCAAACA	758
DB	855	CCAAAGCTCTGGAGTGGATCTGGATTTGCTTTTATTTGGTTTCAGCGAACTATTGCCAAACA	914
QY	759	GATTCAGATGGTTTCGGCAGGTTGGTAAGGCCGGTATGGAGAGTATGGATGGTAAATG	818
DB	915	GATTCAGATGGTTTCGGCAGGTTGGTAAGGCCGGTATGGAGAGTATGGATGGTAAATG	974
QY	819	GGCTGCTGAAAAAGTGGCTGTCAAAGTATTTTTTACCACCTGAAGAAAGCTAGCTGGTTTAG	878
DB	975	GGCTGCTGAAAAAGTGGCTGTCAAAGTGTTTTTTACCACCTGAAGAAAGCTAGCTGGTTTAG	1034
QY	879	AGAAACAGAAATCTACACAGACGGTGTAAATGGCTCATAGAAATATATCTGGTTTATATAGC	938
DB	1035	AGAAACAGAAATCTACACAGACGGTGTAAATGGCTCATAGAAATATATCTGGTTTATATAGC	1094
QY	939	TGCAGACATTAAGGACACCGGTTCCCTGGACTCAGCTGTATTTGATTACTGATTACCATGA	998
DB	1095	TGCAGACATTAAGGACACCGGTTCCCTGGACTCAGCTGTATTTGATTACTGATTACCATGA	1154
QY	999	GAATGGGTCTCTCTATGACTTCTCTGAAATGTGTCACCTGGACACACAGAGCCCTACTCAA	1058
DB	1155	AAATGGATCTCTCTATGACTTCTCTGAAATGTGTCACCTAGACACACAGAGCCCTACTCAA	1214
QY	1059	GTTAGCTTATCTGCTGCTGCTGTGTCACCTCCACACAGAAATTTATGGCAGCA	1118
DB	1215	GTTAGCTTATCTGCTGCTGCTGTGTCACCTCCACACAGAAATTTATGGTACCCA	1274
QY	1119	AGGCAAGCTGCAATTTGCTCATCGAGACCTGAAGGCAAAACATCTTTATTAAGAAAA	1178
DB	1275	AGGCAAGCTGCAATTTGCTCATCGAGACCTGAAGGCAAAACATCTTTATTAAGAAAA	1334
QY	1179	TGCTAGTTGCTCTATTGCTGACTCGGCTAGCTGTAAATTTCAACAGTGACACAAATGA	1238
DB	1335	TGCAAGTTGCTGTATTGCTGACTGGGCTAGCTGTAAATTTCAACAGTGATACAAATGA	1394
QY	1239	AGTTGACATACCTTTGAAACACACAGGGTGGGCAACAGGGGTACATGGCTCCAGAGTGT	1298
DB	1395	AGTTGACATACCTTTGAAATACACAGGGTGGGCAACAGGGGTACATGGCTCCAGAGTGT	1454
QY	1299	GGACAGAGCTGAGTAAACCAATTTCCAGCCCTACATCATGCTGGCTGACATCTACAGCTT	1358
DB	1455	GGATGAAAGCTGAAATTAACCAATTTCCAGCCCTACATCATGCTGGCTGACATCTATAGCTT	1514
QY	1359	TGCTTTGATCATTTGGGAGATGGCCGCTGCTGTATTACAGGAGGAATCGTGGAGGAATA	1418
DB	1515	TGCTTTGATCATTTGGGAGATGGCCGCTGCTGTATTACAGGAGGAATCGTGGAGGAATA	1574
QY	1419	TCAATTACCATAATTAACAATGGTGCCTAGTGACCCCTCTTATGAAGACATCGTGAGGT	1478
DB	1575	TCAATTACCATAATTAACAATGGTGCCTAGTGACCCCTATGAGGACATCGTGAGGT	1634
QY	1479	CGTGTGTGTAAGCCCTTGGGCCAATCGTCTCTAAACCGCTGGAACAGTGATGAATGTCT	1538
DB	1635	TGTTGTGTGTAAGCCCTTGGGCCAATCGTGTCTAAACCGCTGGAACAGTGATGAATGTCT	1694
QY	1539	TCGAGCCGTTTTTGAAGCTGATGTCAAGATGCTGGGCCCAATTAATCCAGCATCCAGACTCAC	1598
DB	1695	TCGAGCAGTTTTTGAAGCTAATGTCAAGATGTTGGGCCCAATTAATCCAGCTCCAGACTCAC	1754
QY	1599	AGCTTTGAGAAATCAAGAGACGCTCCGAAAGATGTTGAATCCAGGATGTAAGATTG	1658
DB	1755	AGCTTTGAGAAATCAAGAGACACTTGCAGAAATGTTGAATCCAGGATGTAAGATTG	1814
QY	1659	AC-----AACAGTTTTTGAGAAAGATTTAGACTGCAAGAAATTC-----ACCCAGGAAG	1710
DB	1815	ACAATTAACCAATTTTGAGGGAGAAATTTAGACTGCAAGAACTTTCTTCCACCAAGGAATGG	1874

QY 1711 GTGGAGTTAGCAGTGGAGTGGGCTTGGTTTCCAGACTCTCTCTCTACCATCTT 1770
Db 1875 GTGGGATTAGCATGGAAATAGGATGTTGACTTGGTTTCCAGACTCTCTCTCTCTA-CATCTT 1933
QY 1771 CACAGGCTCTAACAGTAACCTTTTCAGGACTCTGCAGAAATGC 1813
Db 1934 CACAGGCTCTAACAGTAACCTTACCGTACTCTACAGAAATAC 1976

RESULT 6
US-08-436-265-13
Sequence 13, Application US/08436265
Patent No. 6316217
GENERAL INFORMATION:
APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
APPLICANT: Franzon, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-October-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. 6316217ember-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 9304680.3
FILING DATE: 8-March-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 9311047.6
FILING DATE: 28-May-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 9136099.2
FILING DATE: 3-August-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-October-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kohlei, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD 5298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2070 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO

; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 217..1812
US-08-436-265-13
Query Match 87.2%; Score 1581.4; DB 3; Length 2070;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 1678; Conservative 0; Mismatches 96; Indels 9; Gaps 3;
QY 39 CAGGACACGTGGGAATTCGACAAATGACTCAGCTATACACTTACATCAGATTAATCTGGGAC 98
Db 195 CAGGACGCGTGGCAATCAGCAATGACTCAGCTATACACTTACATCAGATTAATCTGGGAC 254
QY 99 CTGCTGTTTCATCTTCTCATGTTTCAAGGCGCAGAAATCTAGATAGTATGCTCCATGGTAC 158
Db 255 CTGCTGTTTCATCTTCTCATGTTTCAAGGCGCAGAAATCTAGATAGTATGCTCCATGGCAC 314
QY 159 TGGTATGAAATCAGACGTGGACCGGAAAGCCGGAATGAGAGTGCAGCTTACAGCCAGA 218
Db 315 TGGTATGAAATCAGACGTGGACCGGAAAGCCGGAATGAGAGTGCAGCTTACAGCCAGA 374
QY 219 GGACACCTTACCTTTCTTAAATGCTATGCTCAGGACACTGCCCAGATGAGCTATTTAA 278
Db 375 GGATACCTTGGCTTTCTTAAAGTGTATTTGCTCAGGACACTGCCCAGATGAGCTATTTAA 434
QY 279 TAACACATGCATACTAATGCGCATTTGCTTGGCCATTATAGAAGAGATGATCAGGAGA 338
Db 435 TAACACATGCATACTAATGCGCATTTGCTTGGCCATTATAGAAGAGATGATCAGGAGA 494
QY 339 AACACGTTAACTTCTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTC 398
Db 495 AACACATTAATCTTCTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTC 554
QY 399 ACCAAAGCCGAGCTACCCAGGACAAATAGATGTTGTCGGACCAATTTGTGCAACCAATA 458
Db 555 ACCAAAGCCGAGCTACCCAGGACAAATAGATGTTGTCGGACCAATTTGTGCAACCAATA 614
QY 459 TTTGAGCCTACACTGCCCCCTGCTTATAGGCCCATTTCTTGTATGCGCAGCGTCCGATG 518
Db 615 TTTGAGCCTACACTGCCCCCTGCTTATAGGCCCATTTCTTGTATGCGCAGCGTCCGATG 674
QY 519 GCTGCTGTGCTCATCTCTATGGTGTCTGTATTTGTCGCCATGATCGTCTTCTCCAGCTG 578
Db 675 GCTGCTGTGCTCATCTCTATGGTGTCTGTATTTGTCGCCATGATCGTCTTCTCCAGCTG 734
QY 579 CTTCTGTTACAAACATTAATCTGTAAGAGTATCTCAAGCAGAGGTGCTTACAAACCGTACTT 638
Db 735 CTTTGTCTTAAGCATTTATTTGAAGTATCTCAAGCAGAGGTGCTTACAAACCGTACTT 794
QY 639 GGAACAGGATGAAGCATTTATTTCCAGTAGGAGAAATCATTTGAAGACCTGATTTGACCAATC 698
Db 795 GGAACAGGATGAAGCATTTATTTCCAGTAGGAGAAATCATTTGAAGACCTGATTTGACCAATC 854
QY 699 ACAAGGCTCTGCTAGTGGATCTGGATTAACCTTTTATTTGTTTCCAGCAACTATTTGCCAAACA 758
Db 855 CCAAGGCTCTGGAGTGGATCTGGATTCGCTTTTATTTGTTTCCAGCAACTATTTGCCAAACA 914
QY 759 GATTACAGATGTTTGGCAGAGTTGGTAAAGGCGCGGTATGAGAGAGTATCGATGGGTAAATG 818
Db 915 GATTACAGATGTTTGGCAGAGTTGGTAAAGGCGCGGTATGAGAGAGTATCGATGGGTAAATG 974
QY 819 CCGTGGTCAAAAAGTGGCTGTCAAAGTATTTTACCACTGAAGAGCTAGCTGCTTTAG 878
Db 975 CCGTGGTCAAAAAGTGGCTGTCAAAGTATTTTACCACTGAAGAGCTAGCTGCTTTAG 1034
QY 879 AGAAACAGAAATCTACCAGACGGTGTAAATGCGTCATGAAATATATCTTGGTTTTATAGC 938
Db 1035 AGAAACAGAAATCTACCAGACGGTGTAAATGCGTCATGAAATATATCTTGGTTTTATAGC 1094


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;
; ATTORNEY/AGENT INFORMATION:
; NAME: Hersko, Bart S.
; REGISTRATION NUMBER: 32,572
; REFERENCE/DOCKET NUMBER: 5474R
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (513) 627-0633
; TELEFAX: (513) 627-0260
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2402 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLSCULE TYPE: DNA (genomic)
;
US-08-462-467B-11

Query Match      86.8%; Score 1574.2; DB 3; Length 2402;
Best Local Similarity 94.2%; Pred. No. 0;
Matches 1669; Conservative 0; Mismatches 93; Indels 9; Gaps 3;

QY 51 GAATTGGCAATGACTCAGCTATACACTTACATCAGATTACTGGAGGCTGTCTGTTCAT 110
Db 1 GAAATCAGACAATGACTCAGCTATACACTTACATCAGATTACTGGAGGCTGTCTGTTCAT 60

QY 111 CATTTCTCATGTTCAAGGCGAGAACTAGATAGTATGCTCCATGGTGTGCTATGAATC 170
Db 61 CATTTCTCATGTTCAAGGCGAGAACTAGATAGTATGCTCCATGGCAGCTGGTATGAATC 120

QY 171 AGACGTGGACCAAGAAAGCCGGAATGGAGTGACGTTAGCACAGAGGACACCTTACC 230
Db 121 AGACATTGGACCAAGAAAGCCGGAATGGAGTGACTTATAGCACAGAGGATACCTTACC 180

QY 231 TTTCCTTAAATGCTATTGCTCAGGACACTGCCAGATGATGCTATTAATACACATGCAT 290
Db 181 TTTCCTTAAATGCTATTGCTCAGGACACTGCCAGATGATGCTATTAATACACATGCAT 240

QY 291 AACTAATGCCATTCGTTTGCATTTAGCAATATAGAAAGATGATCAGGAGAAACACGTTAAC 350
Db 241 AACTAATGCCATTCGTTTGCATTTAGCAATATAGAAAGATGATCAGGAGAAACACATTAAC 300

QY 351 TTCTGGGTGTATGAAGTGAAGGCTCTGATTTTCAATGCAAGGATTCACCAAAAGCCCA 410
Db 301 TTCTGGGTGTATGAAGTGAAGGCTCTGATTTTCAATGCAAGGATTCACCGAAAGCCCA 360

QY 411 GCTACGACGACAATAGAAATGTTGTCGACCAATTTGTGCAACCAATATTTGACGCTTAC 470
Db 361 GCTACGACGACAATAGAAATGTTGTCGACCAATTTGTGCAACCAATATTTGACGCTTAC 420

QY 471 ACTGCCCCCTGTGCTTATAGGCCCATCTTTGATGCGCAGCGTCGATGGCTGGCTGTGCT 530
Db 421 ACTGCCCCCTGTGCTTATAGGCCCATCTTTGATGCGCAGCATCCGATGGCTGGCTGTGCT 480

QY 531 CATCTCTATGGCTGTCTGATTTGTCGCCATGATCGTCTTCTCCAGTGTCTTCTGTACAA 590
Db 481 CATTTCCATGGCTGTCTGATATAGTTGCTATGATCATCTTCTCCAGTGTCTTGTGTATAA 540

QY 591 ACATTCATGTAAGAGTATCTCAAGCAGAGGTCGTTCAACCGTGTACTGGAAACAGGATGA 650
Db 541 GCATTTATTGTAAGAGTATCTCAAGCAGAGGTCGTTTACAACCGTGTATTTGGAACAGGATGA 600

QY 651 AGCATTTATTCCAGTAGGAGATCACTGAAAGACCTGATTGACCACTCACAAGCTCTGG 710
Db 601 AGCATTTATTCCAGTAGGAGATCACTGAAAGACCTGATTGACCACTCACAAGCTCTGG 660

QY 711 TAGTGGATCTGGATTACCTTTTATTTGTTTCCAGGAACTATTGCAAAACAGATTTCAGATGGT 770
Db 661 GAGTGGATCTGGATTACCTTTTATTTGTTTCCAGGAACTATTGCAAAACAGATTTCAGATGGT 720

QY 771 TCGGCGAGGTTGGTAAGGCGCGGTATGGAGAGTATGGATGGGTAAATGGCGTGGTGAATA 830
Db 721 TCGGCGAGGTTGGTAAGGCGCGGTATGGAGAGTATGGATGGGTAAATGGCGTGGTGAATA 780

QY 831 AGTGGCTGTCAAAGTATTTTTTACCACCTCAAGAACTAGCTGGTTTATAGAGAAACAGAAAT 890
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Db 781 AGTGGCTGTCAAAGTATTTTTTACCACCTGAAGAACTAGCTGGTTTATAGAGAAACAGAAAT 840
QY 891 CTACCAGACGGTGTAAATCGCGTCATGAAAAATATATCTTGGTTTATATAGCTGCAGACATTAA 950
Db 841 CTACCAGACGGTGTAAATCGCGTCATGAAAAATATATCTTGGTTTATATAGCTGCAGACATTAA 900
QY 951 AGGCACCGGTTCTCTGGACTCAGCTGTATTTGATTAATCTGATTACCATGAGAAATGGGTCTCT 1010
Db 901 AGGCACCTGGTTCTCTGGACTCAGCTGTATTTGATTAATCTGATTACCATGAGAAATGGATCTCT 960
QY 1011 CTATGACTTCTCTGAAATGTCACCTCGACACAGAGCCCTACTCAAGTTAGCTTATTC 1070
Db 961 CTATGACTTCTCTGAAATGTCACCTCGACACAGAGCCCTACTCAAGTTAGCTTATTC 1020
QY 1071 TGCTGCTGTGTGCTGTGCTCCACCTCCACACAGAAATTTATGGCAGCAGCAAGCCCTGC 1130
Db 1021 TGCTGCTGTGTGCTGTGCTCCACCTCCACACAGAAATTTATGGTACCCAGGGAAGCCCTGC 1080
QY 1131 AATTGCTCATCGAGACCTGAAAGAGCAAAAAATCCCTTATTAAGAAAAATGGTAGTTGCTG 1190
Db 1081 AATTGCTCATCGAGACCTGAAAGAGCAAAAAATCCCTTATTAAGAAAAATGGAAGTTGCTG 1140
QY 1191 TATTGCTGACCTGGGCTAGCTGTAAATTTCAACAGTGCACACAAATGAAGTTGACATACC 1250
Db 1141 TATTGCTGACCTGGGCTAGCTGTAAATTTCAACAGTGCATCAAAATGAAGTTGACATACC 1200
QY 1251 CTTGAACACCAAGGTTGGGCACAGCGGTACATGCTCCAGAAAGTCTGGAGCAGAGCCT 1310
Db 1201 CTTGAATACCAAGGTTGGGCACCAAGCGGTACATGGCTCCAGAAAGTCTGGATGAAAGCCT 1260
QY 1311 GAGTAAAAACCAATTTCCAGCCCTACATCATGGCTGACATCTACAGCTTTGGTTGATCAT 1370
Db 1261 GAATAAAAACCAATTTCCAGCCCTACATCATGGCTGACATCTATAGCTTTGGTTGATCAT 1320
QY 1371 TTGGGAGATGCGCGTCTGCTTATTAAGAGGAGGATCGTGGAGGAATATCAATTAACATA 1430
Db 1321 TTGGGAAATGCGTCTGCTTATTAAGAGGAGGATCGTGGAGGAATATCAATTAACATA 1380
QY 1431 TTACAACATGCTGCTAGTGACCCCATCTTATGAAGACATGGGTGAGGTGCTGTGTGAA 1490
Db 1381 TTACAACATGCTGCTAGTGACCCCATCTTATGAAGACATGGGTGAGGTGCTGTGTGAA 1440
QY 1491 ACGTTTGGGCAATTCGCTCTTAACCGCTGAAACAGTGAATGAATGCTTTCGAGCCGTTTT 1550
Db 1441 ACGTTTGGGCAATTCGCTCTTAACCGCTGAAACAGCGATGAATGCTTTCGAGCAGTTTT 1500
QY 1551 GAAGCTGATGTCAGAAATGCTGGGCCCAATAATCCAGCATCCAGACTCCAGACTTTTGAAT 1610
Db 1501 GAAGCTGATGTCAGAAATGCTGGGCCCAATAATCCAGCTCCAGACTCCAGACTTTTGAAT 1560
QY 1611 CAAGAAGACGCTCGCAAGATGCTTGAATCCAGGATGTAAGATTTTGAC----AAACAG 1666
Db 1561 CAAGAAGACCTTCGCAAAATGCTTGAATCCAGGATGTAAGATTTTGAATTTAACA 1620
QY 1667 TTTTGAGAAAGAAATTTAGACTGCAAGAAATTC----ACCCGAGGAGGTTGGAGTTAGCA 1722
Db 1621 TTTTGAGGAGAAATTTAGACTGCAAGAAATTCCTTCAACCCAGGAATGGGTGGGATAGCA 1680
QY 1723 TGGACTAGGATGCTGGCTTGGTTTCCAGACTCTCTCTCTACCATCTTTCACAGGCTGCTA 1782
Db 1681 TGGAAATAGGATGTTGACTTGGTTTCCAGACTCTCTCTCTCTA-CATCTTTCACAGGCTGCTA 1739
QY 1783 ACAGTAAACCTTTTCAGGACTCTGCAGAAATGC 1813
Db 1740 ACAGTAAACCTTACCGCACTCTACAGAAATC 1770
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RESULT 10
US-08-158-735A-3
; Sequence 3, Application US/08158735A
; Patent No. 6248554
; GENERAL INFORMATION:

APPLICANT: COOK, JONATHAN S.
APPLICANT: CORREA, PAUL E.
APPLICANT: KOENIG, BETH B.
APPLICANT: ROSENBAUM, JAN S.
APPLICANT: TING, JERRY
TITLE OF INVENTION: DNA SEQUENCE CODING FOR A BMP RECEPTOR
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESS: THE PROCTER & GAMBLE COMPANY
STREET: 11810 EAST MIAMI RIVER ROAD
CITY: ROSS
STATE: OH
COUNTRY: USA
ZIP: 45061
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,735A
FILING DATE: 24-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CORSTANJE, BRAHM J.
REGISTRATION NUMBER: 34,804
REFERENCE/DOCKET NUMBER: 5088
TELECOMMUNICATION INFORMATION:
TELEPHONE: (513) 627-2858
TELEFAX: (513) 627-0260
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2402 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: join(11...1606)

Query Match 86.8%; Score 1574.2; DB 3; Length 2402;

Best Local Similarity 94.2%; Pred. No. 0;

Matches 1669; Conservative 0; Mismatches 93; Indels 9; Gaps 3;

Qy	471	ACTGCCCCCTGTGTTATAGGCCCAATCTTTGATGGCAGCGTCCGATGGCTGGCTGCT	530
Db	421		
Qy	531	CATCTCTATGGCTGTCTGTATTTGTCGCATGATCGTCTTCTCAGCTGCTTCTGTACAA	590
Db	481		
Qy	591	ACATTACTGTAAAGAGTATCTCAAGCAGAGCGTGTACAAACCGTGACCTTGGAAACAGGATGA	650
Db	541	GCATTATTGPAAGAGTATCTCAAGCAGGGGTCTGTACAAACCGTATTTGGAACAGGATGA	600
Qy	651	AGCATTATTCCAGTAGGAGATCACTGAAAGACCTGATTGACAGCTCAAAAGCTCTGG	710
Db	601	AGCATTATTCCAGTAGGAGATCACTGAAAGACCTGATTGACAGCTCCCAAGCTCTGG	660
Qy	711	TAGTGGATCTGGATTACCTTTTATTTGTTAGCGAACTATTTGCCAAACAGATTACAGATGGT	770
Db	661	GAGTGGATCTGGATTGCTTTTATTTGTTTACGCGAACTATTTGCCAAACAGATTACAGATGGT	720
Qy	771	TCGGCAGGTTGGTAAAGGCGGTATGGAGAAATGATGGATGGGTAAATGGCGTGGTGA	830
Db	721	TCGGCAGGTTGGTAAAGGCGGTATGGAGAAATGATGGATGGGTAAATGGCGTGGTGA	780
Qy	831	AGTGGCTGTCAAAAGTATTTTACCACTGAAGAGCTAGCTGGTGTAGAGAAACAGAAAT	890
Db	781	AGTGGCTGTCAAAAGTATTTTACCACTGAAGAGCTAGCTGGTGTAGAGAAACAGAAAT	840
Qy	891	CTACCAAGCGTGTAAATGGCTCATGAAATATACCTTGGTGTATAGCTCGACACATTA	950
Db	841	CTACCAAGCGTGTAAATGGCTCATGAAATATACCTTGGTGTATAGCTCGACACATTA	900
Qy	951	AGGCACGGTTCCTGACCTCAGCTGTATTTGATTACTGATTACCATGAGATCGGCTCT	1010
Db	901	AGGCACGGTTCCTGACCTCAGCTGTATTTGATTACTGATTACCATGAGATCGGCTCT	960
Qy	1011	CTATGACTTCTGAAATGTCCACCTGGACACACAGAGCCCTACTCAAGTTAGCTTATTC	1070
Db	961	CTATGACTTCTGAAATGTCCACCTGGACACACAGAGCCCTACTCAAGTTAGCTTATTC	1020
Qy	1071	TGCTGCTGTGCTGTGCACTCCACACAGAAATTTATGGCAGCAAGGCAAGCTGCT	1130
Db	1021	TGCTGCTGTGCTGTGCACTCCACACAGAAATTTATGGTACCCCAAGGCAAGCTGCT	1080
Qy	1131	AATTGCTCATCGAGACCTGAAGCAGAAACACCTTTATTAAGAAATAGTGTGCTG	1190
Db	1081	AATTGCTCATCGAGACCTGAAGCAGAAACACCTTTATTAAGAAATAGTGTGCTG	1140
Qy	1191	TATTGCTGACCTGGGCTAGCTGTAAATTTCAACAGTGACACAAATGAAAGTTGACATACC	1250
Db	1141	TATTGCTGACCTGGGCTAGCTGTAAATTTCAACAGTGATACAAATGAAAGTTGACATACC	1200
Qy	1251	CTTGAAACACAGGGTGGGCAACAGGGCGGTACATGGCTCCAGAAAGTCTCGAAGAGCTT	1310
Db	1201	CTTGAAATACAGGGTGGGCAACAGGGCGGTACATGGCTCCAGAAAGTCTCGAAGAGCTT	1260
Qy	1311	GAGTAAACCAATTTCCAGCCCTACATCATGCTGACATCTACAGCTTTGGTTGATCAT	1370
Db	1261	GAGTAAACCAATTTCCAGCCCTACATCATGCTGACATCTATAGCTTTGGTTGATCAT	1320
Qy	1371	TTGGGAGATGGCCCGCTGCTGATTATACAGGAGAAATCGTGGAGGAATATCAATACCATTA	1430
Db	1321	TTGGGAAATGGCTGCTGCTGTTGTTATACAGGAGGAATCGTGGAGGAATATCAATACCATTA	1380
Qy	1431	TTTCAACATGGTGCCTAGTGACCCATCTTTATGAAGACATGCGGTAGGTGCTGTGTGAA	1490
Db	1381	TTTCAACATGGTGCCTAGTGACCCATCTTATGAGGACATGCGGTAGGTGCTGTGTGAA	1440
Qy	1491	ACGCTTGGGGCAATCGTCTCTAAACCGCTGGACAGTGAATGCTTTCGAGCCGTTTT	1550
Db	1441	ACGCTTGGGGCAATCGTCTCTAAACCGCTGGACAGTGAATGCTTTCGAGCCGTTTT	1500
Qy	1551	GAAGCTGATGTGAGAAATGCTGGGCCCAATATCCAGCATCCAGACTCAGACTTTTGAGAAAT	1610

Db 1501 GAAGCTAATGTGAGAAATTTGGCCCATATATCAGGCTCCAGACTCCAGACTTTGAGAAAT 1560
Qy 1611 CAAGAAGACGCTCGCAAAAGATGGTTGAATCCCAAGATGTAAGAATTTGAC----AAACAG 1666
Db 1561 CAAGAAGACACTTGGCAAAATGGTTGAATCCCAAGATGTAAGAATTTGACAAATTAACAA 1620
Qy 1667 TTTTGAGAAAGATTTAGACTGCAAGAAATTC-----ACCGAGGAAGGTTGAGTTAGCA 1722
Db 1621 TTTTGAGGAGAAATTTAGACTGCAAGAAATTCCTTCACCCCAAGGAATGGGTGGGATTTAGCA 1680
Qy 1723 TGGACTAGGATGCGGCTTGGTTTCAGACTCTCTCTCTACCATCTTCACAGGCTGCTA 1782
Db 1681 TGGAAATAGATGTTGACTTGGTTTCAGACTCTCTCTCTA-CACTTCACAGGCTGCTA 1739
Qy 1783 ACAGTAAACCTTTCAGGACTCTGCAGAAATGC 1813
Db 1740 ACAGTAAACCTTACCGCACTCTACAGAATAC 1770

RESULT 11

US-08-334-179A-11
; Sequence 11, Application US/08334179A
; Patent No. 6306622
; GENERAL INFORMATION:
; APPLICANT: ROSENBAUM, JAN S.
; APPLICANT: NOHNO, TSUTOMU
; TITLE OF INVENTION: CDNA ENCODING A BMP TYPE II RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE PROCTER AND GAMBLE COMPANY
; STREET: 11810 EAST MIAMI RIVER ROAD
; CITY: ROSS
; STATE: OH
; COUNTRY: US
; ZIP: 45061
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.30, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICANT NUMBER: US/08/334,179A
; FILING DATE: 04-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CORSTANJE, BRAHM J.
; REGISTRATION NUMBER: 34,804
; REFERENCE/DOCKET NUMBER: 5473
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 513-627-2858
; TELEFAX: 513-627-0260
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2402 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(11..1606)
US-08-334-179A-11

Query Match 86.8%; Score 1574.2; DB 3; Length 2402;
Best Local Similarity 94.2%; Pred. No. 0;
Matches 1669; Conservative 0; Mismatches 93; Indels 9; Gaps 3;
Qy 51 GAATTGGACAATGACTCAGCTATACACTTACATTCAGATTCAGGAGCCTGTCTGTTCAT 110
Db 1 GAATCAGACAATGACTCAGCTATACACTTACATTCAGATTCAGGAGCCTGTCTGTTCAT 60
Qy 111 CATTCTCATGTTCAGGGCAGAAATCTAGATAGTATGCTCCATGGTACTGGTATGAAATC 170

Db 61 CATTCTCATGTTCAGGGCAGAAATCTAGATAGTATGCTCCATGGCACTGGTATGAAATC 120
Qy 171 AGACGTGGACCAAGAAAGCGGAAATGAGCTGACGTGTAGCACACAGAGACACCTTACC 230
Db 121 AGACTTGGACCAAGAAAGCGGAAATGAGCTGACCTTTAGCACACAGAGATACCTTGCC 180
Qy 231 TTTCTTAAATGCTATTGCTCAGGACACTGCCCAGATGATGCTATTATAACACATGCAT 290
Db 181 TTTCTTAAAGTCTATTGCTCAGGACACTGCCCAGATGATGCTATTATAACACATGCAT 240
Qy 291 AACTAATGSCCAATGCTTTGCCATTATAGAAGAAGATGATCAGGAGAGAAACACGTTAAC 350
Db 241 AACTAATGSCCAATGCTTTGCCATTATAGAAGAAGATGATCAGGAGAGAAACACATTAAC 300
Qy 351 TTCTGGGTGTATGAAGGTCTGATTTTCAATGCAAGGATTTCAACAAAAGCCCCA 410
Db 301 TTCTGGGTGTATGAAGGTCTGATTTTCAATGCAAGGATTTCAACAAAAGCCCCA 360
Qy 411 GCTACGCGAGGACAATAGAAATGTTGCGGACCAATTTTGTGCAACCAATATTTCAGGCTAC 470
Db 361 GCTACGCGAGGACAATAGAAATGTTGCGGACCAATTTTGTGCAACCAAGTATTTCAGGCTAC 420
Qy 471 ACTGCCCCCTGTCGTTATAGGCCCAATCTTTGATGCGCAGCGTCCGATGSGCTGCTGCT 530
Db 421 ACTGCCCCCTGTCGTTATAGGTCCTTTTGTATGCGCAGCTCCGATGSGCTGCTGCTGCT 480
Qy 531 CATCTCTATGGCTGCTGTTATTTGCGCCATGATCGCTCTTCTCCAGCTGCTCTCTGTACAA 590
Db 481 CATTTCATGGCTGCTGTTATAGTTGCTATGATCATCTTCTCCAGCTGCTTTTGTATAA 540
Qy 591 ACATTACTGTAAGAGTATCTCAAGCAGAGGTGCTTTACAAACCGTACTTGGAAACAGGATGA 650
Db 541 GCATTATTGTAAGAGTATCTCAAGCAGAGGTGCTTTACAAACCGTACTTGGAAACAGGATGA 600
Qy 651 AGCATTTATTCAGTAGGAGATCACTGAAGACCTGATTGACCACTGACCAAGCTCTCG 710
Db 601 AGCATTTATTCAGTAGGAGATCACTGAAGACCTGATTGACCACTGACCAAGCTCTCG 660
Qy 711 TAGTGGATCTGGATTAACCTTTTATTTGTTTCAGGAACTATTGCAACACAGATTCAGATGT 770
Db 661 GAGTGGATCTGGATTAACCTTTTATTTGTTTCAGGAACTATTGCAACACAGATTCAGATGT 720
Qy 771 TCGCAGGTTGGTAAGGGCGGTATGGAAGATGATGGATGGGTAATAGCGGTGGTGAATA 830
Db 721 TCGCAGGTTGGTAAGGGCGGTATGGAAGATGATGGATGGGTAATAGCGGTGGTGAATA 780
Qy 831 AGTGGCTGCTCAAAGTATTTTACCACCTGAAGACCTAGCTGCTTTAGAGAAACAGAAAT 890
Db 781 AGTGGCTGCTCAAAGTATTTTACCACCTGAAGACCTAGCTGCTTTAGAGAAACAGAAAT 840
Qy 891 CTACCAGAGCGGTGTTAATGCGCTCATGAAAAATATCTTGGTTTTATAGCTGCAGACATTA 950
Db 841 CTACCAGAGCGGTGTTAATGCGCTCATGAAAAATATCTTGGTTTTATAGCTGCAGACATTA 900
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Db 901 AGGCACCGGTTCTCGGACTCAGCTGTATTGATTAATGATTAACATGAGATGGGTCTCT 960
Qy 1011 CTATGACTTCCTGAAATGTCACCTCGACACAGAGCCCTACTCAAGTTAGCTTATTC 1070
Db 961 CTATGACTTCCTGAAATGTCACCTCGACACAGAGCCCTACTCAAGTTAGCTTATTC 1020
Qy 1071 TGCTGCCTGTGCTGTGCCACCTCCACACAGAAAAATTTATGCGACGCAAGCAAGCCTGC 1130
Db 1021 TGCTGCCTGTGCTGTGCCACCTCCACACAGAAAAATTTATGTTACCCCAAGGAGCCTGC 1080
Qy 1131 AATTGCTCATGAGACCTGGAAGAGCAAAAAATTCCTTATTAAAGAAAAATGGTATGCTG 1190
Db 1081 AATTGCTCATGAGACCTGGAAGAGCAAAAAATTCCTTATTAAAGAAAAATGGTATGCTG 1140
Qy 1191 TATTGCTGACCTGGGCTAGCTGTTAAATTCAAACAGTGCACAAATGAAGTTGACATACC 1250

Db 1141 TATTGCTGACCTGGCCCTAGCTGTTTAAATTCACAGTGATACAAATGAAGTTGACATACC 1200
QY 1251 CTTGAACACCAAGGTGGGCACAGCGGTGTACATGCTCCAGAAAGTGTGGACGAGAGCCT 1310
Db 1201 CTTGAATACCAAGGTGGGCACAGCGGTGTACATGCTCCAGAAAGTGTGGATGAAGCCT 1260
QY 1311 GAGTAAACCAATTTCCAGCCCTACATCATCGCTGACATCTATAGCTTTGGTTTGATCAT 1370
Db 1261 GAATAAAACCAATTTCCAGCCCTACATCATCGCTGACATCTATAGCTTTGGTTTGATCAT 1320
QY 1371 TTGGAGATGCGCGTCTGTATTTACAGGAGGATCGTGAGGAATATCAATTACCATA 1430
Db 1321 TTGGAAATGCGTCTGTATTTACAGGAGGATCGTGAGGAATATCAATTACCATA 1380
QY 1431 TTCAACATGCTGCTAGTGACCCATCTTATCAAGACATGCTGAGGTGCTGTGTGAA 1490
Db 1381 TTCAACATGCTGCTAGTGACCCATCTTATGAGACATGCTGAGGTGCTGTGTGAA 1440
QY 1491 ACGTTGGCGCAATCGTCTTAAACCGCTGGAACAGTGATGAATGTCTTCGAGCGTTT 1550
Db 1441 ACGTTGGCGCAATCGTCTTAAACCGCTGGAACAGTGATGAATGTCTTCGAGCGTTT 1500
QY 1551 GAAGCTGATGTCAGAAATGCTGGGCCCATTAATCCAGATCCAGACTCAGCTTTGAGAA 1610
Db 1501 GAAGCTAATGTCAGAAATGCTGGGCCCATTAATCCAGACTCCAGACTCAGCTTTGAGAA 1560
QY 1611 CAAGAAGACGCTCGCAAGATGTTGAATCCAGATGTTAAAGATTTGAC----AAACAG 1666
Db 1561 CAAGAGACACTTCGAAATGTTGAATCCAGATGTTAAAGATTTGACAAATTAACAA 1620
QY 1667 TTTTGAGAGAAATTTAGACTGCAAGAAATTC----ACCCGAGGAAGGTGGAGTTAGCA 1722
Db 1621 TTTTGAGGAGAAATTTAGACTGCAAGAAATTC----ACCCGAGGAAGGTGGAGTTAGCA 1680
QY 1723 TGGACTAGGATGCGGTGTTTCCAGACTCTCTCTCTACCATCTTCACAGCTGCTA 1782
Db 1681 TGGAAATAGGATGTTGACTTGGTTTCCAGACTCTCTCTCTA-CATCTTCACAGCTGCTA 1739
QY 1783 ACAGTAAACCTTTCAGAGACTCTGAGAAATGC 1813
Db 1740 ACAGTAAACCTTTCAGAGACTCTGAGAAATGC 1770

RESULT 12

US-08-158-735A-1
; Sequence 1, Application US/08158735A
; Patent No. 6248554
; GENERAL INFORMATION:
; APPLICANT: COOK, JONATHAN S.
; APPLICANT: CORREA, PAUL E.
; APPLICANT: KOENIG, BETH B.
; APPLICANT: ROSENBAUM, JAN S.
; APPLICANT: TING, JERRY
; TITLE OF INVENTION: DNA SEQUENCE CODING FOR A BMP RECEPTOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE PROCTER & GAMBLE COMPANY
; STREET: 11810 EAST MIAMI RIVER ROAD
; CITY: ROSS
; STATE: OH
; COUNTRY: USA
; ZIP: 45061
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/158,735A
; FILING DATE: 24-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CORSTANJE, BRAHM J.

; REGISTRATION NUMBER: 34,804
; REFERENCE/DOCKET NUMBER: 5088
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (513) 627-2858
; TELEFAX: (513) 627-0260
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2056 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(291..1790)
; US-08-158-735A-1

Query Match 78.6%; Score 1424.4; DB 3; Length 2056;
Best Local Similarity 90.3%; Pred. No. 0;
Matches 1584; Conservative 0; Mismatches 76; Indels 94; Gaps 2;
QY 39 CAGGACACGTCGCAATTTGGACAAATGACTCAGCTATACACTTACATCAGATTACTCTGGGAGC 98
Db 269 CAGGACGCTGCGCAATGACAAATGACTCAGCTATACACTTACATCAGATTACTCTGGGAGC 328
QY 99 CTGCTGTTTCATCATTTCTCATGTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGTGAC 158
Db 329 CTGCTGTTTCATCATTTCTCATGTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGGCAC 388
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Db 389 TGTATGAAATCAGACGTGGACCCAGAAAGACGCGGAAATGGAAGTGAACGTTAGCACGAGA 448
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QY 279 TAACACATGCATAAATAATGGCCATTGCTTGGCAATTATAGAAGAAAGATGATCAGGGAGA 338
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QY 339 AACCAAGTTAACTTTCTGGGTGATGAAGTATGAAGCTCTGATTTTCAATGCAAGGATTC 398
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Db 629 ACCAAAGCCGCTACGACGAGCAATAGAAATGCTTGGCAACCAATTTGTCGAACCAATA 688
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QY 519 GCTGGCTGTGCTCATCTCTATGGCTCTGTATGTCGCAATGATCGTCTTCTCCAGCTG 578
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QY 639 GGAACAGGATGAAGCATTTATTTCAGTAGGAGATCACTGAAAGACTGATTTGACCAAGTC 698
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Db 929 CCAAGCTCTGCGAGTGGATCTGGATTTGCTTTATTTGTTTACAGCAACTATTGCGCAACA 988
QY 759 GATTCAGATGCTTCGCGAGCTTGGTAAAGGCCGTTATGGAAGATGATGATGGTAAATG 818
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QY 819 GCGTGTGAAAAAAGTGGCTGTCAAAGTATTTTTTACCACCTGAAGAGCTAGCTGGTTTAG 878

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Db 1049 GCCTGGTGAAGAGTGGCTGTCAAGTGTCTTTTACCACCTGAGAAGCTAGCTGGTTTAG 1108
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QY 999 GAATGGTCTCTCTATGACTCTCTGAAATGTGCCACCTGGACACAGAGCCCTACTCAA 1058
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QY 1359 TGGTTTGTATCATTTGGAGATGCCGCTGCTGTTATTCAGAGGAGGAAATCGTGAGGAATA 1418
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QY 1479 CGTGTGTGTGAACGCTTGGGCGCAATCGTCTTAACCGCTGGAACAGTGATGAA----- 1533
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QY 1569 CTGGGCCCCATATTCAGACATCCAGACTCAGAGCTTTGAGAAATCAAGAAAGACGCTCGCAAA 1628
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Db 1949 AATGGTTGAATCCAGAGATGAAGATTTGACAAATTTTGAAGGAGATTTTAG 2008
QY 1685 ACTGCAAGAAATTC 1698
Db 2009 ACTGCAAGAAATTC 2022
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RESULT 13
US-08-481-337A-5
; Sequence 5, Application US/08481337A
; Patent No. 5863738
; GENERAL INFORMATION:

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APPLICANT: TEN DIJKE, Peter  
APPLICANT: HEIDIN, Carl-Henrik  
APPLICANT: MIYAZONO, Kohel  
APPLICANT: SAMPATH, Kuber T.  
TITLE OF INVENTION: Morphogenic Protein-Specific Cell  
SURFACE RECEPTORS AND USES THEREOF  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Testa, Hurwitz & Thibault  
STREET: 125 High St.  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/481,337A  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MEYERS, Thomas C.  
REGISTRATION NUMBER: 36,989  
REFERENCE/DOCKET NUMBER: CRP-097CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2932 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 310..1905  
OTHER INFORMATION: /product= "Human ALK3"  
US-08-481-337A-5
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Query Match 76.5%; Score 1387; DB 2; Length 2932;  
Best Local Similarity 87.8%; Pred. No. 0;  
Matches 1561; Conservative 0; Mismatches 205; Indels 11; Gaps 4;  
QY 39 CAGGACAGCTGGCAATTTGACAAATGACCTACAGCTATACATCAGAGTTACTGGGAGC 98  
Db 288 CAGGAAACATTAACAATTTGAACAAATGACCTACAGCTATACATTTACATCAGAGTTACTGGGAGC 347  
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Db 348 CTATTTGTTTCATCTTCTCGTGTTCAGGACAGAAATCTGGATAGTATGCTTTCATGGCAC 407  
QY 159 TGGTATGAAATCAGAGCTGGACCAAGAGAGCGGAAATTTGAGAGTGAACCTTAGCACCAGA 218  
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Db 528 TAAACATGCATTAACCTTCTGGGTGATGAAGTATGAAGGATTCGATTTTCAATGAAGGATTC 647  
QY 339 AACCAAGTAACTTCTGGGTGATGAAGTATGAAGGCTCTGATTTTCAATGAAGGATTC 398  
Db 588 AACCAAGTAACTTCTGGGTGATGAAGTATGAAGGATTCGATTTTCAATGAAGGATTC 647  
QY 399 ACCAAAGCCAGCTACGAGGACAAATGAGTGTTCGAGCAAAATTTTGTGCAACCAATA 458
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Db 648 TCCAAAAGCCAGCTACGCCGGAACAATAGATGTTGTCGACCAAAATTTATGTAACCAAGTA 707
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Db 708 TTTGCAACCAACACTGCCCTGCTGCTATAGGTCGGTTTTTGTGCGAGCATTTGATG 767
Qy 519 GCTGGCTGTCTCATCTCTATGCTGTCTGTATTTGTCGCCATGATCTCTTCTCCAGCTG 578
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Qy 639 GGAACAGAGTAAGCATTTATTTCCAGTAGAGATCACTCAAGACCTGATTGACAGATC 698
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Qy 699 ACAAGCTCTGGTAGTGATCTGGATTTACCTTTATTTGTTTACGCGAACTATTGCCAAACA 758
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Db 1548 GGACGAAGCTTGAACCAAAACCACTTCCAGCCCTACATCATGGCTGACATCTTACAGCTT 1607
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Db 1668 CCAATTGCCATATTACAAATGTTACCGAGTGATCGTTCATACGAAGATATGCTGAGGT 1727
Qy 1479 CGTGTGTGAACCGTTGCGGCAATCGTCTCTAAACCGCTGGAACAGTGATGATGCT 1538
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Qy 1539 TCAGACCGTTTTGAAGCTGATGTCAGAATGCTGGGCCCAATATCCAGCATCCAGACTCAC 1598
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Qy 1599 AGCTTTGAGAATCAAGAAGACGCTCGCAAGATGTTGAATCCAGGATGTAAGAATTTG 1658
Db 1848 AGCATTTGAGAATTTAAGAAGACGCTTCCCAAGATGTTGAATCCCAAGATGTAAGAATCTG 1907
Qy 1659 A-----CAACAGTTTTGAGAAGAAATTTAGACTGCAAGAA-----ATTACCCGAGGAAG 1709
Db 1908 ATGTTTAAACCAATCGGAGGAGAACTCTAGACTGCAAGAACTGTTTTTATCCCATGGCATG 1967
Qy 1710 GGTGGAGTTAGCATGACT-AGGATGTCGCTTGGTTTTCCAGACTCTCTCTC- TACCA 1767
Db 1968 GGTGGAATTAGAGTGAATGAAGATGTTAACTTGGTTCTCAGACTCTTTCTTCACTACGT 2027
Qy 1768 CTTACAGGCTGCTAACAGTAACCTTTCCAGGACTCT 1804
Db 2028 GTTACAGGCTGCTAATATTAACCTTTCCAGTACTCT 2064

RESULT 14

US-09-382-256-5
; Sequence 5, Application US/09382256A
; Patent No. 6207814
; GENERAL INFORMATION:
; APPLICANT: MIYAZONO, Kohei
; TEN DIJKE, Petra
; FRANZEN, Petra
; YAMASHITA, Hidetoshi
; HEUDIN, Carl-Henrik
; TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS
; HAVING SERINE THREONINE KINASE DOMAINS,
; AND THEIR USE
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/382,256A
; FILING DATE: 24-Aug-1999
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/02367
; FILING DATE: No. 6207814ember 17, 1993
; APPLICATION NUMBER: GB 9224057.1
; FILING DATE: No. 6207814ember 17, 1992
; APPLICATION NUMBER: GB 9304677.9
; FILING DATE: March 8, 1993
; APPLICATION NUMBER: GB 9304680.3
; FILING DATE: March 8, 1993
; APPLICATION NUMBER: 9311047.6
; FILING DATE: May 28, 1993
; APPLICATION NUMBER: 9313763.6
; FILING DATE: July 2, 1993
; APPLICATION NUMBER: 9316099.2
; FILING DATE: August 3, 1993
; APPLICATION NUMBER: 321344.5
; FILING DATE: October 15, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6207814man D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5298.1

RESULT 15

US-09-395-115-5
Sequence 5, Application US/09395115
Patent No. 6271365
GENERAL INFORMATION:
APPLICANT: Miyazono, Kohsei; Dijke, Peter Ten;
APPLICANTS: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/395,115
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-October-1995
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. 6271365ember-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6271365ember-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304680.3
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9311047.6
FILING DATE: 28-May-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 93136099.2
FILING DATE: 3-August-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-October-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kohlei, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD 5298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2932 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 310..1905

US-09-395-115-5

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GenCore version 5.1.6
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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 19587084

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1750.4	96.5	3003	9	US-10-868-497-90
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6	1750.4	96.5	3167	6	US-10-463-190-120
7	1750.4	96.5	3167	9	US-10-868-497-88
8	1750.4	96.5	3167	9	US-10-868-497-89
9	1581.4	87.2	2070	3	US-09-903-068-13
10	1581.4	87.2	2070	9	US-10-739-413-13
11	1574.2	86.8	2402	3	US-09-742-153-11
12	1424.4	78.6	2056	7	US-10-641-319-3
13	1387	76.5	2932	3	US-09-903-068-5
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15	1387	76.5	2932	6	US-10-286-152A-37
16	1387	76.5	2932	6	US-10-463-190-116
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18	1387	76.5	2932	9	US-10-868-497-85
19	1387	76.5	2932	9	US-10-492-380-37
20	1387	76.5	2932	9	US-10-450-763-22861
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22	1374.6	75.8	2623	5	US-10-153-217-1
23	1343	74.1	1599	9	US-10-745-237-307

24	1258.8	69.4	2730	9	US-10-450-763-22868	Sequence 22868, A
25	1104	60.9	1743	8	US-10-128-558-48	Sequence 48, Appl
26	978.2	54.0	1185	6	US-10-029-386-20369	Sequence 20369, A
27	918	50.6	1929	8	US-10-128-558-49	Sequence 49, Appl
28	810.4	44.7	1695	9	US-10-450-763-22867	Sequence 22867, A
29	773.8	42.7	2659	8	US-10-487-556-21	Sequence 21, Appl
30	716	39.5	1952	3	US-09-903-068-17	Sequence 17, Appl
31	716	39.5	1952	3	US-09-982-543A-7	Sequence 7, Appl
32	716	39.5	1952	9	US-10-739-413-17	Sequence 17, Appl
33	716	39.5	1952	10	US-11-098-889-7	Sequence 7, Appl
34	707.6	39.0	1575	6	US-10-463-190-117	Sequence 117, App
35	707.6	39.0	1575	9	US-10-868-497-86	Sequence 86, Appl
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37	707.6	39.0	2032	6	US-10-286-152A-39	Sequence 39, Appl
38	707.6	39.0	2032	6	US-10-139-814-13	Sequence 13, Appl
39	707.6	39.0	2032	6	US-10-172-118-570	Sequence 570, App
40	707.6	39.0	2032	6	US-10-295-027-67	Sequence 67, Appl
41	707.6	39.0	2032	6	US-10-295-027-788	Sequence 788, App
42	707.6	39.0	2032	6	US-10-295-027-836	Sequence 836, App
43	707.6	39.0	2032	6	US-10-295-027-880	Sequence 880, App
44	707.6	39.0	2032	6	US-10-173-999-63	Sequence 63, Appl
45	707.6	39.0	2032	6	US-10-463-190-118	Sequence 118, App

ALIGNMENTS

RESULT 1
US-09-874-628-1
; Sequence 1, Application US/09874628
; Patent No. US20020137133A1
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, John
; CELESTE, Anthony J.
; THIES, R. Scott
; YAMAJI, No. US20020137133A1oru
; TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute Inc.- Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/874,628
; APPLICATION NUMBER: US/09/874,628
; FILING DATE: 05-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/123,934
; FILING DATE: 17-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, Steven R
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 876 1170
; TELEFAX: 617 876 5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1813 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: CPK1-23a


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; NAME/KEY: CDS
; LOCATION: 61...1656
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-874-628-1

Query Match      100.0%; Score 1813; DB 3; Length 1813;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1261 AGGTGGGCACACGCGGTACATGGCTCCAGAGTGTCTGAGAGAGCTTGAGTAAAAAC 1320
Db 1261 AGGTGGGCACACGCGGTACATGGCTCCAGAGTGTCTGAGAGAGCTTGAGTAAAAAC 1320

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Qy 1741 TGGTTTCCAGACTCTCTCTTACCATCTTCCAGGCTGCTTACAGTAAACCTTTTCAGGA 1800
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Qy 1801 CTCTGCAGAATGC 1813
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; Publication No. US20040142417A1
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, John
; CELESTE, Anthony J.
; THIES, R. Scott
; YAMAJI, Noboru
; TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19

;;
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genetics Institute Inc.- Legal Affairs
;; STREET: 87 CambridgePark Drive
;; CITY: Cambridge
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02140
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
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;; SOFTWARE: Patentin Release #1.0, Version #1.25
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;; APPLICATION NUMBER: US/10/600,645
;; FILING DATE: 23-Jun-2003
;; CLASSIFICATION: 530
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;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/123,934A
;; FILING DATE: 17-SEP-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: LAZAR, Steven R
;; REGISTRATION NUMBER: 32,618
;; REFERENCE/DOCKET NUMBER: 5203
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617 876 1170
;; TELEFAX: 617 876 5851
;;
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1813 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; IMMEDIATE SOURCE:
;; CLONE: CFK1-23a
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 61..1656
;; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-600-645-1

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGTGGATCCCCGGGCTGCAGGAATTCGCGGCGCCAGGACACGTGCGAATTGGACA 60
DB 1 CTAGTGGATCCCCGGGCTGCAGGAATTCGCGGCGCCAGGACACGTGCGAATTGGACA 60

QY 61 ATGACTCAGCTATACACTTACATCAGATTACTGGGAGCCGTCTGTTTCATCTCTCAT 120
DB 61 ATGACTCAGCTATACACTTACATCAGATTACTGGGAGCCGTCTGTTTCATCTCTCAT 120

QY 121 GTTCAAGGGCAGAACTCTAGATAGTATGCTCCATGGTACTGTTGATGAATCAGACGTGGAC 180
DB 121 GTTCAAGGGCAGAACTCTAGATAGTATGCTCCATGGTACTGTTGATGAATCAGACGTGGAC 180

QY 181 CAGAAGAGCCGGAATATGAGTGTAGCTTACGACCGAGGACACCTTTCCTTAAAA 240
DB 181 CAGAAGAGCCGGAATATGAGTGTAGCTTACGACCGAGGACACCTTTCCTTAAAA 240

QY 241 TGCATTGTCTCAGACACTGCCAGATGACGCTATTAAATTAACACATGCAATGATGGC 300
DB 241 TGCATTGTCTCAGACACTGCCAGATGACGCTATTAAATTAACACATGCAATGATGGC 300

QY 301 CATTGCTTTGCCATTATAGAAGATGATCAGGAGAAACACGTTAACTTCGGGTGT 360
DB 301 CATTGCTTTGCCATTATAGAAGATGATCAGGAGAAACACGTTAACTTCGGGTGT 360

QY 361 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGATTTCAACAAAGCCAGCTACGACG 420
DB 361 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGATTTCAACAAAGCCAGCTACGACG 420

QY 421 ACAATAGAATGTTGTGCGACCAATTTGTGCAACCAATATTTGCGACCTACACTGCCCCCT 480
DB 421 ACAATAGAATGTTGTGCGACCAATTTGTGCAACCAATATTTGCGACCTACACTGCCCCCT 480

QY 481 GTCGTTATAGGCCCAATTCCTTTGATGGCAGCGTCCGATGGCTGCTGCTCATCTCTATG 540
DB 481 GTCGTTATAGGCCCAATTCCTTTGATGGCAGCGTCCGATGGCTGCTGCTCATCTCTATG 540

QY 541 GCTGCTCTGATTTGTCGCCCATGCTCTTCTCCAGCTGCTTCTGTTTCAACACATTACTGT 600
DB 541 GCTGCTCTGATTTGTCGCCCATGCTCTTCTCCAGCTGCTTCTGTTTCAACACATTACTGT 600

QY 601 AAGAGTATCTCAAGCAGAGGTCGTTTCAACCGTGACTTGGAAACAGGATGAAGCATTTATT 660
DB 601 AAGAGTATCTCAAGCAGAGGTCGTTTCAACCGTGACTTGGAAACAGGATGAAGCATTTATT 660

QY 661 CCAGTAGGAGAAATCACTGAAAGACCTGATTGACAGTCAAAAAGCTCTGGTAGTGATCT 720
DB 661 CCAGTAGGAGAAATCACTGAAAGACCTGATTGACAGTCAAAAAGCTCTGGTAGTGATCT 720

QY 721 GGATTACCTTTTATGTTGTTGAGCGAATCTATGCGCAACAGATTGCGCAGGTT 780
DB 721 GGATTACCTTTTATGTTGTTGAGCGAATCTATGCGCAACAGATTGCGCAGGTT 780

QY 781 GGTAAAGCGCGGTATGAGAGAAATGATGGGTGAAATGGCGTGTGAAAAGTGGCTGTC 840
DB 781 GGTAAAGCGCGGTATGAGAGAAATGATGGGTGAAATGGCGTGTGAAAAGTGGCTGTC 840

QY 841 AAAGTATTTTTTACCACCTGAAGAAAGCTAGCTGGTTTAGAGAAAACAGAAATCTACACG 900
DB 841 AAAGTATTTTTTACCACCTGAAGAAAGCTAGCTGGTTTAGAGAAAACAGAAATCTACACG 900

QY 901 GTGTTAATGGCTCATGAAAATATATCTGTTTATAGCTGCAGACATTAAGGACCGGT 960
DB 901 GTGTTAATGGCTCATGAAAATATATCTGTTTATAGCTGCAGACATTAAGGACCGGT 960

QY 961 TCCTGGACTCAGCTGATTTGTTGATTTACTGATTCACATGAGAAATGGGTCTCTCTATGACTTC 1020
DB 961 TCCTGGACTCAGCTGATTTGTTGATTTACTGATTCACATGAGAAATGGGTCTCTCTATGACTTC 1020

QY 1021 CTGAAATGTGCCACCTCGACACCCAGAGCCCTACTCAAGTTAGCTTTATTTCTGCTGCTGT 1080
DB 1021 CTGAAATGTGCCACCTCGACACCCAGAGCCCTACTCAAGTTAGCTTTATTTCTGCTGCTGT 1080

QY 1081 GGTCTGTGCACCTCCACACAGAAATTTATGGCAGCAAGGCAAGCCTGCAATTTGCTCAT 1140
DB 1081 GGTCTGTGCACCTCCACACAGAAATTTATGGCAGCAAGGCAAGCCTGCAATTTGCTCAT 1140

QY 1141 CGAGACCTCAAGAGCAAAAACATCTTTTAAAGAAAATGGTATGTTGCTGTTGCTGAC 1200
DB 1141 CGAGACCTCAAGAGCAAAAACATCTTTTAAAGAAAATGGTATGTTGCTGTTGCTGAC 1200

QY 1201 CTGGGCTAGCTGTTAAATTTCAACAGTGTGACACAAATGAAAGTTGACATACCTTTGAACACC 1260
DB 1201 CTGGGCTAGCTGTTAAATTTCAACAGTGTGACACAAATGAAAGTTGACATACCTTTGAACACC 1260

QY 1261 AGGTTGGGACACAGCGGTACATGGCTCCAGAAAGTGTGACAGAGCCGTGAGTAAAC 1320
DB 1261 AGGTTGGGACACAGCGGTACATGGCTCCAGAAAGTGTGACAGAGCCGTGAGTAAAC 1320

QY 1321 CATTTCCAGCCCTACATCATGCTGACATCTACAGCTTTTGGTTTGTATCTTTGGGAGATG 1380
DB 1321 CATTTCCAGCCCTACATCATGCTGACATCTACAGCTTTTGGTTTGTATCTTTGGGAGATG 1380

QY 1381 GCGCGTCTGCTGATTTACAGGAGGAATCGTGGAGGAATCAATTTACCATATTAACAACATG 1440
DB 1381 GCGCGTCTGCTGATTTACAGGAGGAATCGTGGAGGAATCAATTTACCATATTAACAACATG 1440

QY 1441 GTGCTCTAGTGACCCATCTTTTGAAGACATGCGTGAGGTGCTGTGTGAAAACGCTTGGCG 1500
DB 1441 GTGCTCTAGTGACCCATCTTTTGAAGACATGCGTGAGGTGCTGTGTGAAAACGCTTGGCG 1500

QY 1501 CCAATCGTCTCTAAACCGCTGGAACAGTGTGATGAATGCTTCTCGAGCCGCTTTTGAAGCTGATG 1560

1501	Db	CCAATCGTCTTAACCGCTGGAACAGATGATGAATGTCTTCGAGCGGTTTTGAAGCTCATG	1560
1561	Qy	TCAGAATGCTGGGCCCAATAATCCAGCATCCAGACTCAACGCTTTGAGAATCAAGAAGACG	1620
1561	Db	TCAGAATGCTGGGCCCAATAATCCAGCATCCAGACTCAACGCTTTGAGAATCAAGAAGACG	1620
1621	Qy	CTCGAAAGATGTTTGAATCCAGGATGTAAGAATTTGACAAACAGTTTTTGAGAAAGAAT	1680
1621	Db	CTCGAAAGATGTTTGAATCCAGGATGTAAGAATTTGACAAACAGTTTTTGAGAAAGAAT	1680
1681	Qy	TTAGACTGCAAGAAATTCACCCGAGGAAGGGTGGAGTTACGATGGACTAGGATGTCGGCT	1740
1681	Db	TTAGACTGCAAGAAATTCACCCGAGGAAGGGTGGAGTTACGATGGACTAGGATGTCGGCT	1740
1741	Qy	TGGTTTCCAGACTCTCTCCTCTACCATCTTTCACAGGCTGCTAACAGGTAAACCTTTTCAGGA	1800
1741	Db	TGGTTTCCAGACTCTCTCCTCTACCATCTTTCACAGGCTGCTAACAGGTAAACCTTTTCAGGA	1800
1801	Qy	CTCTGCAGAATGC	1813
1801	Db	CTCTGCAGAATGC	1813

RESULT 3

US-10-463-190-121

US-10-463-190-121
: Sequence 121. Application US/10463190

; sequence 121, Application US/10
: Publication No. US20040009535A1; PUBLICATION NO: US20
: GENERAL INFORMATION:

; GENERAL INFORMATION:
: APPLICANT: Brinkow Mary E

APPLICANT: Galag, David J.

APPLICANT: Galas, David J.

APPLICANT: Kovacevich, Brian

APPLICANT: Mulligan, John T.
APPLICANT: [REDACTED]
APPLICANT: [REDACTED]

APPLICANT: Paeper, Bryan W.

; APPLICANT: Van Ness, Jeffrey

APPLICANT: Winkler, David G.

; TITLE OF INVENTION: COMPOSITIONS AND MEHTODS FOR

; TITLE OF INVENTION: INCREASES

; FILE REFERENCE: 240083.508C2

; CURRENT APPLICATION NUMBER: US/1

; CURRENT FILING DATE: 200

; NUMBER OF SEQ ID NOS: 143

; SOFTWARE: Fast

; SEQ ID NO 121

; LENGTH: 30

TYPE: DNA

ORGANISM: Rat

Query Match 96.5%: Score 1750.4: DB 6: Length 3003:

Query Match	Best Local Similarity	Pred No	Score
96.5%	99.6%	0	1/50.4

Best Local Similarity 99.6%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 6; Indels 2; Cons 2.

Qy	30	TGCGGCCGACAGGACACGTGGAAATTGGACAATGACTCAGCTACACTTACATCAGATT	89
Db	52	TGCGGCCGACAGGACACGTGGAAATTGGACAATGACTCAGCTATACACTTACATCAGATT	111
Qy	90	ACTGGGAGCCTGTCGTGTTTCATCATTTCTCTCAATGTTCAAGGGCAGAACTCTAGATAGTATGCT	149
Db	112	ACTGGGAGCCTGTCGTGTTTCATCATTTCTCATGTTCAAGGGCAGAACTCTAGATAGTATGCT	171
Qy	150	CCATGGTACTGGTATGAAATCAGACGTTGGACCGAGAACGCCGAAATAATGGAGTGAAGCTT	209
Db	172	CCATGGTACTGGTATGAAATCAGACGTTGGACCGAGAACGCCGAAATAATGGAGTGAAGCTT	231
Qy	210	AGCACACAGAGACACCTTTACCTTTCTTAAATGCTATTGCTCAGGACACTGCCCCAGATGA	269
Db	232	AGCACACAGAGACACCTTTACCTTTCTTAAATGCTATTGCTCAGGACACTGCCCCAGATGA	291
Qy	270	CGCTATTAAACACATGCATAACTAATGGCCATTGCTTTGCCATTATAGAAGAAGATGA	329
Db	292	CGCTATTAAACACACATGCATAACTAATGGCCATTGCTTTGCCATTATAGAAGAAGATGA	351

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Db 1432 GGAGGAATATCAATTTACCATATTACACATGGTGCCTAGTGACCCATCTTTATGAAGACAT 1491
Qy 1470 GCGTGAGTCTGCTGTGTGTAACCGCTTGGGCCCAATCGTCTCTAAACCGCTGGACAGTGA 1529
Db 1492 GCGTGAGTCTGCTGTGTGTAACCGCTTGGGCCCAATCGTCTCTAAACCGCTGGAAACAGTGA 1551
Qy 1530 TGAATGCTTTCGAGCCGCTTTTGAAGCTGATGTCAGAATGCTGGGCCCAATTAATCCAGCATC 1589
Db 1552 TGAATGCTTTCGAGCCGCTTTTGAAGCTGATGTCAGAATGCTGGGCCCAATTAATCCAGCATC 1611
Qy 1590 CAGACTCACAGCTTTGAGAATCAAGAAGACGCTCGCAAGAGTGTGTAATCCAGGATGT 1649
Db 1612 CAGACTCACAGCTTTGAGAATCAAGAAGACGCTCGCAAGAGTGTGTAATCCAGGATGT 1671
Qy 1650 AAGATTGTGACAAACAGTTTTTGAAAAGAAATTTAGACTGCAAGAAAATTCACCCCGAGGAAG 1709
Db 1672 AAGATTGTGACAAACAGTTTTTGAAAAGAAATTTAGACTGCAAGAAAATTCACCCCGAGGAAG 1731
Qy 1710 GGTGGAGTTAGCATGGACTAGGATGTGCGGCTTGGTTTTCCAGACTCTCTCCTCTACCATCT 1769
Db 1732 GGTGGAGTTAGCATGGACTAGGATGTGCGGCTTGGTTTTCCAGACTCTCTCCTCTCTA-CACT 1790
Qy 1770 TCAGAGCTGCTAAACAGTAACCTTTTCAGGACTCTGCAGAAATGC 1813
Db 1791 TCAGAGCTGCTAACAGTAAA-CTTTTCAGGACTCTGCAGAAATGC 1833

RESULT 4
US-10-868-497-90
; Sequence 90, Application US/10868497
; Publication No. US2005010683A1
; GENERAL INFORMATION:
; APPLICANT: Winkler, David G.
; APPLICANT: Shi, Jiye
; APPLICANT: Lacham, John
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR SCLEROSTIN AND
; FILE OF INVENTION: METHODS FOR INCREASING BONE MINERALIZATION
; CURRENT APPLICATION NUMBER: US/10/868,497
; CURRENT FILING DATE: 2004-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 3003
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-868-497-90

Query Match 96.5%; Score 1750.4; DB 9; Length 3003;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

Qy 30 TGGCGCGCCGAGACAGCTGCGAATTGGACAAATGACTCAGCTATACACTTACATCAGATT 89
Db 52 TGGCGCGCGAGACAGACAGCTGCGAATTGGACAAATGACTCAGCTATACACTTACATCAGATT 111
Qy 90 ACTGGGAGCCTGCTGTTCAATCTTCTCATGTTTCAAGGGCAGAAATCTAGATAGTATGCT 149
Db 112 ACTGGGAGCCTGCTGTTCAATCTTCTCATGTTTCAAGGGCAGAAATCTAGATAGTATGCT 171
Qy 150 CCATGTTACTGGTATGAAATCAGACGTGGACCAAGAGAAGCCGGAATAATGGAGTGACGTT 209
Db 172 CCATGTTACTGGTATGAAATCAGACGTGGACCAAGAGAAGCCGGAATAATGGAGTGACGTT 231
Qy 210 AGCACAGAGGACACCTTACCTTTCTTAAATGCTATTGCTCAGGACACTGCCAGATGA 269
Db 232 AGCACAGAGGACACCTTACCTTTCTTAAATGCTATTGCTCAGGACACTGCCAGATGA 291
Qy 270 CGCTATTATAACACATGCATACTAATGGCCATTCGTTGCCATTATAGAAGAAATGA 329
Db 292 CGCTATTATAACACATGCATACTAATGGCCATTCGTTGCCATTATAGAAGAAATGA 351
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Qy 330 TCAGGGAGAAAACCAAGTAACTTCTGGTGTATGAAGTATGAAGGCTCTGATTTTCAATG 389
Db 352 TCAGGGAGAAAACCAAGTAACTTCTGGTGTATGAAGTATGAAGGCTCTGATTTTCAATG 411
Qy 390 CAAGGATTCACAAAAGCCAGCTACGACGAGCAATAGAAATGTTGTGCGACCAATTTGTG 449
Db 412 CAAGGATTCACAAAAGCCAGCTACGACGAGCAATAGAAATGTTGTGCGACCAATTTGTG 471
Qy 450 CAACCAATATTTTCAGCCTACACTGCCCCCTGCTGTTATAGGCCATCTTTTGTATGCGAG 509
Db 472 CAACCAATATTTTCAGCCTACACTGCCCCCTGCTGTTATAGGCCATCTTTTGTATGCGAG 531
Qy 510 CGTCCGATGGCTGGCTGTGCTCATCTCTATGGCTGTCTGTATTTGTGCCCATGATCGCTT 569
Db 532 CGTCCGATGGCTGGCTGTGCTCATCTCTATGGCTGTCTGTATTTGTGCCCATGATCGCTT 591
Qy 570 CTCAGCTGCTTCTGTTTACAAACATTTACTGTATAGAGTATCTCAAGCAGAGGTCGTTACAA 629
Db 592 CTCAGCTGCTTCTGTTTACAAACATTTACTGTAAAGATATCTCAAGCAGAGGTCGTTACAA 651
Qy 630 CCGTGACTTGGAAACAGGATGAAGCATTTATTCAGTAGGAGAAATCACTGAAGAACCTGAT 689
Db 652 CCGTGACTTGGAAACAGGATGAAGCATTTATTCAGTAGGAGAAATCACTGAAGAACCTGAT 711
Qy 690 TGACCAAGTACACAAAGCTCTGGTAGTGGATCTGGATTACCTTTATTTGGTTTCAGGCAACTAT 749
Db 712 TGACCAAGTACACAAAGCTCTGGTAGTGGATCTGGATTACCTTTATTTGGTTTCAGGCAACTAT 771
Qy 750 TGCACCAAGATTCAGATGGTTTCGGCAGGTTGGTAAGGGCCGGTATGGAGAAAGTATGGAT 809
Db 772 TGCACCAAGATTCAGATGGTTTCGGCAGGTTGGTAAGGGCCGGTATGGAGAAAGTATGGAT 831
Qy 810 GGGTAAATGCGGTGGTGAAGAAAGTGGCTGTCAAGTATTTTACCACCTCAAGAACCTAG 869
Db 832 GGGTAAATGCGGTGGTGAAGAAAGTGGCTGTCAAGTATTTTACCACCTCAAGAACCTAG 891
Qy 870 CTGGTTTAGAGAAAACAGAAATCTACACAGACGGTGTAAATGCGTCATGAAAATATACTTG 929
Db 892 CTGGTTTAGAGAAAACAGAAATCTACACAGACGGTGTAAATGCGTCATGAAAATATACTTG 951
Qy 930 TTTTATAGCTGCAGACATTTAAAGGCAACCGGTTCTCGGACTCAGCTGTATTTGATTAAGTGA 989
Db 952 TTTTATAGCTGCAGACATTTAAAGGCAACCGGTTCTCGGACTCAGCTGTATTTGATTAAGTGA 1011
Qy 990 TTACCATGAGAAATGGGTCTCTCTATGACTTCCGAAATGTCACACCTCGACACCAAGGC 1049
Db 1012 TTACCATGAGAAATGGGTCTCTCTATGACTTCCGAAATGTCACACCTCGACACCAAGGC 1071
Qy 1050 CCTACTCAAGTTAGCTTTATTTCTGCTGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1109
Db 1072 CCTACTCAAGTTAGCTTTATTTCTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1131
Qy 1110 TGGCAGCAAGGCAAGCCTGCAATTTGCTCATCGAGACCTGAAGAGCAAAAACATCCTTAT 1169
Db 1132 TGGCAGCAAGGCAAGCCTGCAATTTGCTCATCGAGACCTGAAGAGCAAAAACATCCTTAT 1191
Qy 1170 TAAGAAAAATGCTAGTTGCTGTATTTGCTGACCTGGGCTGCTGTTAAATTTCAACAGTGA 1229
Db 1192 TAAGAAAAATGCTAGTTGCTGTATTTGCTGACCTGGGCTGCTGTTAAATTTCAACAGTGA 1251
Qy 1230 CACAAATGAAGTTGACATACCTTTGAACACAGGGTGGGCAACAGGGGTGACATGGCTCC 1289
Db 1252 CACAAATGAAGTTGACATACCTTTGAACACAGGGTGGGCAACAGGGGTGACATGGCTCC 1311
Qy 1290 AGAAGTGTGGA CGAGAGCCTGAGTAAAAACCAATTTCCAGCCCTACATCATGCTGACAT 1349
Db 1312 AGAAGTGTGGA CGAGAGCCTGAGTAAAAACCAATTTCCAGCCCTACATCATGCTGACAT 1371
Qy 1350 CTACAGCTTTGCTTTGATCATTTGGAGATGGCCCGTCCCTGTATTTACAGGAGGAATCGT 1409
Db 1372 CTACAGCTTTGCTTTGATCATTTGGAGATGGCCCGTCCCTGTATTTACAGGAGGAATCGT 1431
Qy 1410 GGAGGAATATCAATTACCATATTAACAATGCTGCTAGTGACCCATCTTTATGAAGACAT 1469
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Db	1432	GGAGGAATATCAATTACCATATTAACAACATGGTGGCCCTAGTGACCCATCTTTATGAAGACAT	1491
Qy	1470	CGCTGAGGTCGTGTGTGTGAAAAACGCTTTCGGGCCAATCGTCTCTAAACGCGCTGGAAACAGTGGA	1529
Db	1492	CGCTGAGGTCGTGTGTGTGAAAAACGCTTTCGGGCCAATCGTCTCTAAACGCGCTGGAAACAGTGGA	1551
Qy	1530	TGAATGCTTTCGAGCCGCTTTTGAAGCTGTATGTTCAGAAATGCTGGGCCCAATTAATCCAGCATC	1589
Db	1552	TGAATGCTTTCGAGCCGCTTTTGAAGCTGTATGTTCAGAAATGCTGGGCCCAATTAATCCAGCATC	1611
Qy	1590	CAGACTCACAGCTTTTGAGAATCAAGAAGACGCTCGCAAAGATGGTTGAAATCCAGGATGT	1649
Db	1612	CAGACTCACAGCTTTTGAGAATCAAGAAGACGCTCGCAAAGATGGTTGAAATCCAGGATGT	1671
Qy	1650	AAAGATTGACAAACAGTTTTTGAGAAAGAAATTTAGACTGCAAGAAATTCACCCGAGGAAG	1709
Db	1672	AAAGATTGACAAACAGTTTTTGAGAAAGAAATTTAGACTGCAAGAAATTCACCCGAGGAAG	1731
Qy	1710	GGTGGAGTTAGCATGGACTAGGATGTCGGCTTGCTTTCCAGACTCTCTCTCTTACCATCT	1769
Db	1732	GGTGGAGTTAGCATGGACTAGGATGTCGGCTTGCTTTCCAGACTCTCTCTCTTACCATCT	1790
Qy	1770	TCACAGGCTGCTAACAGTAAACCTTTTCAGGACTCTGCAGAATGC	1813
Db	1791	TCACAGGCTGCTAACAGTAAA-CTTTTCAGGACTCTGCAGAATGC	1833

RESULT 5

US-10-463-190-119
; Sequence 119, Application US/10463190
; Publication No. US20040009535A1

; GENERAL INFORMATION:
 ; APPLICANT: Brunkow, Mary E.
 ; APPLICANT: Galas, David J.
 ; APPLICANT: Kovacevich, Brian
 ; APPLICANT: Mulligan, John T.
 ; APPLICANT: Paepfer, Bryan W.
 ; APPLICANT: Van Ness, Jeffrey
 ; APPLICANT: Winkler, David G.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 ; TITLE OF INVENTION: INCREASING BONE MINERALIZATION

```
Query Match          96.5%; Score 1750.4; DB 6; Length 3167;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 6; Indels 2; Gaps 2;
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Qy	90	ACTGGGAGCCTCTGTGTTTCATCATTTTCTCATGTTCAAGGGCAGAANTCTAGATAGTAGCT	149
Db	255	ACTGGGAGCCTCTGTGTTTCATCATTTTCTCATGTTCAAGGGCAGAANTCTAGATAGTAGCT	314

Qy	150 CCATGGTACTGTTGAATCAGACGTGGACCAGAAGCCGAAAAATGGAGTGACGTT	209
Db	315 CCATGGTACTGTTGAATCAGACGTGGACCAGAAGCCGAAAAATGGAGTGACGTT	374

Qy 210 AGCACCAGGACACCTTACTTTTCCTTAAATGCTATTGTCTCAGGACACTGCCCATGA 269
|||||
Db 375 AGCACCGAGGACACCTTACTTTTCCTTAAATGCTATTGTCTCAGGACACTGCCCATGA 434

QY	270	CGCTATTAAATAAACACATGCATAACTAATAGGCCAATTGCTTTGGCCATTATTAGAGAAAGATGA	329
DB	435	CGCTATTAAATAAACACATGCATAAATAATAGGCCAATTGCTTTGGCCATTATTAGAGAAAGATGA	494
QY	330	TCAGGGAGAAACCAACGTTAACTTCTGGGTGATGAAGTATGAAGGCTCTGATTTTCAATG	389
DB	495	TCAGGGAGAAACCAACGTTAACTTCTGGGTGATGAAGTATGAAGGCTCTGATTTTCAATG	554
QY	390	CAAGGATTCACCAAAAGCCACGCTAGCGAGGACAAATAGAAATGTTGTGCGACCAATTTGTG	449
DB	555	CAAGGATTCACCAAAAGCCACGCTAGCGAGGACAAATAGAAATGTTGTGCGACCAATTTGTG	614
QY	450	CAACCAATAATTTGAGCCTACACTGCCCCCTGCTGTTATAGGCCCAATCTCTTTGATGGCAG	509
DB	615	CAACCAATAATTTGAGCCTACACTGCCCCCTGCTGTTATAGGCCCAATCTCTTTGATGGCAG	674
QY	510	CGTCCGATGGCTGGCTGTGCTCATCTATAGGCGTCTGTTATTTGTCGCCATGATCTGCTTT	569
DB	675	CGTCCGATGGCTGGCTGTGCTCATCTATAGGCGTCTGTTATTTGTCGCCATGATCTGCTTT	734
QY	570	CTCCAGCTGCTTCTGTTTACAAAACATTACTGTAAGAGTATCTCAAGCAGAGGTCGTTACAA	629
DB	735	CTCCAGCTGCTTCTGTTTACAAAACATTACTGTAAGAGTATCTCAAGCAGAGGTCGTTACAA	794
QY	630	CCGTGACTTCGGAACAGGATGAAGCATTTATTCAGTAGGAGAAATCACTGAAAGACCTGAT	689
DB	795	CCGTGACTTCGGAACAGGATGAAGCATTTATTCAGTAGGAGAAATCACTGAAAGACCTGAT	854
QY	690	TGACCAGTCAAAAGCTCTGGTAGTGGATCTGATTTACCTTTATTTGGTTACGCGAACTAT	749
DB	855	TGACCAGTCAAAAGCTCTGGTAGTGGATCTGATTTACCTTTATTTGGTTACGCGAACTAT	914
QY	750	TGCCAAACAGATTCCAGATGGTTCCGACAGGTTGGTAAAGGCCCGGTATGGAGAACTATGGAT	809
DB	915	TGCCAAACAGATTCCAGATGGTTCCGACAGGTTGGTAAAGGCCCGGTATGGAGAACTATGGAT	974
QY	810	GGGTAAATGGCGTGGTGA AAAAGTGGCTGTCAAAGTATTTTTTACCACCTGAAGAACTAG	869
DB	975	GGGTAAATGGCGTGGTGA AAAAGTGGCTGTCAAAGTATTTTTTACCACCTGAAGAACTAG	1034
QY	870	CTGGTTTAGAGAAACAGAAATCTTACCAGACGGTGTAAATGCGTTCATGAAATATACTTGG	929
DB	1035	CTGGTTTAGAGAAACAGAAATCTTACCAGACGGTGTAAATGCGTTCATGAAATATACTTGG	1094
QY	930	TTTTTATAGCTGCAGACATTTAAAGGCACCGGTTCTCTGGACTTCAGCTGTATTGTGTTACTGA	989
DB	1095	TTTTTATAGCTGCAGACATTTAAAGGCACCGGTTCTCTGGACTTCAGCTGTATTGTGTTACTGA	1154
QY	990	TTACCATGAGAATGGGTCTCTCTATGACTTCTCTGAAATGTGCCACCTCGACACCCAGAGC	1049
DB	1155	TTACCATGAGAATGGGTCTCTCTATGACTTCTCTGAAATGTGCCACCTCGACACCCAGAGC	1214
QY	1050	CCTACTCAAGTTAGCTTTATTTCTGCTGCTGTGTGCTGTGGCCACTCCACACAGAAATTTTA	1109
DB	1215	CCTACTCAAGTTAGCTTTATTTCTGCTGCTGTGTGCTGTGGCCACTCCACACAGAAATTTTA	1274
QY	1110	TGGCAGCAGGCAAGCCCTGCAATTCCTCATTCGAGACCTTGAGAGCAAAAACATCCTTAT	1169
DB	1275	TGGCAGCAGGCAAGCCCTGCAATTCCTCATTCGAGACCTTGAGAGCAAAAACATCCTTAT	1334
QY	1170	TAGAAAAATGGTAGTTGCTGTATGTGCTGACCTGGGCGCTAGCTGTTTAAATTTCAACAGTGA	1229
DB	1335	TAGAAAAATGGTAGTTGCTGTATTCCTGACCTTGGGCGCTAGCTGTTTAAATTTCAACAGTGA	1394
QY	1230	CACAAATGAAGTTGACATACCCTTTGAACACCGAGGTTGGGCAACGCGGGTACATGCGTCC	1289
DB	1395	CACAAATGAAGTTGACATACCCTTTGAACACCGAGGTTGGGCAACGCGGGTACATGCGTCC	1454
QY	1290	AGAAGTCTCGACGAGAGCCTGAGTAAANACATTTTCCAGCCCTACATCATGCTCTGACAT	1349
DB	1455	AGAAGTCTCGACGAGAGCCTGAGTAAANACATTTTCCAGCCCTACATCATGCTCTGACAT	1514
QY	1350	CTACAGCTTTGGTTTGAATCATTTTTGGAGATGGCCCGCTCGCTGTATTATACAGGAGGAATCGT	1409

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Db 1515 CTACAGCTTTGGTTGGATCATTTGGGAGATGGCCCGTGGCTGTATTACAGAGGAATCGT 1574
Qy 1410 GGAGGAATATCAATACCATATTACAACATGGTCCCTAGTAGTGAACCCATCTTATGAAGACAT 1469
Db 1575 GGAGGAATATCAATACCATATTACAACATGGTCCCTAGTAGTGAACCCATCTTATGAAGACAT 1634
Qy 1470 GCGTAGGTCGTGTGTGTGAAACGCTTTGCGGCCAATCGTCTCTAAACCGCTGGAACAGTGA 1529
Db 1635 GCGTAGGTCGTGTGTGTGAAACGCTTTGCGGCCAATCGTCTCTAAACCGCTGGAACAGTGA 1694
Qy 1530 TGAATGCTTCGAGCCGCTTTGAAGCTGTATGAGATGTGAGATGTGAGATGTGAGATGTGAGATGT 1649
Db 1695 TGAATGCTTCGAGCCGCTTTGAAGCTGTATGAGATGTGAGATGTGAGATGTGAGATGTGAGATGT 1754
Qy 1590 CAGACTCACAGCTTTGAGAAATCAAGAAGACGCTCGCAAGATGTTGAAATCCCAAGGATGT 1649
Db 1755 CAGACTCACAGCTTTGAGAAATCAAGAAGACGCTCGCAAGATGTTGAAATCCCAAGGATGT 1814
Qy 1650 AAGATTTGACAAACAGCTTTTGAGAAAGAAATTTAGACTGCAAGAAATTTCAACCCGAGGAAG 1709
Db 1815 AAGATTTGACAAACAGCTTTTGAGAAAGAAATTTAGACTGCAAGAAATTTCAACCCGAGGAAG 1874
Qy 1710 GGTGGAGTTAGCATGGACTAGGATGTGCGCTTGGCTTTCCAGACTCTCTCTCTACCATCT 1769
Db 1875 GGTGGAGTTAGCATGGACTAGGATGTGCGCTTGGCTTTCCAGACTCTCTCTCTCTA-CATCT 1933
Qy 1770 TCAGAGCTGCTAACACTTAACCTTTTCAGGACTCTGAGAAATGC 1813
Db 1934 TCAGAGCTGCTAACACTTAAC-CTTTTCAGGACTCTGAGAAATGC 1976

RESULT 6
US-10-463-190-120
; Sequence 120, Application US/10463190
; Publication No. US20040009535A1
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary E.
; APPLICANT: Galas, David J.
; APPLICANT: Kovacevich, Brian
; APPLICANT: Mulligan, John T.
; APPLICANT: Paepker, Bryan W.
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Winkler, David G.
; TITLE OF INVENTION: COMPOSITIONS AND MEHTODS FOR
; FILE REFERENCE: INCREASING BONE MINERALIZATION
; CURRENT FILING DATE: 2003-06-16
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 120
; LENGTH: 3167
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-463-190-120
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Query Match 96.5%; Score 1750.4; DB 6; Length 3167;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

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Db 195 TGGCGCGGACGACAGCTGGCAATTTGGCAATGACTCAGCTATACACTTACATCAGATT 254
Qy 90 ACTGGGAGCTGTCTGTTCATCATTTCTCATGTTTCAAGGGCAGAACTAGATAGTATGCT 149
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Qy 150 CCATGGTACTGGTATGAATTCAGACGTGGACAGAAAGCCGGAATAATGGAGTACGTT 209
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Qy 210 AGCACGAGGACACCTTACCTTTCTTAAATGCTATTGCTCAGGACACTGCCAGATGA 269
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Qy 390 CAAGGATTCACAAAAGCCAGCTACGCAAGCAATAGAAATGTTGTCGAGCAATTTGTG 449
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1470 GGCTGAGGTGCTGTGTGTAACCGCTTGGCGGCAATCGTCTCTAAACCGCTGGAACAGTGA 1529
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1530 TGAATGCTTTCAGCGCTTTTGAAGCTGATGTGAGAAATGCTGGGCCCATTAATCCAGCATC 1589
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1650 AAGAGATTTGACAAACAGTTTTCAGAAAGAAATTTAGACTGCAAGAAATTCACCCGAGGAAG 1709
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1710 GGTGGAGTTAGCATGAGCTAGGATGTCGGCTTGGTTTCAGACTCTCTCTCTACCATCT 1769
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1770 TCACAGGCTGCTAACAGTAACTTTTCAGACTCTGCAAGATGC 1813
1934 TCACAGGCTGCTAACAGTAAA-CTTTCAGGACTCTGCAAGATGC 1976

RESULT 7

US-10-868-497-88
; Sequence 88, Application US/10868497
; Publication No. US20050106683A1
; GENERAL INFORMATION:
; APPLICANT: Winkler, David G.
; APPLICANT: Shi, Jiye
; APPLICANT: Latham, John
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR SCLEROSTIN AND
; TITLE OF INVENTION: METHODS FOR INCREASING BONE MINERALIZATION
; FILE REFERENCE: 60117-128
; CURRENT APPLICATION NUMBER: US/10/868,497
; CURRENT FILING DATE: 2004-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 3167
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-868-497-88

Query Match 96.5%; Score 1750.4; DB 9; Length 3167;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

QY 30 TGGGGCCGCGAGACACGTGCGAATTTGGACAATGACTCAGCTATACACTTACATCAGATT 89
DB 195 TGGCCCGGACAGGACACGTGCGAATTTGGACAATGACTCAGCTATACACTTACATCAGATT 254
QY 90 ACTGGGAGCTGTCTGTTTCATATTCTCATGTTCAAGGGCAGAACTAGATAGTATGCT 149
DB 255 ACTGGGAGCTGTCTGTTTCATATTCTCATGTTCAAGGGCAGAACTAGATAGTATGCT 314
QY 150 CCATGTTACTGTTATGAATTCAGACGTGGACCAAGAAAGCCGGAATAATGGAGTGCAGTT 209
DB 315 CCATGTTACTGTTATGAATTCAGACGTGGACCAAGAAAGCCGGAATAATGGAGTGCAGTT 374

QY 210 AGCACCAGGAGACACTTTTACCTTTTAAATATGCTATTGCTCAGGACACTGCCCCAGATGA 269
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DB 555 CAAGGATTTACCAAAAGCCAGCTACGAGAGACAAATAGAAATGCTTCGAGCAAAATTTG 614
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QY 510 CGTCCGATGGCTGGCTGTCTCATCTCTATGGCTGTCTGTATTTGTCGCCATGATCGTCTT 569
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QY 930 TTTTATAGCTCAGACATTTAAAGGCACCGGTTTCTCGGACTCAGCTGATTTTCACTTACTGA 989
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RESULT 8

US-10-868-497-89
; Sequence 89, Application US/10868497
; Publication No. US20050106683A1
; GENERAL INFORMATION:
; APPLICANT: Winkler, David G.
; APPLICANT: Shi, Jiye
; APPLICANT: Latham, John
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR SCLEROSTIN AND
; TITLE OF INVENTION: METHODS FOR INCREASING BONE MINERALIZATION
; FILE REFERENCE: 60117-128
; CURRENT APPLICATION NUMBER: US/10/868,497
; CURRENT FILING DATE: 2004-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 3167
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-868-497-89

Query Match 96.5%; Score 1750.4; DB 9; Length 3167;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

Qy 30 TGGCGCCGCGCAGGACACGTGCGAATTTGGCAATGCAATGCACTCAGCTATACACTTTACATCAGATT 89
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Db 255 ACTGGGAGCCTGTCTGTTCATCATTTCTCATGTTTCAAGGGCAGAAATCTAGATAGTATGCT 314
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Db 1875 GTGGAGTTAGCATGAGCTAGGATGTGCGGCTTGGTTTCAGAGCTCTCTCTCTA-CATCT 1933
Qy 1770 TCACAGGCTGCTAACAGTAAACCTTTCAGAGCTCTGCAGAAATGC 1813
Db 1934 TCACAGGCTGCTAACAGTAAAC-CTTTCAGAGCTCTGCAGAAATGC 1976

RESULT 9
US-09-903-068-13
; Sequence 13, Application US/09903068
; Patent No. US20020123139A1
; GENERAL INFORMATION:
; APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
; Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
; Having Serine Threonine Kinase Domains And Their Use
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/903,068
; Filing DATE: 11-Jul-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/679,187
; Filing DATE: <Unknown>
; APPLICATION NUMBER: PCT/GB93/02367
; Filing DATE: 17-No. US20020123139A1ember-1993
; APPLICATION NUMBER: 9224057.1
; Filing DATE: 17-No. US20020123139A1ember-1992
; APPLICATION NUMBER: 9304677.9
; Filing DATE: 8-March-1993
; APPLICATION NUMBER: 9304680.3
; Filing DATE: 8-March-1993
; APPLICATION NUMBER: 9311047.6
; Filing DATE: 28-May-1993

APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
APPLICATION NUMBER: 9136099.2
FILING DATE: 3-August-1993
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-October-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kohlei, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD 5298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2070 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Mouse
FEATURE:
NAME/KEY: CDS
LOCATION: 217..1812
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-903-068-13

Query Match 87.2%; Score 1581.4; DB 3; Length 2070;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 1678; Conservative 0; Mismatches 96; Indels 9; Gaps 3;

Qy 39 CAGGACGCTGGCAATTCGACATCAGCTATACATCTACATCAGATTAATCGGAGC 98
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Db 255 CTGCTGTTTCATCATTTCTCATGTTTCAAGGGCAGAAATCTAGATAGTCTCCATGGC 314
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Qy 219 GGACACCTTTACCTTTCTTAAATGCTATTGCTCAGGACACTGCCCCAGATGACGCTATTAA 278
Db 375 GGATACCTTGGCTTTCTTAAAGTGTCTATTGCTCAGGACACTGCCCCAGATGATGCTATTAA 434
Qy 279 TAACACATGCATAACTAATGGCCATTGCTTTGCCATTATAGAAAGATGATCAGGAGA 338
Db 435 TAACACATGCATAACTAATGGCCATTGCTTTGCCATTATAGAAAGATGATCAGGAGA 494
Qy 339 AACACAGTTAACTTCTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATGAAGATTC 398
Db 495 AACACATTAATCTTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATGAAGATTC 554
Qy 399 ACCAAAGCCAGCTACGACGACAAATAGAATGTTTGTGGCAATTTGTGCAACCAATA 458
Db 555 ACCAAAGCCAGCTACGACGACAAATAGAATGTTTGTGGCAATTTGTGCAACCAATA 614
Qy 459 TTTGAGGCTACACTGCCCTCTGCTTTATAGGCCCATTTCTTTGATGGCAGGCTCCGATG 518
Db 615 TTTGAGGCTACACTGCCCTCTGCTTTATAGGTCGGTTCTTTGATGGCAGCATCCGATG 674
Qy 519 GCTGCTGTGCTCATCTCTATGGCTGTCTGTATTTGTCGCATGATCGTCTTCTCCAGCTG 578
Db 675 GCTGCTGTGCTCATTTCCATGGCTGTCTGTATGATGATCATCTCTTCTCCAGCTG 734
Qy 579 CTTCGTTTACAAACATTAATGTAAGAGTATCTCAAGACAGAGGCTCGTTACAACCGTACTT 638

QY 519 GCTGGCTGCTCATCTCTATGCTGCTGTATGTCGCCATGATCGTCTCTCCAGCTG 578
Db |||||
QY 675 GCTGGTTGCTCATTTCTTCATGCTGCTGTATGTTGCTATGATCATCTCTCCAGCTG 734
Db |||||
QY 579 CTTCTGTTTAAACAATTAATTAAGAGTATCTCAAGCAGAGGTGCGTTACAACCGTGACTT 638
Db |||||
QY 735 CTTTGTCTATAAGCATTTATGTAAGAGTATCTCAAGCAGGGGTGCTTACAACCGTGATTT 794
QY 639 GGAACAGGATGAAGCATTTATTCAGTAGAGATCACTGAAAGACCTGATGACAGTTC 698
Db |||||
QY 795 GGAACAGGATGAAGCATTTATTCAGTAGAGATCACTGAAAGACCTGATGACAGTTC 854
QY 699 ACAAGCTCTGCTAGTGGATCTGGATTACCTTTATTTGGTTTACGGAACCTATTGCCAAACA 758
Db |||||
QY 855 CCAAGCTCTGGAGTGGATCTGGATTGCTTTATTTGGTTACGGAACCTATTGCCAAACA 914
QY 759 GATTTCAGATGGTTTCGGCAGGTTGGTAAGGCGCGGTATGGAGAAGTATGATGGGTAATG 818
Db |||||
QY 915 GATTTCAGATGGTTTCGGCAGGTTGGTAAGGCGCGTATGGAGAAGTATGATGGGTAATG 974
QY 819 GCGTGTGAAAAAGTGGCTGTCAAAGTATTTTACCACCTGAAGAGCTAGCTGGTTTATG 878
Db |||||
QY 975 GCGTGTGAAAAAGTGGCTGTCAAAGTATTTTACCACCTGAAGAGCTAGCTGGTTTATG 1034
QY 879 AGAAACAGAAATCTACACAGCGTGTAAATGGCTCATGAAATATACCTTGGTTTATAGC 938
Db |||||
QY 1035 AGAAACAGAAATCTACACAGCGTGTAAATGGCTCATGAAATATACCTTGGTTTATAGC 1094
QY 939 TGCAGACATTAAAGGCACCGGTTCTGGACTCAGCTGTATTTGATTACTGATTACCATGA 998
Db |||||
QY 1095 TGCAGACATTAAAGGCACCGGTTCTGGACTCAGCTGTATTTGATTACTGATTACCATGA 1154
QY 999 GAATGGGTCTCTATATGACTCTCTGAAATGTGCGACCCCTGGACACAGAGCCCTACTCAA 1058
Db |||||
QY 1155 AAATGGATCTCTATATGACTCTCTGAAATGTGCGACCCCTGGACACAGAGCCCTACTCAA 1214
QY 1059 GTTAGCTTATCTGCTGCTGCTGTGCTGTGCGACCTCCACACAGAAATTTATGGACGCA 1118
Db |||||
QY 1215 GTTAGCTTATCTGCTGCTGCTGTGCTGTGCGACCTCCACACAGAAATTTATGGTACCCA 1274
QY 1119 AGGCAAGCCTGCAATTTGCTCATCGAGACCTGGAAGCAAAAAACATCTTTATTAAGAAAA 1178
Db |||||
QY 1275 AGGCAAGCCTGCAATTTGCTCATCGAGACCTGGAAGCAAAAAACATCTTTATTAAGAAAA 1334
QY 1179 TGTGTAGTCTGTATTTGCTGACTGGGCTGCTGTGTTAAATTCACAGTGAACAAATGA 1238
Db |||||
QY 1335 TGGAGTTGCTGTATTTGCTGACTGGGCTGCTGTGTTAAATTCACAGTGAACAAATGA 1394
QY 1239 AGTTGACATACCTTGAACACAGGCTGGGACCCAGCGGTATACATGGCTCCAGAAATGCT 1298
Db |||||
QY 1395 AGTTGACATACCTTGAATACAGGCTGGGACCCAGCGGTATACATGGCTCCAGAAATGCT 1454
QY 1299 GGACGAGAGCCTGAGTAAAAACCATTTCCAGCGCTACATCATGGCTGACATCTACAGCTT 1358
Db |||||
QY 1455 GGATGAACCTGATATAAAACCATTTCCAGCGCTACATCATGGCTGACATCTATAGCTT 1514
QY 1359 TGGTTTGATCATTTGGAGATGGCCGCTGCTGTATTTACAGAGGAATCGTGGAGGAATA 1418
Db |||||
QY 1515 TGGTTTGATCATTTGGAAATGGCTGCTGCTGTTGTTATACAGAGGAAATCGTGGAGGAATA 1574
QY 1419 TCAATTTACCATATTACAACATGGTGGTGTGCTGATGACCATCTTATGAACATCGGTGAGGT 1478
Db |||||
QY 1575 TCAATTTACCATATTACAACATGGTGGTGGTGTGCTGATGAGGACATCGGTGAGGT 1634
QY 1479 CGTGTGTGTGAACGCTTCCGGCCCAATCGCTCTTAACCGCTGGAACAGTGAATGTCT 1538
Db |||||
QY 1635 TGTGTGTGTGAACGCTTCCGGCCCAATCGTGTCTTAACCGCTGGAACAGGATGAATGTCT 1694
QY 1539 TCGAGCCGTTTTGAAGCTGATGTAGAAATGCTGGGCCCAATATCCAGCATCCAGACTCAC 1598
Db |||||
QY 1695 TCGAGCAGTTTTGAAGCTAATGTAGAAATGTTGGGCCCAATATCCAGCCTCCAGACTCAC 1754
QY 1599 AGCTTTGAGAATCAAGAACACGCTCGCAAAAGATGGTTGAATCCAGGATGTAAGATTTG 1658

Db 1755 AGCTTTGAGATCAAGAAGACACTTGCAGAAATGGTTGATCCAGGATGTAAGATTTG 1814
QY 1659 AC----AAACAGTTTTTGAGAAAGAAATTTAGACTGCAAGAAATTC-----ACCCGAGGAAG 1710
Db |||||
QY 1815 ACAATTAACAATTTTGAGGGAGAAATTTAGACTGCAAGAAATTTCTTACCCCAAGGAATGG 1874
QY 1711 GTGGAGTTAGCTAGCTAGGATGCGGCTTGGTTTCCAGACTCTCTCTCTACCATCTT 1770
Db |||||
QY 1875 GTGGGATTTAGCATGGAATAGGATGTTGACTTGGTTTCCAGACTCTCTCTCTA-CATCTT 1933
QY 1771 CACAGCTGCTAAACAGTAAACCTTTCCAGACTCTCTCAGAAATGC 1813
Db |||||
QY 1934 CACAGCTGCTAAACAGTAAACCTTACCCTACTCTACAGAAATAC 1976
RESULT 11
US-09-742-153-11
; Sequence 11, Application US/09742153
; Publication No. US20030096296A1
; GENERAL INFORMATION:
; APPLICANT: Rosenbaum, Jan S
; TITLE OF INVENTION: The Use of a BMP Protein Receptor
; Co-Transfected with a Type II BMP Receptor and a Type I
; BMP Receptor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Procter & Gamble Company
; STREET: 11810 East Miami River Road
; CITY: Ross
; STATE: OH
; COUNTRY: USA
; ZIP: 45061
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/742,153
; FILING DATE: 20-Dec-2000
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,467
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hersko, Bart S.
; REGISTRATION NUMBER: 32,572
; REFERENCE/DOCKET NUMBER: 5474R
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (513) 627-0633
; TELEFAX: (513) 627-0260
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2402 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-742-153-11
Query Match 86.8%; Score 1574.2; DB 3; Length 2402;
Best Local Similarity 94.2%; Pred. No. 0;
Matches 1669; Conservative 0; Mismatches 93; Indels 9; Gaps 3;
QY 51 GAAATTGGCAATGACTCAGCTATACATTACATGATTTACTGGAGGCTGTCTGTTCAT 110
Db |||||
QY 1 GAATCAGACAATGACTCAGCTATACATTACATGATTTACTGGAGGCTGTCTGTTCAT 60
QY 111 CATTTCTCATGTTCAAGGGCAGAAATCTAGATAGTAGTCTCCATGGTACTGGTATGAAATC 170
Db |||||

Db 61 CATTCTCTATGTTCAAGGCGAGAACTAGATAGTATGCTCCATGGCACCTGATGAATC 120
Qy 171 AGACGTGGACCAAGAAAGCGGAAATGGAGTGCAGCTTAGCACCAGAGACACCTTACC 230
Db 121 AGACTTGGACCAAGAAAGCGGAAATGGAGTGCAGCTTAGCACCAGAGATACCTTGCC 180
Qy 231 TTTCTTAAATATGCTATTGCTCAGGACACTGCCAGATGACGCTATTAAATACACATGCAT 290
Db 181 TTTCTTAAAGTCTATTGCTCAGGACACTGCCAGATGACGCTATTAAATACACATGCAT 240
Qy 291 AACTAATGGCCATGCTTTGGCATATAGAAAGATGATCAGGAGAAACACGTTTAA 350
Db 241 AACTAATGGCCATGCTTTGGCATATAGAAAGATGATCAGGAGAAACACCAATTAAC 300
Qy 351 TTTCTGGGTGATGAAGTATGAAGCTCTGATTTTCAATGCAAGATTCACCAAAAGCCCA 410
Db 301 TTTCTGGGTGATGAAGTATGAAGCTCTGATTTTCAATGCAAGATTCACCGAAAGCCCA 360
Qy 411 GCTACGAGGACCAATAGAAATGTTGTGGACCAATTTGTGCAACCAATTTTGCAGCCCTAC 470
Db 361 GCTACGAGGACCAATAGAAATGTTGTGGACCAATTTGTGCAACCAATTTTGCAGCCCTAC 420
Qy 471 ACTGCCCCCTGCTGTTATAGCCCAATTTGTGATGGCAGCGTCCGATGGCTGGCTGCT 530
Db 421 ACTGCCCCCTGCTGTTATAGCCCAATTTGTGATGGCAGCGTCCGATGGCTGGCTGCT 480
Qy 531 CATCTCTATGGCTGCTGTTATGTCGCCATGATGCTCTTCCAGCTGCTTCTGTTACAA 590
Db 481 CATTTCATGGCTGCTGTTATGTTGCTATGATCATCTTCCAGCTGCTTTTGTGCTATAA 540
Qy 591 ACATTACTGTAAAGATATCTCAAGCAGAGGTGCTTACCAACCGTGACCTTGGAAACAGGATGA 650
Db 541 GCATTATTGTAAAGATATCTCAAGCAGGCGTCTGTACCAACCGTGATTTGGAAACAGGATGA 600
Qy 651 AGCATTATTTCCAGTAGGAGAAATCACTGAAAGACCTGATTTGACAGTCAAAAGCTCTGG 710
Db 601 AGCATTATTTCCAGTAGGAGAAATCAITGAAAGACCTGATTTGACAGTCCCAAAGCTCTGG 660
Qy 711 TAGTGATCTGGATTAACCTTTATTTGTTTCCAGCAACTATTGCCAACAGATTACAGATGGT 770
Db 661 GAGTGATCTGGATTTGCTTTTATTTGGTTTACGCAACTATTGTTGCCAACAGATTACAGATGGT 720
Qy 771 TCGGCAGGTTGTTAAGGCGCGTATGGAGAAATGATGGTGGTAAATGGCGTGGTGAATA 830
Db 721 TCGGCAGGTTGTTAAGGCGCGTATGGAGAAATGATGGTGGTAAATGGCGTGGTGAATA 780
Qy 831 AGTGGCTGTCAAAAGTATTTTTTACCACTGAAGAGCTAGCTGTTTAGAGAAACAGAAAT 890
Db 781 AGTGGCTGTCAAAAGTATTTTTTACCACTGAAGAGCTAGCTGTTTAGAGAAACAGAAAT 840
Qy 891 CTACCCAGCGTCTTAATGCGTCATGAAATATATCTTGGTTTATAGCTGCACACATTAA 950
Db 841 CTACCCAGCGTCTTAATGCGTCATGAAATATATCTTGGTTTATAGCTGCACACATTAA 900
Qy 951 AGGCACCGTCTCCTGGACTCAGCTGATTTGATTTACTGATTACCATGAGAAATGGGCTCT 1010
Db 901 AGGCACCGTCTCCTGGACTCAGCTGATTTGATTTACTGATTACCATGAGAAATGGATCTCT 960
Qy 1011 CTATGATCTTCTGAAATGTGCCACCTCGGACACACAGAGCCCTACTCAAGTTAGCTTTATC 1070
Db 961 CTATGATCTTCTGAAATGTGCCACCTTAGACACACAGAGCCCTACTCAAGTTAGCTTTATC 1020
Qy 1071 TGGTGGCTGTGGTCTGTGCCACCTCCACACAGAAATTTATGGACCGCAAGCGGAGCTGC 1130
Db 1021 TGGTGGCTGTGGTCTGTGCCACCTCCACACAGAAATTTATGGTACCAAGGGAAGCGCTGC 1080
Qy 1131 AATTGCTCATCGAGACTGAAGAGCAAAACATCTTTATTAAGAAAAATGGTATTTGGCTG 1190
Db 1081 AATTGCTCATCGAGACTGAAGAGCAAAACATCTTTATTAAGAAAAATGGAAATTTGGCTG 1140
Qy 1191 TATTGCTGACCTGGGCTAGCTGTTAAATTTCAA CAGTGACACAAATGAAGTTGACATACC 1250
Db 1141 TATTGCTGACCTGGGCTAGCTGTTAAATTTCAA CAGTGACATGATACAAATGAAGTTGACATACC 1200

Qy 1251 CTTGAACACACAGGTTGGGACACAGCGGTATACATGGCTCCAGAAAGTGTCTGGACGAGCCT 1310
Db 1201 CTTGAATATACAGGGTGGGACACAGCGGTATACATGGCTCCAGAAAGTGTCTGGATGAAGCCT 1260
Qy 1311 GAGTAAAAACCAATTTCCAGCCCTATACATCATGGCTGACATCTACAGCTTTTGGTTGATCAT 1370
Db 1261 GAATAAAAAACCAATTTCCAGCCCTATACATCATGGCTGACATCTATAGCTTTTGGTTGATCAT 1320
Qy 1371 TTGGGAGATGGCCCGTGGCTGTATTACAGAGAGAAATCGTGGAGAAATATCAATTACCATA 1430
Db 1321 TTGGGAAATGGCTGCTGCTGTTGATTACAGAGAGAAATCGTGGAGAAATATCAATTACCATA 1380
Qy 1431 TTAACAACATGGTCCAGTACGACCATCTTATGAAGACATGCGTGAGCTCGTGTGTGGA 1490
Db 1381 TTAACAACATGGTCCAGTACGACCATCTTATGAGGACATCGGTGAGGTTGTGTGTGGA 1440
Qy 1491 ACCTTTGGGCCCAATCGTCTTAAACCGCTGGAA CAGTGATGAATGTCTTCGAGCCGTTT 1550
Db 1441 ACCTTTGGGCCCAATCGTCTTAAACCGCTTGAACACGCGATGAATGTCTTCGAGCAGTTT 1500
Qy 1551 GAAGCTGATGTCAAGATGCTGGGCCCATTAATCCAGATCCAGACTCACAGCTTTGAGAAAT 1610
Db 1501 GAAGCTAATGTCAAGATGTTGGGCCCATTAATCCAGCTCCAGACTCACAGCTTTGAGAAAT 1560
Qy 1611 CAAGAAGACGCTCGCAAAAGATGGTTGAATCCCAAGGATGTAAGATTTGAC- ---AAACAG 1666
Db 1561 CAAGAAGACACTTGGCAAAATGGTTGAATCCCAAGGATGTAAGATTTGACAAATTAACAA 1620
Qy 1667 TTTTGAAGAAAGATTTAGACTGCAAGAAATTC- ---ACCCGAGAAAGGTTGGAGTTAGCA 1722
Db 1621 TTTTGAAGGAGAAATTTAGACTGCAAGAAATTCCTTCCACCAAGGAATGGTGGGATTTAGCA 1680
Qy 1723 TGACCTAGATGTGGCTGGTTTCCAGACTCTCTCTCTACCATCTTCCAGAGCTGCTA 1782
Db 1681 TGGAAATAGATGTGACTTGGTTTCCAGACTCTCTCTCTCTA-CATCTTCCAGGCTGCTA 1739
Qy 1783 ACAGTAAACCTTTACGAGCTCTGCAGAAATGC 1813
Db 1740 ACAGTAAACCTTTACCGCACTCTACAGAAATAC 1770

RESULT 12

US-10-641-319-3
; Sequence 3, Application US/10641319
; Publication No. US20040143863A1
; GENERAL INFORMATION:
; APPLICANT: Li, Linheng
; APPLICANT: Zhang, Jwang
; TITLE OF INVENTION: Hematopoietic Stem Cell Niche Cells
; FILE REFERENCE: 64928
; CURRENT APPLICATION NUMBER: US/10/641,319
; CURRENT FILING DATE: 2003-08-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 2056
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-641-319-3

Query Match 78.6%; Score 1424.4; DB 7; Length 2056;

Best Local Similarity 90.3%; Pred. No. 0;
Matches 1584; Conservative 0; Mismatches 76; Indels 94; Gaps 2;

Qy 39 CAGGACACGCTGGCAATTTGACAAATGACTCAGCTATACACTTACATCAGATTACTGGGAGC 98
Db 269 CAGGACGCTGGCAATCAGCAATGACTCAGCTATACACTTACATCAGATTACTGGGAGC 328
Qy 99 CTGCTGTTTCATCATTTCTCATGTTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGGTAC 158
Db 329 CTGCTGTTTCATCATTTCTCATGTTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGGCAC 388

APPLICATION NUMBER: 9304680.3
FILING DATE: 8-March-1993
APPLICATION NUMBER: 9311047.6
FILING DATE: 28-May-1993
APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
APPLICATION NUMBER: 9136099.2
FILING DATE: 3-August-1993
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-October-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kohlei, Vineet
REGISTRATION NUMBER: 37, 003
REFERENCE/DOCKET NUMBER: LUD 5298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2932 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 310..1905
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-903-068-5

Query Match 76.5%; Score 1387; DB 3; Length 2932;

Best Local Similarity 87.8%; Pred. No. 0;

Matches 1561; Conservative 0; Mismatches 205; Indels 11; Gaps 4;

QY	39	CAGGACACGTCGCAATTTGGCAATGACTCAGCTATACACTTACATCAGATTACTGGAGC	98
DB	288	CAGGAACAATACAAATTTGAACAATGACTCAGCTATACATTTACATCAGATTATTGGAGC	347
QY	99	CTGCTGTTTCATCATTTCTCATGTTCAAGGGCAGAACTAGATAGTATGCTCCATGGTAC	158
DB	348	CTATTGTTTCATCATTTCTGTTTCAAGGACAGAACTGAGTATGCTTCATGGCAC	407
QY	159	TGTTATGAATACAGCTGGACAGAGAAAGCGGAAATGGAGTGAAGTTAGCACAG	218
DB	408	TGGGATGAATACAGCTCCGACAGAGAAAGTCAAGAAATGGAGTAACTTAGCACAG	467
QY	219	GGACACCTTACCTTTCTTAAATGCTATTGCTCAGGACACTGCCAGATGACGCTATTAA	278
DB	468	GGATACCTTGCCCTTTTAAAGTGCTATTGCTCAGGGCACTGCCAGATGATGCTATTAA	527
QY	279	TAAACATGATCAATCAATGCGCATTTGCTTGGCATTATAGAGAAAGATGATCAGGAGA	338
DB	528	TAAACATGATCAATCAATGCGCATTTGCTTGGCATTATAGAGAAAGATGATCAGGAGA	587
QY	339	AACCACTTAACTTCTGGGTGATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTC	398
DB	588	AACCACTTAACTTCTGGGTGATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTC	647
QY	399	ACCAAAAGCCAGCTACGAGGACAAATAGAAATGTTGCGGACCAATTTGCAACCAATA	458
DB	648	TCCAAAGCCAGCTACGCGGACAAATAGAAATGTTGCGGACCAATTTGCAACCAATA	707
QY	459	TTTGACGCTTACACTGCCCCCTGCTGTTATAGGCCCAATCTTTGATGGCAGCGTCCGATG	518
DB	708	TTTGACGCTTACACTGCCCCCTGCTGTTATAGGCCCAATCTTTGATGGCAGCGTCCGATG	767
QY	519	GCTGGCTGCTCATCTCTATGCTGCTGTTATGTCGCCAATGATCGTCTTCTCCAGCTG	578

DB	768	GCTGGTTTTGCTCATTTCTATGGCTGCTGCATAAATTGCTATGATCATCTTCTCCAGCTG	827
QY	579	CTTCTCTTACAAACATTACTGTAAGAGTATCTCAAGCAGAGGTCGTTACAAACGTCGCTT	638
DB	828	CTTTTCTTACAAACATTACTGTAAGAGTATCTCAAGCAGAGGTCGTTACAAACGTCGCTT	887
QY	639	GGAAACAGGATGAAGCAATTTATTCAGTAGGAGAAATCACTGAAAGACCTGATTTGACCA	698
DB	888	GGAAACAGGATGAAGCAATTTATTCAGTAGGAGAAATCACTGAAAGACCTGATTTGACCA	947
QY	699	ACAAAGCTCTGGTAGTGGATCTGGATACCTTTATTTGGTTTACGCGAACTATTTGCCAA	758
DB	948	ACAAAGCTCTGGTAGTGGGTCCTGGATACCTTTATTTGGTTTACGCGAACTATTTGCCAA	1007
QY	759	GATTACAGATGTTTCGGCAGGTTGGTAAGGCGCGTATGGAGAGTATGGATGGGAAATG	818
DB	1008	GATTACAGATGTTTCGGCAGGTTGGTAAGGCGCGTATGGAGAGTATGGATGGGAAATG	1067
QY	819	GCCTGCTGAAAAAGTGGCTGCTCAAGTATTTTTTACCACCTGGAAGAAAGTACGTGGTTT	878
DB	1068	GCCTGCTGAAAAAGTGGCTGCTCAAGTATTTTTTACCACCTGGAAGAAAGTACGTGGTTT	1127
QY	879	AGAAACAGAAATCTACACAGCGGTGTTAATGCGTCTATGAAATATATATCTGGTTTAT	938
DB	1128	AGAAACAGAAATCTACACAACTGCTGCTAATGCGCCATGAAACATATCTGGTTTAT	1187
QY	939	TGCAGACATTTAAAGGCACCGGTTCTGGACTCAGCTGATTTGATTTACTGATTACCAT	998
DB	1188	GGCAGACATTTAAAGGTACAGGTTCTCGGACTCAGCTCTATTTGATTTACTGATTAC	1247
QY	999	GAATGGTCTCTCTATGACTTCTCTGAAATGTGCAACCTGGACACCCAGAGCCCTACT	1058
DB	1248	GAATGGTCTCTCTATGACTTCTCTGAAATGTGCTACACTGACACCCAGAGCCCTGCT	1307
QY	1059	GTTAGCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1118
DB	1308	ATTGGCTTATTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1367
QY	1119	AGGCAAGCTCGAATTTGCTCATCGAGACCTGAGAGCAAAACATCTTTTAAAGAA	1178
DB	1368	AGGCAAGCTCGAATTTGCTCATCGAGACCTTAAAGCAAAACATCTTTTAAAGAA	1427
QY	1179	TGCTAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1238
DB	1428	TGCTAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1487
QY	1239	AGTTGACATACCTTTGAAACACAGAGGTGGGACACAGGCGGTACATGGCTCCAGAA	1298
DB	1488	AGTTGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1547
QY	1299	GGACAGAGCCTGAGTAAACCAATTTCCAGCCCTACATCATGGCTGACATCTACAGCTT	1358
DB	1548	GGACAGAGCCTGAGTAAACCAATTTCCAGCCCTACATCATGGCTGACATCTACAGCTT	1607
QY	1359	TGCTTTGATCATTTGGAGATGGCCCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1418
DB	1608	CGGCTTAATCATTTGGAGATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1667
QY	1419	TCAATTTACATTTTCAACATCGTGTAGTACCCATCTTTATGAAGAATGCGTGGT	1478
DB	1668	CCAAATGCTCATTTCAACATCGTGTAGTACCCATCTTTATGAAGAATGCGTGGT	1727
QY	1479	CGTGTGTGAAACGCTTGGGCGCATCTGCTCTAACCGCTGGAACAGTGAATGCTCT	1538
DB	1728	TGCTGTGTGAAACGCTTGGGCGCATCTGCTCTAACCGCTGGAACAGTGAATGCTCT	1787
QY	1539	TGAGCGCTTTTAAAGCTGATGTCAGAAATGCTGGGCCCAATATCCAGCACTCCAG	1598
DB	1788	ACGAGCAGTTTGAAGCTAATGTCAGAAATGCTGGGCCCAATATCCAGCACTCCAG	1847
QY	1599	AGCTTTGAGAAATCAAGAGACGCTCGCAAGATGTTGAAATCCAGGATGTAAGATTG	1658
DB	1848	AGCATTTGAGAAATCAAGAGACGCTTGGCCAAAGATGGTTGAAATCCCAAGATGTA	1907

QY 1539 TCAGCGCTTTTGAAGCTGATGTGAGAAATCTGGGCCATAAATCCAGACTCCAGACTCAC 1598
DB 1788 ACCGAGCAGTTTGAAGCTAATGTGAGAAATCTGGGCCACAATCCAGCTCCAGACTCAC 1847
QY 1599 AGCTTTGAGAAATCAAGAGACGCTCGCAAGATGGTTGAATCCAGGATGTAAGATTTC 1658
DB 1848 AGCAATTGAGAAATTAAGAGACGCTCGCAAGATGGTTGAATCCCAAGATGTAAGAAATCTG 1907
QY 1659 A----CAAAACAGTTTGGAGAAAGAAATTTAGACTGCAAGAA-----ATTCAACCCGAGGAAG 1709
DB 1908 ATGGTTAAACCATCGGAGGAGAACTCTAGACTGCAAGAAATCTGTTTATACCCATGGCATG 1967
QY 1710 GGTGGAGTTAGCATGGACT-AGGATGTGGCTTTGGTTTCCAGACTCTCTCTCTC-TACCAT 1767
DB 1968 GGTGGAATTAGAGTGGAATAAGGATGTTAACTTTGGTTCTCAGACTCTCTTCTTCACTACGT 2027
QY 1768 CTTTCACAGGCTGTACAGTAAGTAACCTTTCAGGACTCT 1804
DB 2028 GTTCACAGGCTGCTAATATTAAACCTTTCAGTACTCT 2064

RESULT 15
US-10-286-152A-37
; Sequence 37, Application US/10286152A
; Publication No. US20030134308A1
; GENERAL INFORMATION:
; APPLICANT: Alcon Research, Ltd.
; APPLICANT: Clark, Abbot F.
; TITLE OF INVENTION: Bone Morphogenic Proteins (BMP), BMP Receptors and BMP Binding Peptides
; TITLE OF INVENTION: and Their Use in the Diagnosis and Treatment of Glaucoma
; FILE REFERENCE: 2312 US
; CURRENT APPLICATION NUMBER: US/10/286.152A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 2932
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-286-152A-37

Query Match 76.5%; Score 1387; DB 6; Length 2932;
Best Local Similarity 87.8%; Pred. No. 0;
Matches 1561; Conservative 0; Mismatches 205; Indels 11; Gaps 4;

QY 39 CAGGACAGCTGCGAAATGGCAATGACTCAGCTATACACTTACATCAGATTTATGGGAGC 98
DB 288 CAGGAAACATTACAATTTGAACAATGACTCAGCTATACATTTACATCAGATTTATGGGAGC 347
QY 99 CTGCTGTTCATCATTTCTCATGTTCAAGGGCAGAATCTAGATAGTATGCTCCATGGTAC 158
DB 348 CTATTTGTTTCATCATTTCTGTTTCAAGGACAGAATCTGGATAGTATGCTTCATGGCAC 407
QY 159 TGGTATGAATCAGACGTGGACAGAGAGAGCGGAAAATGGAGTGACCTTAGCACCAGA 218
DB 408 TGGGATGAATCAGACTCCGACCAGAAAAGTCAGAAAATGGAGTAACCTTAGCACCAGA 467
QY 219 GGCACCTTACCTTTCTTAAATGCTATTGCTCAGGACACTGCCAGATGACGCTATTAA 278
DB 468 GGTACCTTGCCTTTTAAAGTGCTATTGCTCAGGGCAGCTGCCAGATGATGCTATTAA 527
QY 279 TAACACATGCATAACTAATGGCCATTGCTTGCATTATAGAGAAGATGATCAGGGAGA 338
DB 528 TAACACATGCATAACTAATGGCAATGCTTGGCCATCATAGAGAAGATGATCAGGGAGA 587
QY 339 AACACGTTAACTTCTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTC 398
DB 588 AACACATTAGCTTCAGGGTGTATGAATATGAAGATCTGATTTTCACTGCAAGATTC 647
QY 399 ACCAAAGCCAGCTACGAGGACAAATAGAAATGTTGTCGGACCAATTTGTTGCAACCAATA 458
DB 648 TCCAAAGCCAGCTACGCGCGCAATAGAAATGTTGTCGGACCAATTTATGTAAACCAATA 707

QY 459 TTTGACGCTTACACTGCCCCCTGCTGCTATAGCCCAATCTTTGATGGCAGCGTCCGATG 518
DB 708 TTTGCAACCCACACTGCCCCCTGCTGCTCATAGGTCCGTTTTTTGATGGCAGCATTCGATG 767
QY 519 GCTGGCTGTGCTCATCTCTATAGGCTGTCTGTAATGTGCGCATGATCGTCTTCTCCAGCTG 578
DB 768 GCTGGTTTTGCTCATTTCTATGGCTGTCTGCATAAATTGCTATGATCATCTTCTCCAGCTG 827
QY 579 CTTCTGTTTACAACATTTACTGTAAAGAGTATCTCAAGCAGAGGTCGTTTACAACCGTGACTT 638
DB 828 CTTTGTGTTACAACATTTATTCAGAGAGCATCTCAAGCAGACGCTGTTTACAACTCGTATTT 887
QY 639 GGAACAGGATGAAGCATTTATTCAGTAGGAGAAATCACTGAAAGACGCTGATTGACCAATC 698
DB 888 GGAACAGGATGAAGCATTTATTCAGTTGGAGAAATCACTTAAAGACCTTATTGACCAATC 947
QY 699 ACAAGCTCTGGTAGTGGATCTGGATTAACCTTTATTTGGTTTACGCGAACTATTGCGCAAA 758
DB 948 ACAAGTTCTGGTAGTGGCTGTGGACTACCTTTATTTGGTTTACGCGAACTATTGCGCAAA 1007
QY 759 GATTACAGATGTTTCGGCAGGTTGGTAAGGCGCGTATGGAGAGATATGGATGGTAAATC 818
DB 1008 GATTACAGATGTTTCGGCAGGTTGGTAAGGCGCGTATGGAGAGATATGGATGGCAGAAATC 1067
QY 819 GCGTGTGAAAAAGTGGCTGTCAAAAGTATTTTTTACCACCTGAAAGAGCTAGCTGGTTTAC 878
DB 1068 GCGTGGCGAAAAAGTGGCGGTGAAAGTATTTTACCACCTGAAAGAGCCAGCTGGTTTTC 1127
QY 879 AGAAACAGAAATCTACAGACGGTGTAAATGCGTCTATGAAATATATCTTGGTTTATATAGC 938
DB 1128 AGAAACAGAAATCTACAACTGTGTAAATGCGCCATGAAACATATCTTGGTTTATATAGC 1187
QY 939 TGCAGACATTAAGGACCGGTTCTGGAAGTACGCTGATTTGATTTACTGATTACCATGA 998
DB 1188 GGCAGACATTAAGGAGTACAGGTTCTGGACTCAGCTCTATTTGATTACTGATTACCATGA 1247
QY 999 GAATGGGTCTCTATGACTTCTGAAATGTGCAACCTTGGACACCCAGACAGCCCTACTCAA 1058
DB 1248 AATGGATCTCTATGACTTCTGAAATGTGCTACACTGGACACCCAGAGCCCTGCTTAA 1307
QY 1059 GTTAGCTTATCTGCTGCTGCTGTGTCGCCACCTTCCACAGAAATTTATGGCAGCA 1118
DB 1308 ATTTGGCTTATTCAGCTGCTGCTGTGTCGCCACCTTGCACACAGAAATTTATGGCAGCA 1367
QY 1119 AGGCAAGCTGCAATTTGCTCATCGAGACCTGAAAGCAAAAACATCTTTATTAAGAAAA 1178
DB 1368 AGGAAAGCCCGCAATTTGCTCATCGAGACCTTAAAGCAAAAACATCTTTATTAAGAAAA 1427
QY 1179 TGGTAGTTGCTGTATTTGCTGACTTGGGCTTAGCTGTTAAATTTCAACAGTGACACAAATGA 1238
DB 1428 TGGGAGTTGCTGCTATGCTGACTTGGGCTTGTGTTAAATTTCAACAGTGACACAAATGA 1487
QY 1239 AGTTGACATACCTTTGAACACACAGGGTGGGCAACGAGCGGTACATGGCTCCAGAAATGCT 1298
DB 1488 AGTTGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1547
QY 1299 GACAGAGAGCTGAGTAAACCAATTTCCAGGCTTACATCATGGCTGACATCTACAGCTT 1358
DB 1548 GGACGAAAGCCCTGAAACAAAACCACTTCCAGGCTTACATCATGGCTGACATCTACAGCTT 1607
QY 1359 TGGTTTGTATCATTTGGGAGATGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1418
DB 1608 CGGCTTATCATTTGGGAGATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1667
QY 1419 TCAATTACCATAATTAACACATGGTGCCTAGTAGCCCACTTTATGAAGACATCGCTGAGGT 1478
DB 1668 CCAATTGGCATATTAACACATGGTGCCTAGTAGCCCACTTTATGAAGACATCGCTGAGGT 1727
QY 1479 CGTGTGTGTAACGCTTGGCGCAATCGTCTCTAACCGCTGGAACAGTGAATGTCT 1538
DB 1728 TGTGTGTGTAACGCTTGGCGCAATCGTCTCTAACCGCTGGAACAGTGAATGTCT 1787
QY 1539 TCGAGCCGTTTTTGAAGCTGATGTCAGAAATGCTGGGCCCCATAATCCAGCATCCAGACTCAC 1598

Db	1788	ACGAGCAGTTTTGAAGCTTAATGTCAGAAATGCTGGGCCCAAAATCCAGCCTCCAGACTCAC	1847
Qy	1599	AGCTTTTGAGAAATCAAGAAGAAGCGCTCGCAAAAGATGGTTTGAATCCCAGGATGTAAAGATTTG	1658
Db	1848	AGCATTTGAGAAATTAAGAAGAAGCGCTTGCCAAGATGGTTGAATCCCAAGATGTAAAAATCTG	1907
Qy	1659	A-----CAACACAGTTTTTCAGAAAGAAATTTAGACTGCAAGAA-----ATTACCCCGAGGAAG	1709
Db	1908	ATGTTTAAACCATCGGAGGAGAAACTCTAGACTGCAAGAACTGTTTATCCCATGGCAGT	1967
Qy	1710	GGTGGAGTTAGCATGGACT-AGGATGTGGCTGGGTTTCCAGACTCTCTCCTC-TAGCAT	1767
Db	1968	GGTGGAAATTAGGTGGAATTAAGGAATGTTAACTTGGTTCTCAGACTCTTTCTTCTTCACTACGT	2027
Qy	1768	CTTTCACAGGCTGTAAACAGTAAACCTTTTCAGGACTCT	1804
Db	2028	GTTTCACAGGCTGTAAATATTAAACCTTTTCAGTACTCT	2064

Search completed: December 9, 2005, 19:34:45
Job time : 1042 secs

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OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 17:16:24 ; Search time 167 Seconds
(without alignments)
4058.673 Million cell updates/sec

Title: US-10-600-645-1

Perfect score: 1813

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA_New:*
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10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	154.4	8.5	2090	6	US-10-420-192-7
2	55.8	3.1	2197	6	US-10-750-185-35470
3	45.4	2.5	1481	6	US-10-750-185-39254
4	38	2.1	840	6	US-10-750-185-53450
5	36.6	2.0	193363	7	US-11-112-908-32
6	36.4	2.0	94905	7	US-11-117-187-208
7	36.4	2.0	1082144	7	US-11-117-187-211
8	35.6	2.0	82596	7	US-11-117-187-207
9	35.6	2.0	94905	7	US-11-117-187-208
10	35.6	2.0	1082144	7	US-11-117-187-211
11	35.2	1.9	1342	6	US-10-750-185-29585
12	35.2	1.9	40349	7	US-11-117-187-184
13	34.8	1.9	72600	7	US-11-117-187-206
14	33.8	1.9	150038	7	US-11-121-086-23
15	33.6	1.9	1843	6	US-10-750-185-57651
16	33.4	1.8	127340	7	US-11-112-908-35
17	33	1.8	1188	6	US-10-750-185-55126
18	32.8	1.8	2554	8	US-11-132-285-1
19	32.8	1.8	3334	8	US-11-132-285-39
20	32.8	1.8	3501	6	US-10-131-826A-37
21	32.6	1.8	2577	6	US-10-750-185-29680
22	32.6	1.8	3073	7	US-11-113-424-11
23	32.4	1.8	1464	6	US-10-750-185-64192

ALIGNMENTS

RESULT 1

US-10-420-192-7
; Sequence 7, Application US/10420192
; Publication No. US20050260579A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Herbert Y.
; APPLICANT: Wang, Xiao-Fan
; APPLICANT: Weinberg, Robert A.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: TGF-Beta Type Receptor cDNAs Encoded Products and Uses
; TITLE OF INVENTION: Therefore
; FILE REFERENCE: 0399.1086-022
; CURRENT APPLICATION NUMBER: US/10/420,192
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US 09/584,929
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 08/446,936
; PRIOR FILING DATE: 1995-05-23
; PRIOR APPLICATION NUMBER: US 08/311,703
; PRIOR FILING DATE: 1994-09-23
; PRIOR APPLICATION NUMBER: US 07/786,063
; PRIOR FILING DATE: 1991-10-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2090
; TYPE: DNA
; ORGANISM: genomic
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (336)...(2038)
US-10-420-192-7

Query Match 8.5%; Score 154.4; DB 6; Length 2090;

Best Local Similarity 50.8%; Pred.No. 2.4e-40;
Matches 396; Conservative 0; Mismatches 381; Indels 3; Gaps 1;

QY 825 TGAAGAGTGGCTGTCAAGATATTTTACCACTGAAGAGCTAGCTGGTTTAGAGAAAC 884

Db 1148 TGAGACAGTGGCAGTCAAGATCTTCCCTATGAGGAGTATGCCCTCTTGAAGACAGAGAA 1207

QY 885 AGAATCTACACAGACGGTGTATATGCGTCATGAATAATATCTGGTTTATAGCTCAGAA 944

Db 1208 GGACATCTTCTCAGACATCAATCTGAAGCATAGAGACATACCTCAGTCTCCTGACGCTGA 1267

QY 945 CATTAAGGACCGGTTCTGGGACTCAGCTGTATTGATTACTGATTACCATCAGATGCG 1004

Sequence 20, Appl
Sequence 26173, A
Sequence 11, Appl
Sequence 48490, A
Sequence 210, App
Sequence 200, App
Sequence 83, Appl
Sequence 39137, A
Sequence 191, App
Sequence 13, Appl
Sequence 186, App
Sequence 189, App
Sequence 195, App
Sequence 55434, A
Sequence 205, App
Sequence 54, Appl
Sequence 209, App
Sequence 40032, A
Sequence 52435, A
Sequence 4326, App
Sequence 44445, A
Sequence 58049, A

24 32.4 1.8 162289 7 US-11-121-086-20
25 32.2 1.8 1120 6 US-10-750-185-26173
26 32.2 1.8 2105 7 US-11-054-385-11
27 32 1.8 1544 6 US-10-750-185-48490
28 32 1.8 50959 7 US-11-117-187-210
29 32 1.8 79122 7 US-11-117-187-210
30 32 1.8 187745 7 US-11-121-086-83
31 31.8 1.8 2291 6 US-10-750-185-39137
32 31.8 1.8 94618 7 US-11-117-187-191
33 31.6 1.7 2819 8 US-11-112-944-13
34 31.6 1.7 67088 7 US-11-117-187-186
35 31.6 1.7 83391 7 US-11-117-187-189
36 31.6 1.7 90336 7 US-11-117-187-195
37 31.4 1.7 1514 6 US-10-750-185-55434
38 31.4 1.7 85682 7 US-11-117-187-205
39 31.4 1.7 189252 7 US-11-121-086-54
40 31.4 1.7 611587 7 US-11-117-187-209
41 31.2 1.7 827 6 US-10-750-185-40032
42 31.2 1.7 1210 6 US-10-750-185-52435
43 31.2 1.7 3546 6 US-10-793-626-4326
44 31 1.7 1701 6 US-10-750-185-44445
45 31 1.7 1884 6 US-10-750-185-58049

Db 1268 GGAGCGAAGACGGAGTTGGGAAACAATACCTGGCTGATCAGCGCTTCCAGCGCAAGG 1327
QY 1005 GTCTCTTAATGATCTTCTCAAAATGTGCGACCTTGGACACAGAGCCCTACTCAAGTTAGC 1064
Db 1328 CAACTTACAGGAGTACTTACGCGGCGATGTCATCAGCTGGGAGGACCTGCGCAAGCTGG 1387
QY 1065 TTATTTCTGCTGCTGTGCTGTGCGACCTTCCACACAG---AAATTTATGGCAGCGAAG 1121
Db 1388 CAGCTCCCTCGCCCGGGGGAITGCTCACCTCCACAGTGATCACCTCCATGTGGAGGCC 1447
QY 1122 CAAAGCTGCAATTTGCTCATCTGAGACCTGAAGAGCAAAACATCTTTATTAAGAAAAATGG 1181
Db 1448 CAAAGTCCCATCTGTCACAGGACCTCAAGAGCTCCAATATCTCGTGAAGAACGACCT 1507
QY 1182 TAGTTGCTGTATTTGCTGACCTGGGCTAGCTGTAAATTTCAACAGTGACACAAATGAA 1241
Db 1508 AACCTGCTGCCTGTGTGACTTTGGGCTTTCCCTGCGTCTGGACCTACTCTCTGTGTGA 1567
QY 1242 TGACATACCTTGAACACACAGGTTGGGACACAGGCGGTATCATGGCTCCAGAAATGCTGA 1301
Db 1568 TGACCTGGCTTAACAGTGGCGAGGTGGGAACTGCAAGATACATGGCTCCAGAAATGCTGA 1627
QY 1302 CGAGACCTGAGTAAAAACCATTTCCAGCCCTACATCATGGCTGACATCTACAGCTTTGG 1361
Db 1628 ATCCAGGATGAATTTGGAAATGCTGAGTCTTCAAGCAGCGGATGCTACTCCATGCG 1687
QY 1362 TTTGATCATTTGGAGATGGCCGCTGCTGTATTAAGAGGAATCGTGGAGGAATATCA 1421
Db 1688 TCTGGTGTCTGGAAATGACATCTCGCTGTAATGAGTGGGAGAAATGAAAGATTATGA 1747
QY 1422 ATTACATATTACAACATGGTGGCTAGTACACCATCTTATGAAGACATCGTGAGTGT 1481
Db 1748 GCCTCCATTTGGTTCAGAGTGGGAGCACCCCTGTGTCGAAAGCATGAAGGACAACGT 1807
QY 1482 GTGTGTGAACGCTTCGCGCCCAATCTCTTAACCGCTGGAACAGTGATGATGCTTCG 1541
Db 1808 GTTGAGAGATCAGGCGGACCAAAATTCACAGCTTCTGGCTCAACCACCGGATCA 1867
QY 1542 AGCCGTTTTGAAGTGTGATGTCAAGATGTGCGGCCCATATCCAGCATCCAGATCCACAGC 1601
Db 1868 GATGGTGTGAGACGTTGACTGAGTGTGGGAGCACGACCCAGAGGCGCGTCTCACAGC 1927

RESULT 2
US-10-750-185-35470/c
; Sequence 35470, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 35470
; LENGTH: 2197
; TYPE: DNA
; ORGANISM: Bovine 19866880697177
US-10-750-185-35470

Query Match 3.1%; Score 55.8; DB 6; Length 2197;
Best Local Similarity 56.1%; Pred. No. 1.1e-07;
Matches 105; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 1202 TGGGCTAGCTGTTAAATTTCAACAGTGACACAAATGAAGTTGACATACCTTTGAACACCA 1261
Db 1146 TAGGCTTGGCAGTCAATGCAATTTCCAGAGCAACCAATCAGCTGATGTGGGAAACAACCC 1087
QY 1262 GGTGGGACACAGGCGGTACATGGCTCCAGAAAGTCTCGAGAGAGCTGAGTAAACCC 1321
Db 1086 GTGTGGGACCAACAGCTACATGGCCCCCGAAGTCTTTGATGAAACTATCCAGGTGGATT 1027
QY 1322 ATTTCCAGCCCTACATCATGCTGACATCTACAGCTTTTGGTTTGTATCAATTTGGGAGATGG 1381
Db 1026 GTTTTGAATTTTACAAGAGAGTCAATTTGGGCCCTTTGGACTTGTCTGTGGAGGTGG 967
QY 1382 CCCGTCG 1388
Db 966 CCAGGCG 960

RESULT 3
US-10-750-185-39254/c
; Sequence 39254, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 39254
; LENGTH: 1481
; TYPE: DNA
; ORGANISM: Bovine 19866881053886
US-10-750-185-39254

Query Match 2.5%; Score 45.4; DB 6; Length 1481;
Best Local Similarity 65.0%; Pred. No. 0.00023;
Matches 67; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 292 ACTAATGGCCATTGCTTTGCCATTATAGAAGAGATGATCAGGGAGAAACCAACGTTAACT 351
Db 406 ACAGATGGATATTTTTCACGATGATAGAAGAGATGACTCTGGGATGCCCGTGTCACT 347
QY 352 TCTGGTGTATGAAGTATGAAGGCTCTCTGATTTTCAATGCAAGG 394
Db 346 TCTGGATCTAGGACTAGAGGCTCAGATTTTCAAGTGTCCGG 304

RESULT 4
US-10-750-185-53450
; Sequence 53450, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31


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QY 1706 GRAGGTGGAGTTAGCATGGACTAGGAT 1733
DB 1071543 CTAAGTAGTATTCTCTGTTAGAGAT 1071516

RESULT 8
US-11-117-187-207/c
; Sequence 207, Application US/11117187
; Publication No. US20050266560A1
; GENERAL INFORMATION:
; APPLICANT: PREUSS, DAPHNE
; APPLICANT: COPENHAVER, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD:309US
; CURRENT APPLICATION NUMBER: US/11/117,187
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/09/531,120
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,219
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 207
; LENGTH: 82596
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-207

Query Match 2.0%; Score 35.6; DB 7; Length 82596;
Best Local Similarity 57.6%; Pred. No. 6.7; Mismatches 0; Indels 2; Gaps 1;
Matches 83; Conservative 0;

QY 1590 CAGACTCACAGCTTTGAGAATCAAGAAGCGCTCGCAAGATGGTTGAATCCAGGATGT 1649
DB 20705 CACCATCAAAAGCTTTGAGAAGCAATAAGAAGCTATGTCTAGCTTTTGGAGTCAAAATATGA 20646

QY 1650 AAAGATTTGCACAAACAGTTTGTAG--AAAGAAATTTAGACTGCAAGAAATTCACCCGAGGA 1707
DB 20645 CTAGATGTCATGTGGATGATTGAGTATAAGAACTAAACCGCAACTGGTTCCCAAGGGCT 20586

QY 1708 AGGGTGGAGTTAGCATGGACTAGG 1731
DB 20585 AAAGTAGTGTTAGAAGATACAAAG 20562

RESULT 9
US-11-117-187-208/c
; Sequence 208, Application US/11117187
; Publication No. US20050266560A1
; GENERAL INFORMATION:
; APPLICANT: PREUSS, DAPHNE
; APPLICANT: COPENHAVER, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD:309US
; CURRENT APPLICATION NUMBER: US/11/117,187
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/09/531,120
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,219
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 208
; LENGTH: 94905
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-208

Query Match 2.0%; Score 35.6; DB 7; Length 94905;
Best Local Similarity 57.6%; Pred. No. 7.4; Mismatches 0; Indels 2; Gaps 1;
Matches 83; Conservative 0;

QY 1590 CAGACTCACAGCTTTGAGAATCAAGAAGCGCTCGCAAGATGGTTGAATCCAGGATGT 1649
DB 20705 CACCATCAAAAGCTTTGAGAAGCAATAAGAAGCTATGTCTAGCTTTTGGAGTCAAAATATGA 20646

QY 1650 AAAGATTTGCACAAACAGTTTGTAG--AAAGAAATTTAGACTGCAAGAAATTCACCCGAGGA 1707
DB 20645 CTAGATGTCATGTGGATGATTGAGTATAAGAACTAAACCGCAACTGGTTCCCAAGGGCT 20586

QY 1708 AGGGTGGAGTTAGCATGGACTAGG 1731
DB 20585 AAAGTAGTGTTAGAAGATACAAAG 20562

RESULT 10
US-11-117-187-211
; Sequence 211, Application US/11117187
; Publication No. US20050266560A1
; GENERAL INFORMATION:
; APPLICANT: PREUSS, DAPHNE
; APPLICANT: COPENHAVER, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD:309US
; CURRENT APPLICATION NUMBER: US/11/117,187
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/09/531,120
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,219
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 211
; LENGTH: 1082144
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-211

Query Match 2.0%; Score 35.6; DB 7; Length 1082144;
Best Local Similarity 57.6%; Pred. No. 38; Mismatches 0; Indels 2; Gaps 1;
Matches 83; Conservative 0;

QY 1590 CAGACTCACAGCTTTGAGAATCAAGAAGCGCTCGCAAGATGGTTGAATCCAGGATGT 1649
DB 987951 CACCATCAAAAGCTTTGAGAAGCAATAAGAAGCTATGTCTAGCTTTTGGAGTCAAAATATGA 988010

QY 1650 AAAGATTTGCACAAACAGTTTGTAG--AAAGAAATTTAGACTGCAAGAAATTCACCCGAGGA 1707
DB 988011 CTAGATGTCATGTGGATGATTGAGTATAAGAACTAAACCGCAACTGGTTCCCAAGGGCT 988070

QY 1708 AGGGTGGAGTTAGCATGGACTAGG 1731
DB 988071 AAAGTAGTGTTAGAAGATACAAAG 988094

RESULT 11
US-10-750-185-29585/c
; Sequence 29585, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29585
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	Query Match	1.9%;	Score 34.8;	DB 7;	Length 72600;
	Best Local Similarity	56.8%;	Pred. No.11;		
	Matches 84;	Conservative 0;	Mismatches 62;	Indels 2;	Gaps 1;
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Db	59912	TTCCACATCAAGCTTTTGAGAGCAGAGAGGTTGGTTAGTTGTTGGAGTCGAATAT	59853		
Qy	1648	GTAAGATTTTGACAAACAGTTTTTGAG--AAAGAAATTTAGACTGCAAGAAATTTACCCCGAG	1705		
Db	59852	GACTTGATGCTGCTGATGATTGAGTATAGAACTTAACTGCAACCTGATCTTAAAG	59793		
Qy	1706	GAAGGGTGGAGTTAGCATGGACTAGGAT	1733		
Db	59792	CGTAAGTAGTGTTACCTGCTTATAAGT	59765		

Db 59792 CCTAAGTAGTGTACCTTGTATAAGAT 59765

	Query Match	1.9%;	Score 33.8;	DB 7;	Length 150038;
	Best Local Similarity	58.4%;	Pred. No. 40;		
	Matches 59;	Conservative	0;	Mismatches 42;	Indels 0;
	Gaps	0;			
Qy	1626	AAAGATGTTGTAATCCCAAGGTGTAAGACATTTGACAAACATTTTGGAGAAAGATTTTAGA	1695		
Db	76614	AAAGATGATGGGAGGATGCGATGGGAGGATCCGCAAAAGGATGGGAAATGGATGGAGG			
Qy	1686	CTCGAAGAAATTCACCCAGGAAGGGTGGAGTTAGCATGGA	1726		
Db	76554	ATGGGAAGGAAAAATGGATGAGAGGATGATAGAGAAATGGA	76514		

RESULT 15
US-10-750-185-57651/C
; Sequence 57651, Application US/10750185
; Publication NO. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 13:31:58 ; Search time 5033 Seconds

(without alignments)
16853.761 Million cell updates/sec

Title: US-10-600-645-1

Perfect score: 1813

Sequence: 1 CTAGTGGATCCCCGGGCTG.....TTCAGGACTCTGAGAATGC 1813

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1389.6	76.6	1521	10 AY411158	Mus muscu
2	1274.6	70.3	1532	10 AY411156	Homo sapi
3	1002.2	55.3	1532	10 AY411157	Pan trogl
4	774.6	42.7	1121	3 BM473726	AGENCOURT
5	736	40.6	874	1 AU124197	AU124197
6	734	40.5	915	7 CV558493	UI-M-HZO-
7	728.5	40.2	842	8 CX204646	MNS07540
8	717.2	39.6	1911	4 AK086130	Mus muscu
9	715.6	39.5	779	7 CK638737	UI-M-HO-
10	710	39.2	1509	10 AY418115	Mus muscu
11	707.6	39.0	783	6 CF744610	UI-M-GVO-
12	705	38.9	826	8 DR156725	HESC2 69
13	703.8	38.8	763	7 CV557698	UI-M-HZO-
14	702	38.7	1509	10 AY418113	Homo sapi
15	682.6	37.7	769	6 CD351417	UI-M-GIO-
16	672.8	37.1	1509	10 AY418114	Pan trogl
17	668.4	36.9	909	5 BU152346	AGENCOURT
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19	666.5	36.8	772	7 CN460181	UI-M-HO-
20	664.8	36.7	717	7 CO045435	UI-M-HO-
21	664.8	36.7	775	6 CD352514	UI-M-GIO-
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ALIGNMENTS

RESULT 1

AY411158

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Gene

ORIGIN

Query Match

Best Local Similarity

Matches 1452; Conservative

Score 1389.6; DB 10; Length 1521;

Pred. No. 0;

Mismatches 69; Indels 11; Gaps 1;

23	652	36.0	708	7	CN457827	UI-M-HNO-
24	651.2	35.9	736	6	CA749455	UI-M-PVO-
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26	635.8	35.1	689	7	CN535314	UI-M-HSO-
27	629.2	34.7	1073	7	CN643937	ILLUMISEN
28	625.6	34.5	741	6	CF741390	UI-M-GHO-
29	621.6	34.3	849	6	CD244444	AGENCOURT
30	618.4	34.1	750	6	CD804808	UI-M-GWO-
31	616.8	34.0	817	6	CD352073	UI-M-GIO-
32	610	33.6	677	7	CV558110	UI-M-HZO-
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37	590	32.5	773	1	AU123612	AU123612
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41	560.2	30.9	613	7	CN670354	A0891612-
42	556.4	30.7	621	1	AA137882	mq80a04.f
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45	537.2	29.6	702	7	CN534002	UI-M-HO-

AY411158 1521 bp DNA linear GSS 16-DEC-2003
Mus musculus BMPRIA gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

AY411158

AY411158.1 GI:39767126

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 1521)

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, P., Murphy, B.,

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,

Adams, M.D. and Cargill, M.

Inferred nonneutral evolution from human-chimp-mouse orthologous

gene trios

Science 302 (5652), 1960-1963 (2003)

14671302

2 (bases 1 to 1521)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, P., Murphy, B.,

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,

Adams, M.D. and Cargill, M.

Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering

them based on alignment.

Location/Qualifiers

1. .1521

/organism="Mus musculus"

/mol_type="genomic DNA"

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QY	1268	GCACACAGGGGTACATGGCTCCAGAAAGTCTCGACAGAGCCCTGAGTAAAAACCATTTTCC	1327
Db	1141	GCACCAAGCGGTACATGGCTCCAGAAAGTCTCGATGAAAGCCCTGAAATAAAAAACCATTTTCC	1200
QY	1328	AGCCCTTACATCATGGCTGACATCTACAGCTTTTGGTTTGATCATTTGGGAGATGGCCCGTC	1387
Db	1201	AGCCCTTACATCATGGCTGACATCTATAGCTTTTGGTTTGATCATTTGGGAAATGGCTCGTC	1260
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Db	1261	GTT-----GGAATCGTGGAGGAATATCAATTTACCATTTTACAACATGGTGCCCA	1309
QY	1448	GTGACCCATCTTATGAAGACATCGCTGAGGTGCTGTGTGTGTAAGCCCTTTCGCGCCCAATCG	1507
Db	1310	GTGACCCATCTTATGAAGACATCGCTGAGGTGCTGTGTGTGTAAGCCCTTTCGCGCCCAATCG	1369
QY	1508	TCTCTAACCGCTGGAAACAGTGAATGTCTTCGAGCCGTTTGAAGCTGATGTGAGAAT	1567
Db	1370	TGTCTAACCGCTGGAAACAGGATGAATGTCTTCGAGCAGTTTGAAGCTAAATGTGAGAAT	1429
QY	1568	GCTGGCCCATTAATCCAGCATCCAGACTCAGAGCTTTCAGATCAAGAGACGCTCGCAA	1627
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QY	1628	AGATGGTTGAATCCCAAGGATGTAAAGATTTGA	1659
Db	1490	AAATGGTTGAATCCCAAGGATGTAAAGATTTGA	1521
RESULT 2			
LOCUS	AY411156	1532 bp	DNA linear GSS 16-DEC-2003
DEFINITION	Homo sapiens BMRP1A gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.		
ACCESSION	AY411156		
VERSION	AY411156.1	GI:39767124	
KEYWORDS	GSS.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 1532)		
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaritwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios		
JOURNAL	Science	302 (5652),	1960-1963 (2003)
PUBMED	14671302		
REFERENCE	2 (bases 1 to 1532)		
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaritwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.		
FEATURES	Location/Qualifiers		
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gene			

ORIGIN

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Best Local Similarity 89.2%; Pred. No. 0;
Matches 1367; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

QY 128 GGCAGAAATCTAGATAGTATGCTCCATGCTGCTGATGAAATCAGACGTTGGACCGAGAA 187
DB 1 GACAGAAATCTGATAGTATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60

QY 188 AGCCGAAATCGAGTACGTTAGCACAGAGGACACCTTACCTTCTTAAATGCTATT 247
DB 61 AGTCAGAAATCGAGTAACTTAGCACAGAGGATACCTTGGCTTTTTTAAAGTCTATT 120

QY 248 GCTCAGGACATGCCAGATGACGCTATTAAACACATGCAATTAATGCTGCTATTGCT 307
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QY 308 TTGCCATTATAGAAAGATGATCAGGAGAAACCACTTAACTTCTGGGTGATGAAGT 367
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QY 368 ATGAGGCTCTGATTTCAATGCAAGGATTCACAAAGCCAGCTACGAGGACAATAG 427
DB 241 ATGAGGATCTGATTTTCAATGCAAGGATTCACAAAGCCAGCTACGAGGACAATAG 300

QY 428 AATGTTGTCGACCAATTTGTCACCAATATTTTCAGCCTACACTGCCCTGCTGCTTA 487
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QY 488 TAGGCCCATTTCTTGATGCGACGCTCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 547
DB 361 TAGGTCGCTTTTCTGATGCGACATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

QY 548 GTATTGTCGCCATGATGCTTCTCCAGCTGCTTCTGTTCAAAACATTAAGTAAAGTA 607
DB 421 GCATAATTGCTATGATCATCTTCTCCAGCTGCTTCTGTTCAAAACATTAAGTAAAG 480

QY 608 TCTCAAGCAGAGGTCGTTTACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 667
DB 481 TCTCAAGCAGAGGTCGTTTACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540

QY 668 GAGATCACTGAAAGACCTGATGACCAAGCTCCTGCTGCTGCTGCTGCTGCTGCTGCT 727
DB 541 GAGATCACTGAAAGACCTGATGACCAAGCTCCTGCTGCTGCTGCTGCTGCTGCTGCT 600

QY 728 CTTATTGCTCAGGAACTATGCTCAACAGATTCAGATGCTGCTGCTGCTGCTGCTGCT 787
DB 601 CTTATTGCTCAGGAACTATGCTCAACAGATTCAGATGCTGCTGCTGCTGCTGCTGCT 660

QY 788 GCCGTATGGAGAGTATGGATGGTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 847
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DB 721 TCTTACCACCTGAAGACCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780

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QY 968 CTCAGCTGATTTGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 1027
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QY 1028 GTGCCACCTCCGACACCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1087
DB 901 GTGCTACATGACACCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960

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DB 961 GCCACCTCCACACAAATTTATGGCAGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020

QY 1148 TGAAGAGCAAAACATCCTTATTAAAGAAAATGGTAGTTGCTGTTATGCTGACCTGGGCC 1207
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QY 1388 GCTGTATTACAGGAGGAATCGTGGAGGAATATCAATTACCATATTACCAATGGTGCCTTA 1447
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QY 1448 GTGACCCATCTTATGAAGACATGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1507
DB 1321 GTGATCCGTCATACGAAGATATGCTGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380

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DB 1381 TGTCTAATCGGTGGAACAGTGAATGCTTACGAGCAGTTTGAAGCTTAATGTCAGAAAT 1440

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QY 1628 AGATGTTGAATCCAGAGATGAAGAATTGA 1659
DB 1501 AGATGTTGAATCCAGAGATGAAGAATTGA 1532

RESULT 3
AY411157
LOCUS
DEFINITION Pan troglodytes BMP1A gene, VIRTUAL TRANSCRIPT, partial sequence,
AY411157
ACCESSION
VERSION AY411157.1 GI:39767125
KEYWORDS
SOURCE
ORGANISM Pan troglodytes (chimpanzee)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pan.
REFERENCE 1 (bases 1 to 1532)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarimal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Fierriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
Gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1532)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarimal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Fierriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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Matches 1082;	Conservative	0;	Mismatches	450;	Indels	0;	Gaps	0;		
Qy	128	GGCAGAAATCTAGATAGTATGCTCCATGGTACTGGTATGAAATCAGAGCTGGACCAAGA	187							
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Qy	188	AGCCGGAATGGAGTCAGCTTAGCACACAGAGACACCTTACCTTTCTTAAATGCTATT	247							
Db	61	AGTCAGAAATGGAGTAACCTTAGCACACAGAGATACCTTGCCTTTTAAAGTGTATT	120							
Qy	248	GCTCAGACACTGCCAGATAGCCTATTAAACACATGCATAACTAAATGGCCATTGCT	307							
Db	121	GCTCAGGNACTGCCNNNGATGCTATTAAANNNNNNNNNNNNNNNNNNNNNNNNN	180							
Qy	308	TTGCCATTATAGAAAGATGATCAGGGAGAAACCAAGTTAACTTCTGGGTGTATGAAGT	367							
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Qy	368	ATGAAGGCTCTGATTTTCAATGCAAGGATTCACCAAAGCCAGCTACGCAGGACCAATAG	427							
Db	241	NN	300							
Qy	428	AATGTTGTCGGACCAATTTGTGCAACCAATATTTGCAGCCTACACTGCCCCCTGTCTGTTA	487							
Db	301	AATGTTGTCGGAACCAATTTATGTAACAGTATTTGCAACCACTGCCCCCTGTGTCTCA	360							
Qy	488	TAGCCCATTTCTTTGATGGCAGCGTCCGATGGCTGGCTGTGCTCATCTCTATGGCTGCT	547							
Db	361	TAGTCCGTTTTTTGATGGCAGCATTCGATGGCTGGTTTGCTCATTTCTATGGCTGCT	420							
Qy	548	GTATTGTCGCATGATCGTCTCTCCAGCTGCTCTGTTTACAAACATTACTGTAAGAGTA	607							
Db	421	GCATAATGCTATGATCATCTCTCCAGCTGCTTTTGTACAAANNNNNNNNNNNNNN	480							
Qy	608	TCTCAAGCAGAGTGGTTTACAACCGTGACTTGGAAACAGGATGAAGCATTTATTCAGTAG	667							
Db	481	NN	540							
Qy	668	GAGAAATCACTGAAGACCTGATTGACCAAGTCAAAAGCTCTGGTGTGGATCTGGATTTAC	727							
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Db	601	NN	660							
Qy	788	GCCGATGTCGAAAGTATGGATGGCTAAATGGCGTGTGAAAAGTGCCTGTCAAAAGTAT	847							
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Qy	908	TGGCTCATGAAATATATCTGGTTTTATAGCTGGCAGACATTAAGGCACCGGTTCTCGGA	967							
Db	781	TGGCCCATGAAACATATCTGGTTTCAAGCGGAGACATTAAGAGGTACAGGTTCTCGGA	840							
Qy	968	CTCAGCTGATTTTGATTACTGATTACCATGAGAAATGGTCTCTCTATGACTTCTCTGAAT	1027							
Db	841	CTCWNCTCTATTGATTACTGATTACCATGAAATGGATCTCTCTATGACTTCTCTGAAT	900							
Qy	1028	GTGCCACCTTGGACACCAAGCCCTACTCAAGTTAGCTTATTCTGCTGCGCTGGTCTGT	1087							

Qy	1008	TCCTCATG-ACCTTCCTGAAATGTGCCACCTTGACACACGAGCCCTACTCAAGTAGCTTT	1066
Db	841	TCCTCATGAACCTTCCTGAAATGTGCTACACTGACACACGAGCCCTGCTTTAAATTGGCTT	900
Qy	1067	ATTCTGCT-CCCTGTGGTCTGTGGCCACCTCCACACAGAAATTTATGGCAGCGCAAGGCAA-	1124
Db	901	ATCAGCTGGCCTGGGNCCTGGGCCACTCTGCCCCAGAAATTTATGGGCCCCCAAGAAAA	960
Qy	1125	-GCGTCAATTTGCTCAT-CGAGACCTTGAACAGCAAAACATCCTTATTAAAGAAAAA	1178
Db	961	GCCCGCAATGGCTCTCTCCAAACCTTAAGGAGCAAAACATCCTCTTCCAAAAAAA	1016
RESULT 5			
LOCUS	AU124197	874 bp	mRNA linear EST 01-AUG-2002
DEFINITION	AU124197 NT2RM2 Homo sapiens cDNA clone NT2RM2001814 5', mRNA sequence.		
ACCESSION	AU124197		
VERSION	AU124197.1	GI:10948913	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.		
	1 (bases 1 to 874)		
	Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and Isogai,T.		
TITLE	HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S., Isogai,T.)		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: genomics@hri.co.jp HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.		
FEATURES			
source	Location/Qualifiers 1..874 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="NT2RM2001814" /cell_type="teratocarcinoma" /cell_line="NT2" /clone_lib="NT2RM2" /notes="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal precursor cells"		
ORIGIN			
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Best Local Similarity	90.1%	Pred. No. 6.6e-209;	
Matches	787; Conservative	0; Mismatches 86; Indels 0; Gaps 0;	
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Qy	410	AGCTACGCAGGACCAATAGAAATGTTGTCGGACCAATTTGTGCACCAATATTTGCAGCCTA	469
Db	61	AGCTACCGCGACCAATAGAAATGTTGTCGGACCAATTTATGTACCAAGTATTTGCACACCA	120
Qy	470	CACTGCCCCCTGCTGTTATAGGCCCAATCTTTTGATGGCAGCGTCGATGGCTGGCTGTGC	529

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QY 650 AAGCATTTATTCCAGTAGAGAAATCACTGAAAGACCTGATTGACCAAGTCACAAAGCTCTG 709
Db 301 AAGCATTTATTCCAGTTGAGAAATCACTAAAGACCTTATTGACCAAGTCACAAAGTTCTG 360
QY 710 GTAGTGGATCTCGATTACCTTTATTGGTTTACGGAACATATTGCCAAACAGATTCAGATGG 769
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QY 770 TTCCGCAAGTTGGTAAGGCGGTATGGAGAGTATGGATGGTAAATGGCGTGTGAAA 829
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QY 830 AAGTGGCTCTCAAGATTTTATTTTACCACTGAAAGAGCTAGCTGGTTTAGAGAGAAACAGAAA 889
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QY 890 TCTACAGACGGTGTAAATGCGTCATGAAATATATCTGGTTTTTATAGTCGAGACATTA 949
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QY 950 AAGGCACCGTTTCTGGACTAGCTGTATTTGATTTACTGATTACCATGAGATGGTCTC 1009
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QY 1130 CAATTGCTCATGAGACCTGAGAGCAAAAACATCTTATTAGAAAATGTAGTTGCT 1189
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QY 1190 GTATTGCTGACCTGGGCTAGCTGTGTTAAATTC 1222
Db 841 GCATTGCTGACCTGGGCTTGGTAAATCA 873

RESULT 6
LOCUS CV558493
DEFINITION UI-M-H20-ctf-1-05-0-UI.r1 NIH_BMAP_H20 Mus musculus cDNA clone
IMAGE:30690220 5', mRNA sequence.
ACCESSION CV558493
VERSION CV558493.1 GI:54445126
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 915)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mouse1.html>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: PYX-5.
FEATURES
source Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="CS7BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30690220"
/tissue_type="whole eye"
/dev_stage="newborn 1,5,15 and embryos 15,16,17,18 dpc"
/lab_host="DH10B (T1 phage
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/note="Organ: Eye; Vector: PYX-Asc; Site:1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into PYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AATAATTAGC. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."

ORIGIN

Query Match 40.5%; Score 734; DB 7; Length 915;
Best Local Similarity 92.5%; Pred. No. 2.7e-208;
Matches 817; Conservative 0; Mismatches 56; Indels 10; Gaps 4;
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Db 1 TGCAGACATTAAGGCACCTGGTTCTGGACTCAGCTGTATTTGATTACTGATTACATGA 60
QY 999 GAATGGGTCTCTATGACTTCTGAAATGTCACCTGGACACACAGAGCCCTACTCAA 1058
Db 61 AAATGGATCTCTCTATGACTTCTGAAATGTCACACTAGACACAGAGCCCTACTCAA 120
QY 1059 GTTAGCTTATTTCTGCTGCTGTGTCTGTGCACCTCCACACAGAAATTTATGGCAGCA 1118
Db 121 GTTAGCTTATTTCTGCTGCTGTGTGTCTGTGCACCTCCACACAGAAATTTATGGTACCA 180
QY 1119 AGGCAAGCCTGCAATTTGCTCATCGAGACCTGAAAGCAAAAACATCTTTATTAAGAAAA 1178
Db 181 AGGGAAGCCTGCAATTTGCTCATCGAGACCTGAAAGCAAAAACATCTTTATTAAGAAAA 240
QY 1179 TGGTATTTGCTGTTATTTGCTGACCTGGGCTAGCTGTTAAATTTCAACAGTGACACAAATGA 1238
Db 241 TGGAAATTTGCTGTTATTTGCTGACCTGGGCTAGCTGTTAAATTTCAACAGTGATACAAATGA 300
QY 1239 AGTTGACATACCTTTGAAACACAGGGTGGGCACCGGGGTACATGGCTCCAGAAAGTGTCT 1298
Db 301 AGTTGACATACCTTTGAATACAGGGTGGGCACCAAGCGGTACATGGCTCCAGAAAGTGTCT 360
QY 1299 GGACAGAGCCTGAGTAAAAACCAATTTCCAGCCCTACATCATTTGGCTGACATCTACAGCTT 1358
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QY 1359 TGGTTTGTATTTGGGAGATGGCCGCTGCTGTTATTACAGAGGAATCGTGGAGGAATA 1418
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QY 1419 TCAATTACCATATTACAAACATGGTGCCTAGTGACCCATCTTTATGAAGACATGCGTGAGGT 1478
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QY 1479 CGTGTGTGTAACGCTTGGGCCAATCGTCTCTAAACCGCTGGAACAGTGATGAATGTCT 1538
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QY 1539 TCGAGCGGTTTGAAGCTGATGTGAGAAATGCTGGGCCCAATTAATCCAGCATCCAGACTCAC 1598
Db 601 TCGAGCAGTTTGAAGCTAATGTGAGAAATGCTGGGCCCAATTAATCCAGCATCCAGACTCAC 660
QY 1599 AGCTTTGAGAAATCAAGAAGCGCTCGCAAGATGGTTGAATCCAGGATGTAAGATTTG 1658
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QY 1659 AC----AAACAGTTTGGAGAAAGATTTAGACTGCAAGAAATTC-----ACCCGAGGAAG 1710
Db 721 ACAATTAACAAATTTTGGGGAGAAATTTAGACTGCAAGAAATTC-----ACCCGAGGAAG 780
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Db 781 GTGGGATTAGCATGGAATAGGATGTGGCTTGGTTTCCAGACTCTCTCTCTA-CATCTT 839
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RESULT 7

CX204646 842 bp mRNA linear EST 29-DEC-2004
LOCUS MNS07540 Mouse Neurosphere Normalized cDNA library Mus musculus
DEFINITION cDNA 5', mRNA sequence.

ACCESSION

CX204646

VERSION

CX204646.1 GI:56859818

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

1. (bases 1 to 842)
Williams, C., Wirtz, V., Lundberg, J. and Frisen, J.
Expressed sequence tags of cDNA clones from murine neurospheres

AUTHORS

Unpublished (2005)

TITLE

Contact: Williams, C.

JOURNAL

Molecular Biotechnology

COMMENT

Institution of Biotechnology
Albano University Center, KTH-Royal Institute of Technology, 106
91 Stockholm, Sweden

FEATURES

source

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/organism="Mus musculus"
/mol_type="mRNA"
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/dev_stage="Adult"
/clone_lib="Mouse Neurosphere Normalized cDNA library"
/note="Organ: Adult brain; Vector: pCMVSPORT6.0; A cDNA
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from neurospheres of adult male and female mice. Custom
normalized cDNA library by Invitrogen/ResGen"

ORIGIN

Query Match 40.2%; Score 728.6; DB 8; Length 842;
Best Local Similarity 93.6%; Pred. No. 1.1e-206;
Matches 793; Conservative 0; Mismatches 49; Indels 5; Gaps 3;
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Db 1 ATCAGGAGAAACACCACTTAACCTTCTGGGTGATGAAGCTCTGATTTTCAAT 60
QY 389 GCAAGGATTCACAAAGCCAGCTACGACAGACAATAGAAATGTTGTTCGACCAATTTGT 448
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QY 509 GCGTCCGATGGCTGTGCTCTCTATAGGCTGTCTGTATGTGCGCATGATCGTCT 568
Db 181 GCATCCGATGGCTGTGCTCTCTATAGGCTGTCTGTATGTGCTATGATCATCT 240
QY 569 TCTCCAGCTGCTTCTTTACAAACATTAAGAGTATCTCAAGCAGAGCTCGTTACA 628
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QY 629 ACCGTGACTTGGAAACAGGATGAAGCATTTATTCAGTAGGAGAAATCACTGAAAGACCTGA 688
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Db 721 CCTACTCAAGTTAGCTTTATTTCTGCTGCTGTGGTCTGTGCCACCTCC-CACAGAAATTT 779
QY 1109 ATGGCAGCAAGGCAAGCTGCAATTTGCTCATCGAGACTGAAGAGCAAAACATCCTTA 1168
Db 780 ATGGTACCCAGGG--AAGCCTGCATTGTCTCATCGAGACCTGA--AAGCAAAAACATCCTTA 835
QY 1169 TTAAGAA 1175
Db 836 TAAAAA 842

RESULT 8

LOCUS

AK086130

DEFINITION

Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched library, clone:930007102 product:bone morphogenetic protein receptor, type 1B, full insert sequence.

ACCESSION

AK086130

VERSION

AK086130.1 GI:26351960

KEYWORDS

HTC; CAP trapper.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

REFERENCE	Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS	Carninci, P. and Hayashizaki, Y.	
JOURNAL	High-efficiency full-length cDNA cloning	
PUBLISHED	Meth. Enzymol. 303, 19-44 (1999)	
REFERENCE	10349636	
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)	
PUBLISHED	11042159	
REFERENCE	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer	
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)	
PUBLISHED	11076861	
REFERENCE	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.	
AUTHORS	Functional annotation of a full-length mouse cDNA collection	
TITLE	Nature 409, 685-690 (2001)	
JOURNAL	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	
REFERENCE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	
AUTHORS	Nature 420, 563-573 (2002)	
TITLE	6 (bases 1 to 1911)	
JOURNAL	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hangaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ono, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	
REFERENCE	Direct Submission	
AUTHORS	Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]	
TITLE	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken	
JOURNAL	Genomic Sciences Center and Genome Science Laboratory in RIKEN	
REFERENCE	Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.	
AUTHORS	Please visit our web site for further details.	
TITLE	URL: http://genome.gsc.riken.jp/	
JOURNAL	URL: http://fantom.gsc.riken.jp/	
REFERENCE	Location/Qualifiers	
AUTHORS	1. 1911	
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JOURNAL	/mol_type="mRNA"	
REFERENCE	/strain="C57BL/6J"	
AUTHORS	/db_xref="FANTOM_DB:D930007102"	
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JOURNAL	/clone="D930007102"	
REFERENCE	FEATURES	
AUTHORS	Source	

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	Matches 1049; Conservative	0; Mismatches 483; Indels 12; Gaps 3;
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Qy	180 CCAGAAGACCGGAAATGAGTACGTTAGCACCAGGAGACACCTTACCTTCTTAA	239
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Qy	190 CACCAAGAA---GGAGATGGAGAGAGTACAGCCGCCACCCCTCGGCCAAGATCTC	246
Db		
Qy	240 ATGCTATTGCTCAGGACACTGCCAGATGACGCTATTAAATACATCATCACTAA	299
Db		
Qy	247 TTGTAATGCCACCACTGTCCGGAAGACTAGTCAACATATCTGCACACAGATGG	306
Db		
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Db		
Qy	307 GTACTGCTTACGATGATAGAAGAAGATGACTCTGGAATGCTGTGTCACTCTGG	366
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Db		
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Db		
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Qy	597 CTGTAAGAGTATCTCAAGACAGAGTCTGTACCAACCGTGACTTGGAAAGGAT	656
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Db		
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Qy	661 CATTCCTCTGGAGAGTCCCTGAGAGACTTGTATCGAGCAGTCTCAGAGCTCG	720
Db		
Qy	717 ATCTGGATTACCTTTATTGTTTTCAGCAACTATTTCGCCAACAGATTAGAT	776
Db		
Qy	721 ATCAGGCTCTCCCTCTGCTGCTCCAAAGGACAATAGCTAAGCAAAATTCAG	780
Db		
Qy	777 GGTGGTGAAGGGCGGTATGGAGAAAGTATGATGGGTGAAATGGGCTGGTGA	836
Db		
Qy	781 GATTGGAAGGCGCTATGCGAGGTTGATGGGGAAGTGGCGTGGAGAAAGGTGC	840
Db		

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QY 841 TGTGAAAGTGTCTTCCACCAGGAGGAGCCAGCTGTTCCGAGAGACTGAGATATATCA 900
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QY 897 GAGCGTGTAAATGCGTCATGAAATATACCTGTTTATAGCTGCGAGACATTAAGGCAC 956
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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 961 TGGTCTGCTGACTGATTTGACCTCATCAGACTATCATGAAACGGCTCCCTTTATGA 1020
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1017 CTTCTGAAATGTGCCACCTTGGACACACAGAGCCCTACTCAAGTTAGCTTATTTCTGCTGC 1076
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1021 CTATCTGAAATCCACCACTTAGAGCCAAAGTCCATGCTGAAGCTAGCTACTCTCTGT 1080
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1077 CTGTGCTGTGCGCACTTCACACAGAGAAATTTATGCGCCAGAGGAGCGCTGCAATTC 1136
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1081 CAGCGGCTATGCCATTTACACACGGAATCTTTAGCACTCAAGGCAAGCAGCAATTCG 1140
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1137 TCATCAGAGCTGAAGAGCAAAACATCTTTATAGAAAAATGGTAGTTGCTGTATTGC 1196
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1141 CQATCAGACTTGAAGATGAACATCTCTGTTGAAGAAAAATGGAACCTTGTGCTATGC 1200
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1201 AGACCTGGGCTTGGCTGTCAAGTTTATAGTACACAAATGAGTTGACATCCACCCAA 1260
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1257 CACAGGTTGGGACACAGGCGGTACATGGCTCAGAAAGTCTGAGAGAGCGCTGAGTAA 1316
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1261 CACCGGTTGGGACCAAGCGCTATATGCCCTCAGAAAGTCTGCGAGAGCTTGAATAG 1320
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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 1561 TATGACAGAGTCTGCGGCGCAGATCTGCTCCAGGCTCAGCGCCCTGAGAGTTAAGAA 1620
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1617 GAGGCTCGAAAGATGGTTGAATCCAGGATGTAAGATTTGAC 1660
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1621 AACCCTTGCCAAATGTCAGAGTCCCAGGACATTAACCTCTGAC 1664
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
CK638737
LOCUS
DEFINITION
IMAGE:30644216 5', mRNA sequence.
EST.
CK638737.1 GI:41364603
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 779)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
```

TITLE
JOURNAL
COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: pYX-5.

FEATURES
source

Location/Qualifiers

1..779
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30644216"
/tissue_type="Upper Head"
/dev_stage="9.5-10.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP H00"
/note="Organ: Head; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAATCGAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."

ORIGIN

Query Match 39.5%; Score 715.6; DB 7; Length 779;
Best Local Similarity 94.9%; Pred. No. 8.5e-203;
Matches 739; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 322 GAAGATGATCAGGAGAACACCTTAACCTCTGGGTGATGAAGTATGAAGCTCTGAT 381
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QY 382 TTTCAATGCAAGGATTCACAAAGCCAGCTACGAGGACAAATAGAAATGTTGCGGACC 441
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 TTTCAATGCAAGGATTCACCGAAGCCAGCTACGAGGACAAATAGAAATGTTGCGGACC 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 442 AATTTGTGAAACAATATTTGAGCCTACACTGCCCCCTGTGCTTATAGCCCAATTTCTTT 501
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QY 121 AATTTGTGCAACCACTATTTGAGCCTACACTGCCCCCTGTTGTTATAGTCCGTTCTTT 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 502 GATGCGAGCTCCGATGGCTGCTGCTCATCTCTATGGCTGCTGTTATGTCGCATG 561
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 GATGCGAGCATCCGATGGCTGTTGCTCATTTTCATGGCTGCTGTTATGTTGTAATG 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 562 ATCTGCTCTTCCAGCTGCTTCTGTTACAAACATTAAGTAAAGATATCTCAAGCAGAGT 621
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 ATCATCTTCTCAGCTGCTTTTGTATAGCATTTATTGAAGTATCTCAAGCAGGGGT 300
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QY 622 CTTTACAACCGTGAATTGGAAACAGGATGAAGCATTTATTCCAGTAGGAGAAATCACTGAAA 681
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 CGTTACAACCGTGAATTGGAAACAGGATGAAGCATTTATTCCAGTAGGAGAAATCACTGAAA 360
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 682 GACCTGATTGACCACTCAAAAGCTCTGCTAGTGCATCTGGATTAACCTTTATGTTCTAG 741
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 361 GACCTGATTGACCACTCCCAAAGCTCTGGGAGTGGATCTGCCCTTTATTTGTTCTAG 420
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 742 CGAACTATTGCCAAACAGATTTCAGATGGTTTCGGCAGGTTGGTAAAGCGCGGTATCGAGAA 801
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||


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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1 (bases 1 to 826)
            NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS    NIH-MGC http://mgi.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: BresaGen, Inc.
            cDNA Library Preparation: Express Genomics, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
            DNA Sequencing by: Laboratory for Genomics and Bioinformatics,
            University of Georgia
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/ILNL at:
            http://image.llnl.gov
            Plate: LLAM 17072 row: g column: 17
            Seq primer: JENREV (CAGGAACAGCTATGACC)
            High quality sequence stop: 826.
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            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:7965451"
            /sex="male"
            /tissue_type="human embryonic stem cells differentiated to
            an early endodermal cell type"
            /cell_type="human embryonic stem cells"
            /cell_line="BG01"
            /lab_host="DH10B-T1 phage-resistant E. coli"
            /clone_lib="NIH_MGC_258"
            /note="Vector: pExpress-1; Site_1: NotI; Site_2: EcoRV;
            RNA obtained from human embryonic stem cells isolated from
            the inner cell mass of blastocyst stage embryos and
            differentiated to an early endodermal cell type. Cell line
            id and NIH Registry designation is BG01. Positive for
            GATA4, Mixl1, Msx1, HNF4alpha expression; negative for AFP
            expression. Passage number 40. cDNA primed using oligo-dT
            primer: 5'-pGACTAGTCTAGATCGGAGCGGCCCT(T)25-3' and
            cloned into the EcoRV/NotI sites of pExpress-1. This
            primary library is non-normalized (normalized primary
            library is NIH_MGC_259). It was constructed by Express
            Genomics (Frederick, MD). Sequence ends have been trimmed
            to exclude vector and regions below Phred quality 16.
            Three-prime sequences are presented as their reverse
            complement and have been trimmed to exclude polyA. Note:
            this is a Mammalian Gene Collection library."

ORIGIN
Query Match      38.9%; Score 705; DB 8; Length 826;
Best Local Similarity 90.8%; Pred. No. 1.3e-199;
Matches 750; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 412 CTACCGGACATAGATGTTGTCGGACCAATTTGTGCAACCAATATTTGACGCTACA 471
Db 1 CTACCGGACATAGATGTTGTCGGACCAATTTGTATGTAACCAATTTGCAACCCACA 60

QY 472 CTGCCCCCTGCTGTTATAGGCCCATCTTTTGTATGGCAGGCTCCGATGGCTGGCTC 531
Db 61 CTGCCCCCTGTTGTATAGTCCGTTTGTATGGCAGGATTCGATGGCTGGTTTGTCT 120

QY 532 ATCTCTATGGCTGCTGTATTTGTCGCCATATGATCGTCTTCTCCAGCTGCTTGTGTACAAA 591
Db 121 ATTTCTATGGCTGCTGTGATATTTGCTATGATCACTTCTCCAGCTGCTTGTGTACAAA 180

QY 592 CATTACTGTAGAGTATCTCAGCAGAGAGGTGCTTACACCGTGACTTGGACAGGATGAA 651

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181 CATATTCCAGAGCATCTCAAGCAGACGTCGTGTACATCGTGTATTGGAAACAGGATGAA 240
652 GCATTTATCCAGTAGGAGAAATCACTGAAAGACCTGATGACCACTCAAAAGCTCTGGT 711
241 GCATTTATCCAGTTGGAGAAATCACTAAAGACCTTATTGACCACTCAAAAGTTCTGGT 300
712 AGTGGATCTGATTTACCTTTATTTGGTTCAGGCACTATTGCGCAACAGATTCAGATGGTT 771
301 AGTGGGCTGGACTACCTTTATTGGTTTCTGAGCACTATTGCGCAACAGATTCAGATGGTC 360
772 CGGCAAGTTGGTAAGGCCGGTATGGAAGAGTATGGAATGGGTAAATGGCGTGGTGAATAA 831
361 CGGCAAGTTGGTAAGGCCGGTATGGAAGAGTATGGAATGGGTAAATGGCGTGGTGAATAA 420
832 GTGGCTGTCAAGATATTTTACCCTCAAGAGAGTACGTGGTTAGAGAAACAGAAATC 891
421 GTGGCGGTGAAGATATTTTACCCTCAAGAGAGTACGTGGTTAGAGAAACAGAAATC 480
892 TACCAGAGCGGTGTTAATGGCTCATGAAATATCTTGGTTTATAGCTGCAGACATTTAA 951
481 TACCAGAGCGGTGTTAATGGCTCATGAAATATCTTGGTTTATAGCTGCAGACATTTAA 540
952 GGACCGGTTCTCTGACTCAGCTGATTTGTTGTTTACTGATTTACCATGAGATGGTCTCTC 1011
541 GGTACAGGTTCTCTGACTCAGCTGATTTGTTGTTTACTGATTTACCATGAGATGGTCTCTC 600
1012 TATGACTTCTCTGAAATGTGCCACCTGGACACCGAGAGCCCTACTCAAGTTAGCTTTATCT 1071
601 TATGACTTCTCTGAAATGTGTACACTGGACACCGAGAGCCCTGCTTAAATTTGCTTTATTC 660
1072 GCTGCTGTGCTGTGTCACCTCCACAGAAATTTATGGCAGCAGGAGGAGGCTGCA 1131
661 GCTGCTGTGCTGTGTCACCTCCACAGAAATTTATGGCAGCAGGAGGAGGAGGCTGCA 720
1132 ATTGCTCATCAGACCTCGAAGAGCAAAACATCTTATTAAGAAATATGGTGTGCTGT 1191
721 ATTGCTCATCAGACCTCGAAGAGCAAAACATCTTATTAAGAAATATGGTGTGCTGT 780
1192 ATTGCTGACCTGGGCTAGCTGTTAAATTCACAGTGCACAAATG 1237
781 ATTGCTGACCTGGGCTGCTGTTTAAATTCACAGTGCACAAATG 826

RESULT 13
CV557698
LOCUS      CV557698
DEFINITION UI-M-H2O-ctc-n-16-0-UI.r1 NIH_BMAP_H2O Mus musculus cDNA clone
IMAGE:30695271 5', mRNA sequence.
ACCESSION CV557698
VERSION    CV557698.1 GI:54443523
KEYWORDS   EST.
SOURCE      Mus musculus (house mouse)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
            1 (bases 1 to 763)
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James Lin University of Iowa
            cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/mousefl.html
            This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            Seq primer: pyx-5.
            Location/Qualifiers

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FEATURES


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source
1. .763
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/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGS:30695271"
/tissue_type="whole eye"
/dev_stage="newborn 1.5,15 and embryos 15,16,17,18 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP H20"
/note="Organ: Eye; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AATAATTACG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."
```

Query Match 38.8%; Score 703.8; DB 7; Length 763;
Best Local Similarity 95.2%; Pred. No. 2.9e-199;
Matches 726; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 878 GAGAAACAGAAATCTACAGACGGTGTAAATGGCTCATGAATAATATCTTGGTTTATAG 937
DB 1 GAGAAACAGAAATCTACAGACGGTGTAAATGGCTCATGAATAATATCTTGGTTTATAG 60

QY 938 CTCGAGACATTAAGGACCGGTTCTCGACTGAGCTGATTTGATTACTGATTCACATG 997
DB 61 CTCGAGACATTAAGGACCGGTTCTCGACTGAGCTGATTTGATTACTGATTCACATG 120

QY 998 AGAATGGTCTCTATGACTTCTGAAATGTCCACCTCGGACACAGAGCCCTACTCA 1057
DB 121 AATATGATCTCTATGACTTCTGAAATGTCCACCTAGACACAGAGCCCTACTCA 180

QY 1058 AGTTAGCTTATTCGTGCTGTGGTCTGTGCACCTCCACACAGAAATTTATGGCAGCG 1117
DB 181 AGTTAGCTTATTCGTGCTGTGGTCTGTGCACCTCCACACAGAAATTTATGGTACCC 240

QY 1118 AAGGCAAGCCTGCAATTCATCGAGACCTGAAGAGCAAAACATCTTTAAGAAA 1177
DB 241 AAGGCAAGCCTGCAATTCATCGAGACCTGAAGAGCAAAACATCTTTAAGAAA 300

QY 1178 ATGGTAGTGTCTGCTATTGCTGACCTGGGCTAGCTGTTAAATTCACAGTGACACAAATG 1237
DB 301 ATGGTAGTGTCTGCTATTGCTGACCTGGGCTAGCTGTTAAATTCACAGTGATACAAATG 360

QY 1238 AAGTTGACATACCTTTGAACACCAAGGCTGGGACCAAGGCTGATGGCTCCAGAAATGC 1297
DB 361 AAGTTGACATACCTTTGAATACCAAGGCTGGGACCAAGGCTGATGGCTCCAGAAATGC 420

QY 1298 TGGACGAGACCTGAGTAAACCAATTCAGCCCTACATCATGCTGCTGATCATTCAGCT 1357
DB 421 TGGATGAAACCTGGAATAAAACCAATTCAGCCCTACATCATGCTGCTGATCATTCAGCT 480

QY 1358 TTGGTTTGTATCTTTGGGAGATGGCCGCTGCTGTTATACAGAGCAATCGTGGAGAT 1417
DB 481 TTGGTTTGTATCTTTGGGAAATGGCTGCTGTTATACAGAGCAATCGTGGAGAT 540

QY 1418 ATCAATATACCATATTACAAATCGTGTAGTGACCCATCTTTATGAAGACATCGCTGAGG 1477
DB 541 ATCAATATACCATATTACAAATCGTGTAGTGACCCAGTGACCCATCTTATGAGACATCGCTGAGG 600

QY 1478 TCGTGTGTGAAACCGTTGCGGCCAATCGTCTCTAAACCGCTGGAACAGTGATGATGTC 1537
DB 601 TTGTGTGTGAAACCGTTGCGGCCAATCGTGTCTAAACCGCTGGAACAGCGATGATGTC 660

ORIGIN

Query Match 38.8%; Score 702; DB 10; Length 1509;
Best Local Similarity 68.2%; Pred. No. 1.3e-198;
Matches 1007; Conservative 0; Mismatches 460; Indels 9; Gaps 2;

QY 1538 TTGAGCCGCTTTTGAAGCTGATGCTCAGAAATGCTGGGCCCATATATCCAGCATCCAGACTCA 1597
DB 661 TTGAGCCGCTTTTGAAGCTGATGCTCAGAAATGCTGGGCCCATATATCCAGCATCCAGACTCA 720

QY 1598 CAGCTTTGAGAATCAAGAGAGCGCTCGCAAGAGATGTTGAATC 1640
DB 721 CAGCTTTGAGAATCAAGAGAGCACTTTGCAAAATGTTGAATC 763

RESULT 14
AY418113 1509 bp DNA linear GSS 17-DEC-2003
LOCUS
DEFINITION Homo sapiens BMP1B gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY418113
VERSION AY418113.1 GI:39774073
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1509)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1509)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
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ORIGIN

Query Match 38.7%; Score 702; DB 10; Length 1509;
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Matches 1007; Conservative 0; Mismatches 460; Indels 9; Gaps 2;

QY 187 AAGCCGGAATATGAGTACGCTTACACAGAGGACACCTTACCTTTCTTAAATGCTAT 246
DB 40 AAGAAGAAGAGTGGTGAGAGTACAGCCCCCCCCCGCTCCAAAGGCTCTTGGCTTGTAAA 99

QY 247 TGCTCAGGACACTGCCAGATGACGCTATTATAACACATGATTAACATATGCGCAATGC 306
DB 100 TGCCACCACCTTGTCCAGAGACTCAGTCAACATATTGGACACACAGCGATATTGT 159

QY 307 TTGTCATTTATAGAAAGATGATCAGGGAGAAAACAAGTTAACTTCTGGGTGTATGAAG 366
DB 160 TTCAGATGATAGAAAGAGTACCTGGGTGGCTGTGGTCACTTCTGGTGGCTAGGA 219

QY 367 TATGAGGCTCTGATTTTCAATGCAAGGATTCACCAAGAGCCAGCTAGCGAGCAATA 426
DB 220 CTGAAAGGCTCAGATTTTTCAGTGTCCGGACACTCCCATTTCTCATCAAGAAGATCAATT 279

QY 427 GAATGTTG---TCGGACCAATTTGTGCAACCAATATTTGACGCCCTACACTGCCCCCTGTC 483

Db 280 GAATGCTGCACAGAAAGGAACGAATGTATATAAGACCTACACCCCTACACTGCTCTCAATG 339
Qy 484 GTTATAGGCCCATTTCTTTGATGGCAGCGTCCGATGGCTGGCTGTGCTCATCTCTATGGCT 543
Db 340 AAAAACAAGAGATTTTGTGATGACCTATACACACAGGCTTTACTTATATCTGTACT 399
Qy 544 GTCTGTATTGTGCCATGATCTCTTCTCCAGCTGCTTGTGTTACAAACATTACTGTAAAG 603
Db 400 GTCTGTAGTTTGTCTCTGGTCTCTATCATATATATATATATATATATATATATATATAT 453
Qy 604 AGTATCTCAAGCAGAGGTCGTATCAACCGTGTACTTGGACAGGATGAAGCAATTTATTTCCA 663
Db 454 AGACAAGAAACACAGACCTCGATACAGACTATGGGTAGAACAGGATGAACACTTACATTCCT 513
Qy 664 GTAGAGAAATCACTGAAGACCTGATGACCAAGTCTCGTAGTGTGATCTGGA 723
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Qy 784 AAGGGCCGTATGGAGAACTATGGATGGTAAATGCGTGGTGAAGAGTGGCTGTCAA 843
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Qy 844 GTATTTTACCACCTGAAGAACTAGCTGGTTTAGAGAAACAGAAATCTACACAGCGTG 903
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Db 754 TTGATGAGGCATGAAGAACTTTTGGGTTTCAATGTGTCAGATATCAAGGAGCAGGGTCC 813
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Qy 1024 AAATGTGCCACCTGACACAGACCCCTACTCAAGTTAGCTTATTTCTGCTGCTCTGGT 1083
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Db 1474 GCCAAATGTCAGAGTCCAGGACATTAAACTCTGA 1509
RESULT 15
CD351417
LOCUS
DEFINITION
IMAGE:6856367 5', mRNA sequence.
ACCESSION
CD351417
VERSION
CD351417.1 GI:31142932
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 769)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pyX-5.
Location/Qualifiers
1..769
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6856367"
/tissue_type="whole brain"
/dev_stage="embryo 13.5, 14.5, 16.5, 17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP G10"
/note="Organ: Brain; Vector: pyX- Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Ronald, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pyX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCAGACAG. This library was created for the University
of Iowa Brain Anatomy Project (BMAP). 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

Query Match 37.7%; Score 682.6; DB 6; Length 769;
Best Local Similarity 94.4%; Pred. No. 6.9e-193;
Matches 728; Conservative 0; Mismatches 41; Indels 2; Gaps 2;
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Qy 161 GTATGAATCAGACGCTGGACAGAAAGCCGGAATAATGAGTGACGTTAGCACACAGAGG 220
Db 121 GTATGAATCAGACGCTGGACAGAAAGCCGGAATAATGAGTGACGTTAGCACACAGAGG 180
Qy 221 ACACCTTACCTTCTTAAATGCTATTGCTCAGGACACTGCCCCAGATGACGCTATTAAATA 280
Db 181 ATACCTTGGCCTTCTTAAAGTGCTATTGCTCAGGACACTGCCCCAGATGATGCTATTAAATA 240
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Db 601 AACAGGATGAAGCATTTATTTCCAGTAGGAGAACTCACTGAAAGACCTGATTGACCACTCAC-C 659
Qy 701 AAAGCTCTGGTAGTGGATCTGGATTACCTTTATTGGTTTCAGCGAACTATTGCCAAACAGA 760
Db 660 CAAGCTNCTGGAGTGGATCTGGATTGCCCTTTATTGGTTTCAGCGAACTATTGCCAAACAGA 719
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Search completed: December 9, 2005, 17:16:18
Job time : 5040 secs

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OM protein - protein search, using sw model

Run on: December 3, 2005, 05:59:53 ; Search time 188 Seconds
(without alignments)
1243.348 Million cell updates/sec

Title: US-10-600-645-2
Perfect score: 2838
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2838	100.0	532	2	Aar70237 Bone morph
2	2838	100.0	532	7	Ade61819 Rat Prote
3	2838	100.0	532	7	Ade61815 Rat Prote
4	2838	100.0	532	9	Adw28803 Rat bone
5	2838	100.0	532	9	Adw28802 Rat bone
6	2838	100.0	532	9	Adw28801 Rat bone
7	2838	100.0	532	9	Adw28806 Rat bone
8	2838	100.0	532	9	Adx97416 Rat bone
9	2838	100.0	532	9	Adx97415 Rat bone
10	2838	100.0	532	9	Adx97414 Rat bone
11	2838	100.0	532	9	Adx97419 Rat bone
12	2838	99.5	532	2	Aar74343 BRK-1 pro
13	2823	99.5	532	2	Aar95201 Bone morph
14	2823	99.5	532	2	Aar95225 Mouse BMP
15	2823	99.5	532	2	Aaw6248 Mouse BMP
16	2823	99.5	532	2	Aay3305 Human MAL
17	2823	99.5	532	9	Ady51876 Murine AL
18	2769	97.6	532	2	Aar55368 Human Act
19	2769	97.6	532	2	Aar55207 Human ALK
20	2769	97.6	532	2	Aay33301 Human HAL
21	2769	97.6	532	6	Aae35259 Protein u
22	2769	97.6	532	6	ABO07221 Human p53
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24	2769	97.6	532	7	Ade61821 Human Pro

ALIGNMENTS

RESULT 1
AAR70237

ID AAR70237 standard; protein; 532 AA.

XX AC AAR70237;

XX AC AAR70237;

DT 25-MAR-2003 (revised)

DT 28-SEP-1995 (first entry)

XX Bone morphogenic protein receptor CFK1-23a.

XX Bone morphogenic protein; receptor; serine/threonine kinase; BMP; bone;

KW cartilage; injury; treatment; inhibition.

XX Rattus rattus.

XX WO9507982-A1.

XX 23-MAR-1995.

PF 07-SEP-1994; 94WO-US010080.

PR 17-SEP-1993; 93US-00123934.

XX (GEMY) GENETICS INST INC.

Wozney JM, Celeste AJ, Thies RS, Yamaji N;

WPI; 1995-131350/17.

N-PSDB; AAQ83530.

Truncated BMP and serine/threonine kinase receptor proteins - used to

inhibit the effects of BMP-2 and/or BMP-4.

Claim 16; Page 50-51; 83pp; English.

Truncated bone morphogenic protein (BMP) receptors and serine/threonine kinase receptors may be used in compositions to inhibit the effects of BMP's such as BMP-2 and BMP-4. The truncated receptors prof. comprise the ligand binding domain, but not the serine/threonine kinase and transmembrane domains. The truncated proteins are soluble and will be excreted into supernatant by recombinant mammalian cells expressing them. Such cells can be delivered in a medium or matrix which partially impedes their mobility, thereby localising the cells to a site of bone or cartilage injury. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 532 AA;

SQ

Ade61817 Human Pro
Adq9878 Antagonis
Adw28798 Human bon
Adx07491 Cyclin-de
Adx97411 Human bon
Ady51868 Human ALK
Abg22870 Novel hum
Ady81416 Human act
Abg22877 Novel hum
Ade08017 Novel pro
Adu40387 Novel hum
Aar74342 Truncated
Ade08018 Novel pro
Adu40388 Novel hum
Adg22876 Novel hum
Aae06221 Wild-type
Aae06225 Human BMP
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Abj05538 Breast ca
Abg31268 Human bon
Abj19801 Androgen-

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Query Match 100.0%; Score 2838; DB 2; Length 532;
Best Local Similarity 100.0%; Pred. No. 8.6e-279;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MTQLTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKPKENGVTLPEDTLPLFK 60
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DB 61 CYCSGHCPDDAINNCTITNGHCFALIEEDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRR 120
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DB 121 TTECCRTNLCNQYLQPTLPVVIQPFDDGSVRWLAVLISMAVCIVAMIVFSSCFYKHYC 180
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DB 361 RDLKSKNILIKNGSCCCTADLGLAVKNSDTNEVDIPLNTRVGTTRYNAPEVLDESLSKN 420
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DB 421 HFQPYIMADIYSGFLIIWEMARRCITGGIVEEYQLPYYNMVPSDPSYEDMRVVCVKRLR 480
QY 481 PIVSNRWNDECLRAVLKLMSCWAHNPAISRLTALRIKTKLAKMVESQDVKI 532
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XX
AC ADE61819;
DT
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein AAB33865, SEQ ID NO 7747.
XX
DE Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GSHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
XX
```

GENBANK; AAB33865.

New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 532 AA;

Query Match 100.0%; Score 2838; DB 7; Length 532;
Best Local Similarity 100.0%; Pred. No. 8.6e-279;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CYCSGHCPDDAINNCTITNGHCFALIEEDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRR 120
DB 61 CYCSGHCPDDAINNCTITNGHCFALIEEDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRR 120
QY 121 TTECCRTNLCNQYLQPTLPVVIQPFDDGSVRWLAVLISMAVCIVAMIVFSSCFYKHYC 180
DB 121 TTECCRTNLCNQYLQPTLPVVIQPFDDGSVRWLAVLISMAVCIVAMIVFSSCFYKHYC 180
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DB 241 GKGRYGEVMGKWRGEKAVKVFPTTEASWFRTEIYQTVLMRHNILGFTAAADIKGTG 300
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DB 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAISAACGLCHLHTEIYGTQKPAIAH 360
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QY 481 PIVSNRWSDECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
DB 481 PIVSNRWSDECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532

RESULT 3

ID ADE61815
AC ADE61815 standard; protein; 532 AA.
XX ADE61815;
XX 29-JAN-2004 (first entry)
XX Rat Protein AAB33865, SEQ ID NO 7743.
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX Rattus norvegicus.
XX WO2003016475-A2.
XX 27-FEB-2003.
XX 14-AUG-2002; 2002WO-US025765.
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; AAB33865.
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX Claim 1; Page: 1017pp; English.
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 532 AA;

Query Match 100.0%; Score 2838; DB 7; Length 532;
Best Local Similarity 100.0%; Pred No. 8.6e-279;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MTOLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPFLK 60
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DB 61 CYCSGHCPCDDAINTCITNGHCFALIEEDDQGETTLTSCGMKYEGSDFOCKSPKQALRR 120
QY 121 TIECCRTNLCNOYLOPTLPVVGIFDGSVRWLAVLISMAVCIVAMIVSSFCYKHYC 180
DB 121 TIECCRTNLCNOYLOPTLPVVGIFDGSVRWLAVLISMAVCIVAMIVSSFCYKHYC 180
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DB 181 KSISRRGRYNRLDEDEAFIPVGESLKOLIDQSQSSGSGGLPLLQVORTIAKIQMVQRV 240
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DB 241 GKGRYGEVWGMKGRCVAVKVFVFTTEASWFERETIYQTVLMRHNILGFTAAIDIKGTG 300
QY 301 SWTQLYLITDHYHENGSLYDFLKCATLDTALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
DB 301 SWTQLYLITDHYHENGSLYDFLKCATLDTALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
QY 361 RDLKSKNLIKNGSCCIIADLGLAVKFNDSITNEVDIPLNTRVGTTRRYMAPEVLDESLSKN 420
DB 361 RDLKSKNLIKNGSCCIIADLGLAVKFNDSITNEVDIPLNTRVGTTRRYMAPEVLDESLSKN 420
QY 421 HFQPYIMADIYSFGLIIMEMARRCITGGIVEEYQLPYNNVPSDPSYEDMREVVCVKRLR 480
DB 421 HFQPYIMADIYSFGLIIMEMARRCITGGIVEEYQLPYNNVPSDPSYEDMREVVCVKRLR 480
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RESULT 4

ADW28803
ID ADW28803 standard; protein; 532 AA.
XX AC ADW28803;
XX 07-APR-2005 (first entry)
XX DE Rat bone morphogenetic protein (BMP) receptor type 1 Seq 107.
XX KW receptor; bone morphogenetic protein; bone injury; antibody production;
KW TGF beta antagonist; BMP-antagonist; osteopathic; osteopenias;
XX KW osteoporosis.
XX OS Rattus norvegicus.
XX XX WO2005003158-A2.
XX PD 13-JAN-2005.
XX PF 15-JUN-2004; 2004WO-US018910.
XX PR 16-JUN-2003; 2003US-00463190.
XX PA (CLLT) CELLTech R & D INC.
XX PI Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paepers BW;
PI Van Ness J, Winkler DG;
XX WPI; 2005-081936/09.
XX DR N-PSDB; ADW28817.
XX XX

PT New antibody or antigen-binding fragment that binds specifically to
PT sclerostin polypeptide and which inhibits binding of sclerostin
PT polypeptide to a bone morphogenic protein, useful for increasing bone
PT mineral content or density.
XX
XX
XX Claim 1; SEQ ID NO 107; 205pp; English.
XX
CC This invention relates to a novel antibody or antigen-binding fragment
CC that binds specifically to a sclerostin (SOST) polypeptide and impairs
CC formation of a sclerostin homodimer. Specifically, it refers to an
CC antibody that competitively inhibits binding of the sclerostin
CC polypeptide to a bone morphogenic protein (BMP) Type I receptor binding
CC site or a BMP Type II receptor binding site. The present invention
CC describes a hybridoma cell capable of producing the antibody and a host
CC cell for antibody expression. Furthermore, it provides a nucleic acid
CC molecule encoding a transforming growth factor-beta (TGF-beta) binding
CC protein known as SOST (and also BEER) and methods for detection thereof.
CC Accordingly, such antibodies and osteopathic compositions of the
CC invention can be used for treating osteopenia, osteoporosis, fractures
CC and other disorders related to low bone mineral content and density. As
CC such, these compositions improve bone mineralization and can be described
CC as TGF-beta antagonists and/ or BMP-antagonists. This polypeptide
CC sequence is a bone morphogenetic protein receptor type I given in an
CC exemplification of the invention.
XX
XX Sequence 532 AA;
SO

Query Match	100.0%	Score 2838;	DB 9;	Length 532;
Best Local Similarity	100.0%;	Prod. No. 8.6e-279;		
Matches 532;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MTQLYTYIRLLGACLFIIISHVQGNQDSMLHGTGMKSDVDQKKPEGVGTIAPEDTLP	60	
Db	1	MTQLYTYIRLLGACLFIIISHVQGNQDSMLHGTGMKSDVDQKKPEGVGTIAPEDTLP	60	
Qy	61	CYSGCHPCDDAINNTCITNGHCFAIIEEDDOGETTITSGCMKYEGSPQCKDSPAQLRR	120	
Db	61	CYSGCHPCDDAINNTCITNGHCFAIIEEDDOGETTITSGCMKYEGSPQCKDSPAQLRR	120	
Qy	121	TIECCRNLCNQYLQPTLPVVIQGFDDGSVRWLAVLISMAVCIVAMIVFSSCFYKHYC	180	
Db	121	TIECCRNLCNQYLQPTLPVVIQGFDDGSVRWLAVLISMAVCIVAMIVFSSCFYKHYC	180	
Qy	181	KS1SSRGYNRDLQDEAFIPVGSLSKDLIDQSSGSGGLPLLQVORTIAKQITQMRQV	240	
Db	181	KS1SSRGYNRDLQDEAFIPVGSLSKDLIDQSSGSGGLPLLQVORTIAKQITQMRQV	240	
Qy	241	GKGRYGEVMGKWRGEKVAVKVFPTTBEASWFRETEIYQTVLMRHNILGFIADIKGTG	300	
Db	241	GKGRYGEVMGKWRGEKVAVKVFPTTBEASWFRETEIYQTVLMRHNILGFIADIKGTG	300	
Qy	301	SWTQLYLITDYHENGSLYDFLKCATLDTLRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH	360	
Db	301	SWTQLYLITDYHENGSLYDFLKCATLDTLRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH	360	
Qy	361	RDLSKKNILIKONGSCCIIADGLGAVKENSQDNEVDIPLNTRVGTTRRYMAPVLDESLSKN	420	
Db	361	RDLSKKNILIKONGSCCIIADGLGAVKENSQDNEVDIPLNTRVGTTRRYMAPVLDESLSKN	420	
Qy	421	HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYINMVPSPDPSYEDMREVCVKRLR	480	
Db	421	HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYINMVPSPDPSYEDMREVCVKRLR	480	
Qy	481	PIVSNRWNSECLRAVLKLMSECAWHPASRLTALRIKKTIAKVVESQDVKI	532	
Db	481	PIVSNRWNSECLRAVLKLMSECAWHPASRLTALRIKKTIAKVVESQDVKI	532	

RESULT 5
ADW28802
ID ADW28802 standard; protein; 532 AA.
XX
AC ADW28802;

XX	
DT	07-APR-2005 (first entry)
DE	Rat bone morphogenetic protein (BMP) receptor type 1 Seq 106.
XX	
KW	receptor; bone morphogenetic protein; bone injury; antibody production;
KW	TGF beta antagonist; BMP-antagonist; osteopathic; osteopenias;
KW	osteoporosis.
XX	
OS	Rattus norvegicus.
XX	
PN	WO2005003158-A2.
XX	
PD	13-JAN-2005.
XX	
XX	15-JUN-2004; 2004WO-US018910.
XX	
PR	16-JUN-2003; 2003US-00463190.
XX	(CLLT) CELLTECH R & D INC.
PA	
PI	Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paepker BW;
PI	Van Ness J, Winkler DG;
XX	
DR	WPI; 2005-081936/09.
DR	N-PSDB; ADW28816.
DR	
XX	
PT	New antibody or antigen-binding fragment that binds specifically to
PT	sclerostin polypeptide and which inhibits binding of sclerostin
PT	polypeptide to a bone morphogenic protein, useful for increasing bone
PT	mineral content or density.
XX	
PS	Claim 1; SEQ ID NO 106; 205pp; English.
XX	
CC	This invention relates to a novel antibody or antigen-binding fragment
CC	that binds specifically to a sclerostin (SOST) polypeptide and impairs
CC	formation of a sclerostin homodimer. Specifically, it refers to an
CC	antibody that competitively inhibits binding of the sclerostin
CC	polypeptide to a bone morphogenic protein (BMP) Type I receptor binding
CC	site or a BMP Type II receptor binding site. The present invention
CC	describes a hybridoma cell capable of producing the antibody and a host
CC	cell for antibody expression. Furthermore, it provides a nucleic acid
CC	molecule encoding a transforming growth factor-beta (TGF-beta) binding
CC	protein known as SOST (and also BEER) and methods for detection thereof.
CC	Accordingly, such antibodies and osteopathic compositions of the
CC	invention can be used for treating osteopenia, osteoporosis, fractures
CC	and other disorders related to low bone mineral content and density. As
CC	such, these compositions improve bone mineralization and can be described
CC	as TGF-beta antagonists and/or BMP-antagonists. This polypeptide
CC	sequence is a bone morphogenetic protein receptor type 1 given in an
CC	exemplification of the invention.
XX	
SQ	Sequence 532 AA;
SQ	

	Query Match	100.0%;	Score 2838;	DB 9;	Length 532;
	Best Local Similarity	100.0%;	Pred. No. 8.e-279;		
	Matches 532;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MTQLYTYIRLLGACLFII	SHVQGNLDSMLHGTGKMSD	VDQKPKENGVTTLAPEDTLPFLK	60
Db	1	MTQLYTYIRLLGACLFII	SHVQGNLDSMLHGTGKMSD	VDQKPKENGVTTLAPEDTLPFLK	60
Qy	61	CYCSGHCPDDAINTCIT	NGHCFATIEEDDQGETTLT	SGCMKYEGSDFOCKDSPKAQLRR	120
Db	61	CYCSGHCPDDAINTCIT	NGHCFATIEEDDQGETTLT	SGCMKYEGSDFOCKDSPKAQLRR	120
Qy	121	TIECCRTNLCNQYLQPTLP	PVWLGPFDDGSVRMLAVLI	ISMAVCIVAMIVESSCFYKHVC	180
Db	121	TIECCRTNLCNQYLQPTLP	PVWLGPFDDGSVRMLAVLI	ISMAVCIVAMIVESSCFYKHVC	180
Qy	181	KSTISSRGYNRDLQOEAF	TPVGESIKDLIDQSSGSGSLP	LLVQRTIAKIQIMVROV	240
Db	181	KSTISSRGYNRDLQOEAF	TPVGESIKDLIDQSSGSGSLP	LLVQRTIAKIQIMVROV	240

Qy	241	KGGRYGEVWGMKGWRGEKVAVKVFFPTTEEASWFRTEIYOTVLMRHNENILGPTAADIKG7G	300
Db	241	KGGRYGEVWGMKGWRGEKVAVKVFFPTTEEASWFRTEIYOTVLMRHNENILGPTAADIKG7G	300
Qy	301	SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAYSAACGLCHLHTEIYGTQGRPAIAH	360
Db	301	SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAYSAACGLCHLHTEIYGTQGRPAIAH	360
Qy	361	RDLSKNILIKNGSCCCTADGLAVKFNSTNNEVDIPLNTRVGTTRYMAPEVLDESLSKN	420
Db	361	RDLSKNILIKNGSCCCTADGLAVKFNSTNNEVDIPLNTRVGTTRYMAPEVLDESLSKN	420
Qy	421	HFQPYIMADIYSFGLLIWEMARRCITGGIVEEYQLPYNNWPSDPSYEDMREVVCCVKLR	480
Db	421	HFQPYIMADIYSFGLLIWEMARRCITGGIVEEYQLPYNNWPSDPSYEDMREVVCCVKLR	480
Qy	481	PIVSNRNNWDBCLRAVLKMLSCWAHNPAISRALTALRIKKTAKMVESSQDVKI	532
Db	481	PIVSNRNNWDBCLRAVLKMLSCWAHNPAISRALTALRIKKTAKMVESSQDVKI	532

RESULT 6	
ADW28801	
ID	ADW28801 standard; protein; 532 AA.
XX	
XX	ADW28801;
XX	
DT	07-APR-2005 (first entry)
XX	
DE	Rat bone morphogenetic protein (BMP) receptor type 1 Seq 105.
XX	
KW	receptor; bone morphogenetic protein; bone injury; antibody production;
KW	TGF beta antagonist; BMP-antagonist; osteopathic; osteopenias;
KW	osteoporosis.
XX	
OS	Rattus sp.
OS	
XX	
PN	W02005003158-A2.
XX	
PD	13-JAN-2005.
XX	
XX	15-JUN-2004; 2004WO-US018910.
PF	
PP	16-JUN-2003; 2003US-00463190.
PR	
XX	
PA	(CLLT) CELLTECH R & D INC.
XX	
PI	Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paepser BW;
PI	Van Ness J, Winkler DG;
XX	
DR	WPI; 2005-081936/09.
DR	N-PSDB; ADW28815.
XX	
PT	New antibody or antigen-binding fragment that binds specifically to
PT	sclerostin polypeptide and which inhibits binding of sclerostin
PT	polypeptide to a bone morphogenic protein, useful for increasing bone
PT	mineral content or density.
XX	
PS	Claim 1; SEQ ID NO 105; 205pp; English.
XX	
CC	This invention relates to a novel antibody or antigen-binding fragment
CC	that binds specifically to a sclerostin (SOST) polypeptide and impairs
CC	formation of a sclerostin homodimer. Specifically, it refers to an
CC	antibody that competitively inhibits binding of the sclerostin
CC	polypeptide to a bone morphogenic protein (BMP) Type I receptor binding
CC	site or a BMP Type II receptor binding site. The present invention
CC	describes a hybridoma cell capable of producing the antibody and a host
CC	cell for antibody expression. Furthermore, it provides a nucleic acid
CC	molecule encoding a transforming growth factor-beta (TGF-beta) binding
CC	protein known as SOST (and also BEER) and methods for detection thereof
CC	Accordingly, such antibodies and osteopathic compositions of the
CC	invention can be used for treating osteopenia, osteoporosis, fractures

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(CLLT ) CELLTECH R & D INC.
PA Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paepers BW;
PI Van Ness J, Winkler DG;
XX WPI; 2005-081936/09.
XX
XX New antibody or antigen-binding fragment that binds specifically to
PT sclerostin polypeptide and which inhibits binding of sclerostin
PT polypeptide to a bone morphogenic protein, useful for increasing bone
PT mineral content or density.
XX
XX Claim 1; SEQ ID NO 110; 205pp; English.
XX
XX This invention relates to a novel antibody or antigen-binding fragment
CC that binds specifically to a sclerostin (SOST) polypeptide and impairs
CC formation of a sclerostin homodimer. Specifically, it refers to an
CC antibody that competitively inhibits binding of the sclerostin
CC polypeptide to a bone morphogenic protein (BMP) Type I receptor binding
CC site or a BMP Type II receptor binding site. The present invention
CC describes a hybridoma cell capable of producing the antibody and a host
CC cell for antibody expression. Furthermore, it provides a nucleic acid
CC molecule encoding a transforming growth factor-beta (TGF-beta) binding
CC protein known as SOST (and also BBER) and methods for detection thereof.
CC Accordingly, such antibodies and osteopathic compositions of the
CC invention can be used for treating osteopenia, osteoporosis, fractures
CC and other disorders related to low bone mineral content and density. As
CC such, these compositions improve bone mineralization and can be described
CC as TGF-beta antagonists and/ or BMP-antagonists. This polypeptide
CC sequence is a bone morphogenic protein receptor type 1 given in an
CC exemplification of the invention.
XX
XX Sequence 532 AA;
SQ
Query Match 100.0%; Score 2838; DB 9; Length 532;
Best Local Similarity 100.0%; Pred. No. 8.6e-279;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPAPEDTLPLFK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPAPEDTLPLFK 60
QY 61 CYCSGHCDDALNNCTITNGHCFALIEDDQGETTLTSGCMKYESDFQCKDSPKAQLRR 120
Db 61 CYCSGHCDDALNNCTITNGHCFALIEDDQGETTLTSGCMKYESDFQCKDSPKAQLRR 120
QY 121 TIECCTRNLCNQYLOPTLPVPIGFFDGSVRLAVLISMAVICIVAMIVFSSCFYKHYC 180
Db 121 TIECCTRNLCNQYLOPTLPVPIGFFDGSVRLAVLISMAVICIVAMIVFSSCFYKHYC 180
QY 181 KSISRRGRYNRDLQDEAFIPVGESLKDLDQSQSGSGSLPLLVQRTIAKQIQMVQRV 240
Db 181 KSISRRGRYNRDLQDEAFIPVGESLKDLDQSQSGSGSLPLLVQRTIAKQIQMVQRV 240
QY 241 KGGRYGEVWGMKRGKAVKVFPTTEASFRETEIYQTVLMRHENILGFIADIKGTG 300
Db 241 KGGRYGEVWGMKRGKAVKVFPTTEASFRETEIYQTVLMRHENILGFIADIKGTG 300
QY 301 SWTQLYLITDHYENGSLYDFLKCATLDTRALLKLAYSACGLCHLHTIYGTQCKPAT 360
Db 301 SWTQLYLITDHYENGSLYDFLKCATLDTRALLKLAYSACGLCHLHTIYGTQCKPAT 360
QY 361 RDLKSKNLIKNGSCCIIADLGLAVKFNSTDNEVDIPLNTRVGTTRYNAPEVLDESLSKN 420
Db 361 RDLKSKNLIKNGSCCIIADLGLAVKFNSTDNEVDIPLNTRVGTTRYNAPEVLDESLSKN 420
QY 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYNNMVPSPDSYEDMREVVCVKRLR 480
Db 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYNNMVPSPDSYEDMREVVCVKRLR 480
QY 481 PIVSNRWNNSDECLRAVLKLMSECAHNPNASRLTALRIKTKLAKMVESQDVKI 532
Db 481 PIVSNRWNNSDECLRAVLKLMSECAHNPNASRLTALRIKTKLAKMVESQDVKI 532
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RESULT 8
ADX97416
ID ADX97416 standard; protein; 532 AA.
XX
XX AC ADX97416;
XX
XX 05-MAY-2005 (first entry)
DT
XX
XX DE Rat bone morphogenic protein type I receptor, SEQ ID 76.
XX
XX KW antibody; sclerostin; SOST; bone morphogenic protein receptor;
KW Transforming Growth Factor; osteopathic; gene therapy; bone repair;
XX osteopenia; osteoporosis; bone injury.
XX
XX OS Rattus norvegicus.
XX
XX FN WO2005014650-A2.
XX
XX PD 17-FEB-2005.
XX
XX PF 15-JUN-2004; 2004WO-US018912.
XX
XX PR 16-JUN-2003; 2003US-0478977P.
XX
XX PA (CLLT ) CELLTECH R & D INC.
XX
XX PI Winkler DG, Shi J, Latham J;
XX
XX DR WPI; 2005-163219/17.
XX
XX DR N-FSDB; ADX97430.
XX
XX New isolated antibody specific for a sclerostin polypeptide, useful for
increasing bone mineralization or for treating or preventing conditions
associated with low bone mineral density, e.g. osteoporosis or
osteopenia.
Claim 1; SEQ ID NO 76; 157pp; English.
XX
XX The invention relates to a novel isolated antibody, or its antigen-
binding fragment, which binds specifically to a sclerostin (SOST)
polypeptide. The SOST polypeptide comprises any of 6 sequences having 190
or 213 amino acids, fully defined in the specification (ADX97341,
ADX97360, ADX97398, ADX97400, ADX97402 or ADX97408). The antibody
competitively inhibits binding of the SOST polypeptide to a bone
morphogenic protein (BMP) Type I Receptor binding site and a BMP Type II
Receptor binding site, where the BMP Type I Receptor binding site is
capable of binding to a BMP Type I Receptor polypeptide. The invention
further comprises: a hybridoma cell producing the new antibody; a host
cell that is capable of expressing the new antibody; a composition
comprising the new antibody, or its antigen-binding fragment, and a
physiological carrier; an immunogen comprising a peptide comprising 6, 7,
8, 9, 10, 11, 12, or at least 21-50 or 20-75 consecutive amino acids of
the SOST polypeptide; methods for producing an antibody that specifically
binds to the SOST polypeptide; and methods for identifying an antibody
that modulates a Transforming Growth Factor (TGF)-beta signaling pathway,
that impairs binding of a BMP to the SOST polypeptide, that impairs SOST
homodimer formation, or that increases bone mineral content. The novel
antibody and compositions have osteopathic activity. The SOST nucleic
acids may be used in gene therapy. The composition and methods are useful
for increasing bone mineralization, which may treat or prevent diseases
or conditions associated with low bone mineral density, such as
osteopenia, osteoporosis or bone fractures. This sequence represents a
rat bone morphogenic protein type I receptor of the invention.
XX
XX Sequence 532 AA;
QY
Query Match 100.0%; Score 2838; DB 9; Length 532;
Best Local Similarity 100.0%; Pred. No. 8.6e-279;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPAPEDTLPLFK 60
```

Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTTLAPEDTLPFLK 60
Qy 61 CYSGCHCPDDAINNNTCTGNHCFALIEDDQGETTLTSGCMKYEGSDFOCKDSPKQALRR 120
Db 61 CYSGCHCPDDAINNNTCTGNHCFALIEDDQGETTLTSGCMKYEGSDFOCKDSPKQALRR 120
Qy 121 TIECCRTNLCNOYLQPTLPVWIGPFDGSRVRLAVLISMAVCIVAMIVFSSFCYKHYC 180
Db 121 TIECCRTNLCNOYLQPTLPVWIGPFDGSRVRLAVLISMAVCIVAMIVFSSFCYKHYC 180
Qy 181 KSISRRGRYNRDLQDEAFIPVGESLKDLIDQSQSGSGGLPLLQRTIAKIQMVROV 240
Db 181 KSISRRGRYNRDLQDEAFIPVGESLKDLIDQSQSGSGGLPLLQRTIAKIQMVROV 240
Qy 241 GKGRYGVMMGKWRGEKVAVKVFFTEASWFRTEIYQTVLMRHNILGFIADIKGTG 300
Db 241 GKGRYGVMMGKWRGEKVAVKVFFTEASWFRTEIYQTVLMRHNILGFIADIKGTG 300
Qy 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Qy 361 RDLKSKNLIKKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSKN 420
Db 361 RDLKSKNLIKKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSKN 420
Qy 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYNNVPSDPSYEDMRVVCVKRLR 480
Db 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYNNVPSDPSYEDMRVVCVKRLR 480
Qy 481 PIVSNRWNSECLRAVLKLMSECAWNPASRLTALRIKKTAKWVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAWNPASRLTALRIKKTAKWVESQDVKI 532

RESULT 9

ADX97415
ID ADX97415 standard; protein; 532 AA.
AC ADX97415;
XX
XX 05-MAY-2005 (first entry)
XX Rat bone morphogenic protein type I receptor, SEQ ID 75.
XX antibody; sclerostin; SOST; bone morphogenic protein receptor;
XX Transforming Growth Factor; osteopathic; gene therapy; bone repair;
XX osteopenia; osteoporosis; bone injury.
XX Rattus norvegicus.
XX WO2005014650-A2.
XX
XX 17-FEB-2005.
XX
XX 15-JUN-2004; 2004WO-US018912.
XX
XX 16-JUN-2003; 2003US-0478977P.
XX
XX (CLLT) CELTECH R & D INC.
XX Winkler DG, Shi J, Latham J;
XX
XX WPI; 2005-163219/17.
XX N-PSDB; ADX97429.
XX
XX New isolated antibody specific for a sclerostin polypeptide, useful for
XX increasing bone mineralization or for treating or preventing conditions
XX associated with low bone mineral density, e.g. osteoporosis or
XX osteopenia.
XX
XX Claim 1; SEQ ID NO 75; 157pp; English.

XX The invention relates to a novel isolated antibody, or its antigen-
CC binding fragment, which binds specifically to a sclerostin (SOST)
CC polypeptide. The SOST polypeptide comprises any of 6 sequences having 190
CC or 213 amino acids, fully defined in the specification (ADX97341,
CC ADX97360, ADX97398, ADX97400, ADX97402 or ADX97408). The antibody
CC competitively inhibits binding of the SOST polypeptide to a BMP Type II
CC morphogenic protein (BMP) Type I Receptor binding site and a BMP Type II
CC Receptor binding site, where the BMP Type I Receptor binding site is
CC capable of binding to a BMP Type I Receptor polypeptide. The invention
CC further comprises: a hybridoma cell producing the new antibody; a host
CC cell that is capable of expressing the new antibody; a composition
CC comprising the new antibody, or its antigen-binding fragment, and a
CC physiological carrier; an immunogen comprising a peptide comprising 6, 7,
CC 8, 9, 10, 11, 12, or at least 21-50 or 20-75 consecutive amino acids of
CC the SOST polypeptide; methods for producing an antibody that specifically
CC binds to the SOST polypeptide; and methods for identifying an antibody
CC that modulates a Transforming Growth Factor (TGF)-beta signaling pathway,
CC that impairs binding of a BMP to the SOST polypeptide, that impairs SOST
CC homodimer formation, or that increases bone mineral content. The novel
CC antibody and compositions have osteopathic activity. The SOST nucleic
CC acids may be used in gene therapy. The composition and methods are useful
CC for increasing bone mineralization, which may treat or prevent diseases
CC or conditions associated with low bone mineral density, such as
CC osteopenia, osteoporosis or bone fractures. This sequence represents a
CC rat bone morphogenic protein type I receptor of the invention.
XX
SQ Sequence 532 AA;

Query Match 100.0%; Score 2838; DB 9; Length 532;
Best Local Similarity 100.0%; Pred. No. 8.6e-279;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTTLAPEDTLPFLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTTLAPEDTLPFLK 60
Qy 61 CYSGCHCPDDAINNNTCTGNHCFALIEDDQGETTLTSGCMKYEGSDFOCKDSPKQALRR 120
Db 61 CYSGCHCPDDAINNNTCTGNHCFALIEDDQGETTLTSGCMKYEGSDFOCKDSPKQALRR 120
Qy 121 TIECCRTNLCNOYLQPTLPVWIGPFDGSRVRLAVLISMAVCIVAMIVFSSFCYKHYC 180
Db 121 TIECCRTNLCNOYLQPTLPVWIGPFDGSRVRLAVLISMAVCIVAMIVFSSFCYKHYC 180
Qy 181 KSISRRGRYNRDLQDEAFIPVGESLKDLIDQSQSGSGGLPLLQRTIAKIQMVROV 240
Db 181 KSISRRGRYNRDLQDEAFIPVGESLKDLIDQSQSGSGGLPLLQRTIAKIQMVROV 240
Qy 241 GKGRYGVMMGKWRGEKVAVKVFFTEASWFRTEIYQTVLMRHNILGFIADIKGTG 300
Db 241 GKGRYGVMMGKWRGEKVAVKVFFTEASWFRTEIYQTVLMRHNILGFIADIKGTG 300
Qy 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Qy 361 RDLKSKNLIKKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSKN 420
Db 361 RDLKSKNLIKKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSKN 420
Qy 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYNNVPSDPSYEDMRVVCVKRLR 480
Db 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYNNVPSDPSYEDMRVVCVKRLR 480
Qy 481 PIVSNRWNSECLRAVLKLMSECAWNPASRLTALRIKKTAKWVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAWNPASRLTALRIKKTAKWVESQDVKI 532
RESULT 10
ADX97414
ID ADX97414 standard; protein; 532 AA.

XX AC ADX97414;
XX DT 05-MAY-2005 (first entry)
XX DE Rat bone morphogenic protein type I receptor, SEQ ID 74.
XX KW antibody; sclerostin; SOST; bone morphogenic protein receptor;
XX KW Transforming Growth Factor; osteopathic; gene therapy; bone repair;
XX KW osteopenia; osteoporosis; bone injury.
XX OS Rattus sp.
XX PN WO2005014650-A2.
XX PD 17-FEB-2005.
XX PF 15-JUN-2004; 2004WO-US018912.
XX PR 16-JUN-2003; 2003US-0478977P.
XX PA (CLLT) CELLTech R & D INC.
XX PI Winkler DG, Shi J, Latham J;
XX PI WPI; 2005-163219/17.
XX DR N-PSDB; ADX97428.
XX
XX New isolated antibody specific for a sclerostin polypeptide, useful for
XX PT increasing bone mineralization or for treating or preventing conditions
XX PT associated with low bone mineral density, e.g. osteoporosis or
XX PT osteopenia.
XX PS Claim 1; SEQ ID NO 74; 157pp; English.
XX
XX The invention relates to a novel isolated antibody, or its antigen-
XX CC binding fragment, which binds specifically to a sclerostin (SOST)
XX CC polypeptide. The SOST polypeptide comprises any of 6 sequences having 190
XX CC or 213 amino acids, fully defined in the specification (ADX97341,
XX CC ADX97360, ADX97398, ADX97400, ADX97402 or ADX97408). The antibody
XX CC competitively inhibits binding of the SOST polypeptide to a bone
XX CC morphogenic protein (BMP) Type I Receptor binding site and a BMP Type II
XX CC Receptor binding site, where the BMP Type I Receptor binding site is
XX CC capable of binding to a BMP type I Receptor polypeptide. The invention
XX CC further comprises: a hybridoma cell producing the new antibody; a host
XX CC cell that is capable of expressing the new antibody; a composition
XX CC comprising the new antibody, or its antigen-binding fragment, and a
XX CC physiological carrier; an immunogen comprising a peptide comprising 6, 7,
XX CC 8, 9, 10, 11, 12, or at least 21-50 or 20-75 consecutive amino acids of
XX CC the SOST polypeptide; methods for producing an antibody that specifically
XX CC binds to the SOST polypeptide; and methods for identifying an antibody
XX CC that modulates a Transforming Growth Factor (TGF)-beta signaling pathway,
XX CC that impairs binding of a BMP to the SOST polypeptide, that impairs SOST
XX CC homodimer formation, or that increases bone mineral content. The novel
XX CC antibody and compositions have osteopathic activity. The SOST nucleic
XX CC acids may be used in gene therapy. The composition and methods are useful
XX CC for increasing bone mineralization, which may treat or prevent diseases
XX CC or conditions associated with low bone mineral density, such as
XX CC osteopenia, osteoporosis or bone fractures. This sequence represents a
XX CC rat bone morphogenic protein type I receptor of the invention.
XX SQ Sequence 532 AA;
Query Match 100.0%; Score 2838; DB 9; Length 532;
Best Local Similarity 100.0%; Pred. No. 8.6e-279;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTQLYTYRLLGACLFISHVQGNLDSMLHGTGMSKSDVDQKPKNGVTLPEDTLPLFK 60
DB 1 MTQLYTYRLLGACLFISHVQGNLDSMLHGTGMSKSDVDQKPKNGVTLPEDTLPLFK 60
QY 61 CYCSGHCPDDAINTTCITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
|||||

Db 61 CYCSGHCPDDAINTTCITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
QY 121 TIECRTLNCQYLQPTLPVPVIGFFDGSVRWLAVLISMVAVCIAMIVFSSCFYKHYC 180
|||||
Db 121 TIECRTLNCQYLQPTLPVPVIGFFDGSVRWLAVLISMVAVCIAMIVFSSCFYKHYC 180
QY 181 KSISRGHYNRLDQDEAFIPVGSLSKDLIDQSQSSGSGGLPLLVQRTIAKIQIMVRQV 240
Db 181 KSISRGHYNRLDQDEAFIPVGSLSKDLIDQSQSSGSGGLPLLVQRTIAKIQIMVRQV 240
QY 241 GKGRYGEVVMGKWRGEKVAVKVFVFTTEBASFPRETEIYQTVLMRHNILGFTAAADIKGTG 300
Db 241 GKGRYGEVVMGKWRGEKVAVKVFVFTTEBASFPRETEIYQTVLMRHNILGFTAAADIKGTG 300
QY 301 SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAISAACGLCHLHTEIYGTQKPAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAISAACGLCHLHTEIYGTQKPAIAH 360
QY 361 RDLXKNLIIKNGSCCCTIADILGLAVKFNDSNDNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
Db 361 RDLXKNLIIKNGSCCCTIADILGLAVKFNDSNDNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
QY 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEYQLPYNNMVPSPDSYEDMRVWCVKRLR 480
Db 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEYQLPYNNMVPSPDSYEDMRVWCVKRLR 480
QY 481 PIVSNRWNDSDECLRAVLKMLSECWAHNPASRLTALRIKKTAKMYESQDVKI 532
Db 481 PIVSNRWNDSDECLRAVLKMLSECWAHNPASRLTALRIKKTAKMYESQDVKI 532
RESULT 11
ADX97419
ID ADX97419 standard; protein; 532 AA.
XX AC ADX97419;
XX DT 05-MAY-2005 (first entry)
XX DE Rat bone morphogenic protein type Ia receptor, SEQ ID 79.
XX KW antibody; sclerostin; SOST; bone morphogenic protein receptor;
XX KW Transforming Growth Factor; osteopathic; gene therapy; bone repair;
XX KW osteopenia; osteoporosis; bone injury.
XX OS Rattus sp.
XX PN WO2005014650-A2.
XX PD 17-FEB-2005.
XX PF 15-JUN-2004; 2004WO-US018912.
XX PR 16-JUN-2003; 2003US-0478977P.
XX PA (CLLT) CELLTech R & D INC.
XX PI Winkler DG, Shi J, Latham J;
XX PI WPI; 2005-163219/17.
XX
XX New isolated antibody specific for a sclerostin polypeptide, useful for
XX PT increasing bone mineralization or for treating or preventing conditions
XX PT associated with low bone mineral density, e.g. osteoporosis or
XX PT osteopenia.
XX PS Claim 1; SEQ ID NO 79; 157pp; English.
XX
XX The invention relates to a novel isolated antibody, or its antigen-
XX CC binding fragment, which binds specifically to a sclerostin (SOST)
XX CC polypeptide. The SOST polypeptide comprises any of 6 sequences having 190
XX CC or 213 amino acids, fully defined in the specification (ADX97341,
XX CC ADX97360, ADX97398, ADX97400, ADX97402 or ADX97408). The antibody
XX CC competitively inhibits binding of the SOST polypeptide to a bone
XX CC morphogenic protein (BMP) Type I Receptor binding site and a BMP Type II
XX CC Receptor binding site, where the BMP Type I Receptor binding site is
XX CC capable of binding to a BMP type I Receptor polypeptide. The invention
XX CC further comprises: a hybridoma cell producing the new antibody; a host
XX CC cell that is capable of expressing the new antibody; a composition
XX CC comprising the new antibody, or its antigen-binding fragment, and a
XX CC physiological carrier; an immunogen comprising a peptide comprising 6, 7,
XX CC 8, 9, 10, 11, 12, or at least 21-50 or 20-75 consecutive amino acids of
XX CC the SOST polypeptide; methods for producing an antibody that specifically
XX CC binds to the SOST polypeptide; and methods for identifying an antibody
XX CC that modulates a Transforming Growth Factor (TGF)-beta signaling pathway,
XX CC that impairs binding of a BMP to the SOST polypeptide, that impairs SOST
XX CC homodimer formation, or that increases bone mineral content. The novel
XX CC antibody and compositions have osteopathic activity. The SOST nucleic
XX CC acids may be used in gene therapy. The composition and methods are useful
XX CC for increasing bone mineralization, which may treat or prevent diseases
XX CC or conditions associated with low bone mineral density, such as
XX CC osteopenia, osteoporosis or bone fractures. This sequence represents a
XX CC rat bone morphogenic protein type I receptor of the invention.
XX SQ Sequence 532 AA;
Query Match 100.0%; Score 2838; DB 9; Length 532;
Best Local Similarity 100.0%; Pred. No. 8.6e-279;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTQLYTYRLLGACLFISHVQGNLDSMLHGTGMSKSDVDQKPKNGVTLPEDTLPLFK 60
DB 1 MTQLYTYRLLGACLFISHVQGNLDSMLHGTGMSKSDVDQKPKNGVTLPEDTLPLFK 60
QY 61 CYCSGHCPDDAINTTCITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
|||||

competitively inhibits binding of the SOST polypeptide to a bone morphogenic protein (BMP) Type I Receptor binding site and a BMP Type II Receptor binding site, where the BMP Type I Receptor binding site is capable of binding to a BMP Type I Receptor polypeptide. The invention further comprises: a hybridoma cell producing the new antibody; a host cell that is capable of expressing the new antibody; a composition comprising the new antibody, or its antigen-binding fragment, and a physiological carrier; an immunogen comprising a peptide comprising 6, 7, 8, 9, 10, 11, 12, or at least 21-50 or 20-75 consecutive amino acids of the SOST polypeptide; methods for producing an antibody that specifically binds to the SOST polypeptide; and methods for identifying an antibody that modulates a Transforming Growth Factor (TGF)-beta signaling pathway, that impairs binding of a BMP to the SOST polypeptide, that impairs SOST homodimer formation, or that increases bone mineral content. The novel antibody and compositions have osteopathic activity. The SOST nucleic acids may be used in gene therapy. The composition and methods are useful for increasing bone mineralization, which may treat or prevent diseases or conditions associated with low bone mineral density, such as osteopenia, osteoporosis or bone fractures. This sequence represents a rat bone morphogenic protein type Ia receptor of the invention.

XX Sequence 532 AA;

Query Match 100.0%; Score 2838; DB 9; Length 532;

Best Local Similarity 100.0%; Pred. No. 8.6e-279;

Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMSDVKQKPKENGVTLPEDTLPFLK 60

Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMSDVKQKPKENGVTLPEDTLPFLK 60

Qy 61 CYCSGHCPCDDAINNCTITNGHCFIIEEDDQGETTLTSGCMKYGSDFOCKDSPKQALRR 120

Db 61 CYCSGHCPCDDAINNCTITNGHCFIIEEDDQGETTLTSGCMKYGSDFOCKDSPKQALRR 120

Qy 121 TIECCRTNLCNQYLQPTLPVPIGPFDDGSRVRLAVLISMVAVCIAMIVFSSCFYKHYC 180

Db 121 TIECCRTNLCNQYLQPTLPVPIGPFDDGSRVRLAVLISMVAVCIAMIVFSSCFYKHYC 180

Qy 181 KSISRRGRVNRDLQDEAFIPVGSLSKDLIDQSQSGSGSLPLLVORTIAKQIQMVROV 240

Db 181 KSISRRGRVNRDLQDEAFIPVGSLSKDLIDQSQSGSGSLPLLVORTIAKQIQMVROV 240

Qy 241 GKGRYGVMMGKWRGEKAVKVPFTTEASWPRETEIYQTVLMRHNILGFIAADIKGTG 300

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Qy 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360

Db 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360

Qy 361 RDLKSKNILIKONGSCCIIADGLAVKFNSTNEVDPLNTRVGTTRRYMAPEVLDESLSKN 420

Db 361 RDLKSKNILIKONGSCCIIADGLAVKFNSTNEVDPLNTRVGTTRRYMAPEVLDESLSKN 420

Qy 421 HFQPIYINADIYSFGLIIWEMARRCITGIVVEEQLPYNNVPDPSYEDNREVVVCVKRLR 480

Db 421 HFQPIYINADIYSFGLIIWEMARRCITGIVVEEQLPYNNVPDPSYEDNREVVVCVKRLR 480

Qy 481 PIVSNRWNSECLRAVLKLMSECAWNPASRLTALRIKKTAKWVSQDVKI 532

Db 481 PIVSNRWNSECLRAVLKLMSECAWNPASRLTALRIKKTAKWVSQDVKI 532

RESULT 12

AAR74343

ID AAR74343 standard; protein; 532 AA.

XX

AC AAR74343;

XX

DT 25-MAR-2003 (revised)

XX 01-NOV-1995 (first entry)

XX

DE BRK-1 protein.

XX BRK-1; BMP receptor kinase protein-1; bone morphogenetic protein.

XX Mus sp.

XX Key Location/Qualifiers

FH Peptide 1..23

FT Domain /label= Sig_peptide

FT Domain 24..152

FT Domain /label= Extracellular_ligand_binding_domain

FT Domain 153..176

FT Domain /label= Transmembrane_domain

FT Domain 177..532

XX /label= Intracellular_kinase_domain

XX WO9514778-A2.

XX 01-JUN-1995.

XX 23-NOV-1994; 94WO-US013534.

XX 24-NOV-1993; 93US-00158735.

XX (PROC) PROCTER & GAMBLE CO.

XX Cook JS, Correa PE, Koenig BB, Rosenbaum JS, Ting J;

XX WPI; 1995-206935/27.

XX N-PSDB; AAQ90184.

XX New bone morphogenetic protein receptor kinase protein - used for

XX identifying cpds. capable of binding it and for developing therapeutic

XX cpds. and detection system(s).

XX Claim 1; Page 29-32; 49pp; English.

XX A cDNA library prepared from NIH3T3 poly-A RNA was screened with J159 PCR

XX fragment to isolate clone BRK-1 (sequence given in AAQ90184) encoding the

XX full-length BMP receptor kinase protein (AAR74343). Vectors including the

XX DNA were used to express recombinant BRK-1 in CHO and COS-7 hosts.

XX (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 532 AA;

Query Match 99.5%; Score 2823; DB 2; Length 532;

Best Local Similarity 98.9%; Pred. No. 2.9e-277;

Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMSDVKQKPKENGVTLPEDTLPFLK 60

Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMSDVKQKPKENGVTLPEDTLPFLK 60

Qy 61 CYCSGHCPCDDAINNCTITNGHCFIIEEDDQGETTLTSGCMKYGSDFOCKDSPKQALRR 120

Db 61 CYCSGHCPCDDAINNCTITNGHCFIIEEDDQGETTLTSGCMKYGSDFOCKDSPKQALRR 120

Qy 121 TIECCRTNLCNQYLQPTLPVPIGPFDDGSRVRLAVLISMVAVCIAMIVFSSCFYKHYC 180

Db 121 TIECCRTNLCNQYLQPTLPVPIGPFDDGSRVRLAVLISMVAVCIAMIVFSSCFYKHYC 180

Qy 181 KSISRRGRVNRDLQDEAFIPVGSLSKDLIDQSQSGSGSLPLLVORTIAKQIQMVROV 240

Db 181 KSISRRGRVNRDLQDEAFIPVGSLSKDLIDQSQSGSGSLPLLVORTIAKQIQMVROV 240

Qy 241 GKGRYGVMMGKWRGEKAVKVPFTTEASWPRETEIYQTVLMRHNILGFIAADIKGTG 300

Db 241 GKGRYGVMMGKWRGEKAVKVPFTTEASWPRETEIYQTVLMRHNILGFIAADIKGTG 300

Qy 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360

Db 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360

361	QY	RDLSKSNILIKKNGSCCIIADGLAVKFNSTDNEVDIPLNTRVGTGRYMAPEVLDES	420
361	Db	RDLSKSNILIKKNGSCCIIADGLAVKFNSTDNEVDIPLNTRVGTGRYMAPEVLDES	420
421	QY	HFOPTIMADIYSFGLIIWEMARRCITGGIVEEYQLPYNNMVPSPDPSYEDMREVCVKRLR	480
421	Db	HFOPTIMADIYSFGLIIWEMARRCITGGIVEEYQLPYNNMVPSPDPSYEDMREVCVKRLR	480
481	QY	PIVSNRNWNSDECLRAVLKLMGECWAHPASRLTALRIKKTAKNWSQDVKI	532
481	Db	PIVSNRNWNSDECLRAVLKLMGECWAHPASRLTALRIKKTAKNWSQDVKI	532

RESULT 13

AAR96201

AA96201
ID AAR96201 standard: protein: 532 AA.

XX
XX

AC AAR96201;

2000

DT 22-AUG-1996 (first entry)

XX
19 OCT-NOV-77 (JSTT)

DE Bone morphogenetic protein

XX
XX
STANBORD AVE
STANFORD

Mouse: bone morphogenetic

KW Mouse; bone morphogenetic
KW bone morphogenetic protein

KW bone morphogenetic protein
KW bone disorder; osteoporosis

bone disorder; osteogenic; bone disorder; osteogenic; bone disorder; osteogenic;

KW drug screening; reporter g
KW hormone-releasing element

KW hormone-responsive element

XX 8

OS Mus musculus.

XX

FH	Key	Location/Q
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FT /note= "pe

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PN WO9614412-A2.

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PD 17-MAY-1996.

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23456789

PF 30-OCT-1995; 95WO-US0140

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1555T-1500-00
047050-0000

PR 04-NOV-1994: 94US-003341

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04-NOV-1954; 3403-003341

XX PA (PROC) PROCTER & GAMBLE C

FA / FROU / FROU & GAMBLE C
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PT Rosenbaum JS. Nohno T.

PI
XX
ROSENBAUM JS, Nonno T;

XX
DP WPT: 1096-251763/25

DR WPI; 1996-251762/25.
DR N-BCDR: AAT37339

DR N-PSDB; AAT27228.
YY

XX
DT
TODAY

Isolated bone morphogenic

determine if a test cpd. i.

PT BMP receptor kinase protein

CC	by monitoring reporter gene expression
XX	Sequence 532 AA;
XX	Query Match 99.5%; Score 2823; DB 2; Length 532;
XX	Best Local Similarity 98.9%; Pred. No. 2.9e-277;
XX	Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
Qy	1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTMGKSDVDOKKPPENGVTLAPEDTLUPFLK 60
Db	1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTMGKSDLDQKKPPENGVTLAPEDTLUPFLK 60
Qy	61 CYSGHGPCDDAINNTCITNGHCFPAIIIEEDDQGETTLTSGCMKYEGSDFQKDSPKAQLRR 120
Db	61 CYSGHGPCDDAINNTCITNGHCFPAIIIEEDDQGETTLTSGCMKYEGSDFQKDSPKAQLRR 120
Qy	121 TIECCRTNLCNQYLOPTLPVVI GPPFDGSVRWLAVLISMAVCIVAMIVFSSCFYKHYC 180
Db	121 TIECCRTNLCNQYLOPTLPVVI GPPFDGSIRWLAVLISMAVCIVAMIVFSSCFYKHYC 180
Qy	181 KSISSSRGYNRDLDEQDEAFIPVGESIKDLIDQSSGSGSLPLLVORTIAQIQMVROV 240
Db	181 KSISSSRGYNRDLDEQDEAFIPVGESIKDLIDQSSGSGSLPLLVORTIAQIQMVROV 240
Qy	241 GKGRYGEVMWGWKRGKAVKVPFTTTEASWFRETEIYQTVLMRHENILGFTAADIKGTG 300
Db	241 GKGRYGEVMWGWKRGKAVKVPFTTTEASWFRETEIYQTVLMRHENILGFTAADIKGTG 300
Qy	301 SWTQLYLIIDYHENGSLYDPLKCATLDTRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Db	301 SWTQLYLIIDYHENGSLYDPLKCATLDTRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Qy	361 RDLKSNLILIKNGSCCIADGLAVKFNSDTNEVDIPLNTRVGTTRYMAPEVLDESLSKN 420
Db	361 RDLKSNLILIKNGSCCIADGLAVKFNSDTNEVDIPLNTRVGTTRYMAPEVLDESLSKN 420
Qy	421 HFOPYIMADIYSFGLIIEWMARRCITGGIVEEYQLPYNNVPSDPSYEDMREVVCVKRLR 480
Db	421 HFOPYIMADIYSFGLIIEWMARRCITGGIVEEYQLPYNNVPSDPSYEDMREVVCVKRLR 480
Qy	481 PIVSNRWNSEDCIRAVLKLMSCEWHAHPASRLTALRIKKTAKWVESQDVKI 532
Db	481 PIVSNRWNSEDCIRAVLKLMSCEWHAHPASRLTALRIKKTAKWVESQDVKI 532
RESULT 14	
AAR95225	standard; protein; 532 AA.
XX	AAR95225;
XX	31-DEC-1996 (first entry)
XX	Mouse BMP type I receptor kinase protein (BRK-1).
XX	BMP type II receptor kinase-3; BRK-3; bone morphogenetic protein;
XX	BMP type I receptor kinase; BRK-1; BMP receptor.
XX	Mus sp.
XX	WO9614579-A1.
XX	17-MAY-1996.
XX	30-OCT-1995; 95WO-US014027.
XX	04-NOV-1994; 94US-00334178.
XX	05-JUN-1995; 95US-00462467.
XX	(PROC) PROCTER & GAMBLE CO.
XX	Rosenbaum JS;
XX	

DR WP1; 1996-251887/25.
XX N-PSDB; AAT95225.
PT Assays for bone morphogenetic protein activities - using complex of BMP
PT type I receptor kinase protein and BMP receptor kinase protein BRK-3.
XX
PS Claim 2; Page 66-67; 101pp; English.
XX
CC Full-length mouse bone morphogenetic protein (BMP) type I receptor kinase
CC protein-1 (BRK-1) (AAR95225) is a receptor capable of binding BMP and
CC transducing a signal initiated by the binding. Its amino acid sequence
CC was deduced from a cDNA clone (AAT28021). A BMP receptor kinase protein
CC complex formed of full-length, incomplete or soluble BMP type I receptor
CC kinase protein and full-length, incomplete or soluble BMP type II
CC receptor kinase-3 (BRK-3) (see also AAR95222-24 and AAR95226-34) is
CC useful for screening cpds. for BMP receptor affinity or for determining
CC the concentration of a BMP receptor ligand in a clinical sample. The
CC complex can be expressed by host cells co-transfected with vectors
CC carrying the appropriate DNA sequences (see also AAT28018-30)
XX
SQ Sequence 532 AA;

Query Match 99.5%; Score 2823; DB 2; Length 532;
Best Local Similarity 98.9%; Pred. No. 2.9e-277;
Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDOKKPENGVTLAPEDTLPFLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDLDOKKPENGVTLAPEDTLPFLK 60

QY 61 CYCSGHCPCDDAINNCTITNGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKQALRR 120
Db 61 CYCSGHCPCDDAINNCTITNGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKQALRR 120

QY 121 TIECCRTNLCNQYLOFTLPPVIGPFDGSRVRLAVLISMAVCIVAMIVFSSCFCKHYC 180
Db 121 TIECCRTNLCNQYLOFTLPPVIGPFDGSRVRLAVLISMAVCIVAMIVFSSCFCKHYC 180

QY 181 KSISSRGYNRDLQDEAFIPVGESLKDLIDQSSGSGSLPLLQVORTIAQIQMVROV 240
Db 181 KSISSRGYNRDLQDEAFIPVGESLKDLIDQSSGSGSLPLLQVORTIAQIQMVROV 240

QY 241 GKGRYGEVVMGKRGKAVKVFPTTEASWPRETEIYQTVLMRHNILGFTAADIKGTG 300
Db 241 GKGRYGEVVMGKRGKAVKVFPTTEASWPRETEIYQTVLMRHNILGFTAADIKGTG 300

QY 301 SWTQLYLITDYHENGSLYDFLKCATLDTDRALLKLAYSAAACGLCHLHTEIYGTGKPAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTDRALLKLAYSAAACGLCHLHTEIYGTGKPAIAH 360

QY 361 RDLKSKNLIKKNGSCCIIADGLAVKFNSDTNEVDIPLNTRVGTTRYMAPEVLDESLSKN 420
Db 361 RDLKSKNLIKKNGSCCIIADGLAVKFNSDTNEVDIPLNTRVGTTRYMAPEVLDESLSKN 420

RESULT 15
AAW86248
ID AAW86248 standard; protein; 532 AA.
XX
AC AAW86248;
XX
DT 16-FEB-1999 (first entry)
XX
DE Mouse BMP receptor kinase protein (BRK) -1.
XX

KW Bone morphogenetic protein; BMP; BMP receptor kinase; ActRIIB receptor;
XX BRK; receptor ligand; drug.
OS Mus sp.
XX W09852038-A1.
PN 19-NOV-1998.
XX
PD 13-MAY-1998; 98WO-US009519.
XX
PF 16-MAY-1997; 97US-0046768P.
XX
PR (PROC) PROCTER & GAMBLE CO.
PA
PI Rosenbaum JS;
XX
PT WPI; 1999-009930/01.
DR N-PSDB; AAV711972.
XX
XX Screening method using bone morphogenetic protein receptor complex -
PT which binds to potential drugs, and ActRIIB receptor used in the complex,
PT also host cells transfected with DNA encoding the complex.
XX
PS Claim 1; Page 88-91; 110pp; English.
XX
CC This represents a mouse BMP receptor kinase protein (BRK)-1. This can be
CC used in the method of the invention of determining whether a compound can
CC bind to a bone morphogenetic protein (BMP) receptor kinase protein
CC complex. The method comprises allowing a compound in a sample to bind to
CC the complex, where the complex is comprised of (i) a BMP; (ii) a BRK
CC protein; (iii) an ActRIIB receptor. The method can be used to determine
CC the concentration of a BMP receptor ligand in a sample by comparing the
CC binding to a standard curve prepared with known concentrations of BMP
CC ligand. The method can also be used to determine whether a test compound
CC produces a signal on binding to a BMP receptor protein complex. The
CC method is useful for determining whether a ligand, such as a known or
CC putative drug, can bind to and/or activate the receptors
XX
SQ Sequence 532 AA;

Query Match 99.5%; Score 2823; DB 2; Length 532;
Best Local Similarity 98.9%; Pred. No. 2.9e-277;
Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDOKKPENGVTLAPEDTLPFLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDLDOKKPENGVTLAPEDTLPFLK 60

QY 61 CYCSGHCPCDDAINNCTITNGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKQALRR 120
Db 61 CYCSGHCPCDDAINNCTITNGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKQALRR 120

QY 121 TIECCRTNLCNQYLOFTLPPVIGPFDGSRVRLAVLISMAVCIVAMIVFSSCFCKHYC 180
Db 121 TIECCRTNLCNQYLOFTLPPVIGPFDGSRVRLAVLISMAVCIVAMIVFSSCFCKHYC 180

QY 181 KSISSRGYNRDLQDEAFIPVGESLKDLIDQSSGSGSLPLLQVORTIAQIQMVROV 240
Db 181 KSISSRGYNRDLQDEAFIPVGESLKDLIDQSSGSGSLPLLQVORTIAQIQMVROV 240

QY 241 GKGRYGEVVMGKRGKAVKVFPTTEASWPRETEIYQTVLMRHNILGFTAADIKGTG 300
Db 241 GKGRYGEVVMGKRGKAVKVFPTTEASWPRETEIYQTVLMRHNILGFTAADIKGTG 300

QY 301 SWTQLYLITDYHENGSLYDFLKCATLDTDRALLKLAYSAAACGLCHLHTEIYGTGKPAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTDRALLKLAYSAAACGLCHLHTEIYGTGKPAIAH 360

QY 361 RDLKSKNLIKKNGSCCIIADGLAVKFNSDTNEVDIPLNTRVGTTRYMAPEVLDESLSKN 420
Db 361 RDLKSKNLIKKNGSCCIIADGLAVKFNSDTNEVDIPLNTRVGTTRYMAPEVLDESLSKN 420

Qy	421	HFQPYIMADIYSFGLIIEWMARRCITGGIVEEYQLPYNNMVPSPSYEDMREVVCVKRLR	480
Db	421	HFQPYIMADIYSFGLIIEWMARRCITGGIVEEYQLPYNNMVPSPSYEDMREVVCVKRLR	480
Qy	481	PIVSNRWNSDECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI	532
Db	481	PIVSNRWNSDECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI	532

Search completed: December 3, 2005, 06:07:43
Job time : 193 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 06:04:29 ; Search time 45 Seconds
(without alignments)
977.410 Million cell updates/sec

Title: US-10-600-645-2

Perfect score: 2838

Sequence: 1 MTQLYTYIRLLGACLFIIHSHVQGNLDSMLHGTGKMSVDVDDQKPKENGVTLPEDTLPFLK 532

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2838	100.0	532	2	US-08-123-934A-2
2	2838	100.0	532	2	US-09-874-628-2
3	2838	100.0	532	4	PCT-US94-10080-2
4	2823	99.5	532	2	US-09-382-256-14
5	2823	99.5	532	2	US-08-158-735A-4
6	2823	99.5	532	2	US-09-395-115-14
7	2823	99.5	532	2	US-08-334-179A-12
8	2823	99.5	532	2	US-08-436-265-14
9	2823	99.5	532	2	US-09-679-187-14
10	2823	99.5	532	2	US-09-267-963D-14
11	2769	97.6	532	1	US-08-481-337A-6
12	2769	97.6	532	2	US-09-382-256-6
13	2769	97.6	532	2	US-09-395-115-6
14	2769	97.6	532	2	US-08-436-265-6
15	2769	97.6	532	2	US-09-679-187-6
16	2769	97.6	532	2	US-08-448-371A-6
17	2769	97.6	532	2	US-09-267-963D-6
18	2769	97.6	532	2	US-09-949-016-6475
19	2769	97.6	532	4	PCT-US95-05467-6
20	2763	97.4	532	2	US-09-949-016-7785
21	2616	92.2	500	2	US-08-158-735A-2
22	1934.5	68.2	502	2	US-08-123-934A-4
23	1934.5	68.2	502	2	US-09-874-628-4
24	1934.5	68.2	502	4	PCT-US94-10080-4
25	1933.5	68.1	502	1	US-08-481-337A-8
26	1933.5	68.1	502	2	US-09-382-256-18
27	1933.5	68.1	502	2	US-09-395-115-18

28	1933.5	68.1	502	2	US-08-436-265-18	Sequence 18, Appl
29	1933.5	68.1	502	2	US-09-679-187-18	Sequence 18, Appl
30	1933.5	68.1	502	2	US-08-448-371A-8	Sequence 8, Appl
31	1933.5	68.1	502	2	US-09-267-963D-18	Sequence 18, Appl
32	1933.5	68.1	502	4	PCT-US95-05467-8	Sequence 8, Appl
33	1926	67.9	502	2	US-08-334-179A-14	Sequence 14, Appl
34	1848.5	65.1	494	2	US-09-949-016-10396	Sequence 10396, A
35	1274	44.9	503	2	US-08-123-934A-10	Sequence 10, Appl
36	1274	44.9	503	2	US-09-874-628-10	Sequence 10, Appl
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38	1268	44.7	501	2	US-09-949-016-9766	Sequence 9766, Ap
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40	1268	44.7	503	2	US-09-395-115-10	Sequence 10, Appl
41	1268	44.7	503	2	US-08-436-265-10	Sequence 10, Appl
42	1268	44.7	503	2	US-09-679-187-10	Sequence 10, Appl
43	1268	44.7	503	2	US-09-267-963D-10	Sequence 10, Appl
44	1268	44.7	503	2	US-09-949-016-6528	Sequence 6528, Ap
45	1263.5	44.5	501	1	US-08-149-105-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-123-934A-2
; Sequence 2, Application US/08123934A
; Patent No. 6291206
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, John
; APPLICANT: CELESTE, Anthony J.
; APPLICANT: THIES, R. Scott
; APPLICANT: YAMAJI, No. 6291206oru
; TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute Inc. - Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,934A
; FILING DATE: 17-SEP-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, Steven R
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 876 1170
; TELEFAX: 617 876 5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-123-934A-2

Query Match 100.0%; Score 2838; DB 2; Length 532;
Best Local Similarity 100.0%; Pred. No. 8.6e-261;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTQLYTYIRLLGACLFIIHSHVQGNLDSMLHGTGKMSVDVDDQKPKENGVTLPEDTLPFLK 60
DB 1 MTQLYTYIRLLGACLFIIHSHVQGNLDSMLHGTGKMSVDVDDQKPKENGVTLPEDTLPFLK 60

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QY 61 CYCSGHCPCDDAINTTCITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKSPKAQLRR 120
DB 61 CYCSGHCPCDDAINTTCITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKSPKAQLRR 120
QY 121 TIECCRTNLCNQYLQPTLPVPPVIGPFDGSRVRLAVLISMAVCIAMIVFSSCFCKYKHC 180
DB 121 TIECCRTNLCNQYLQPTLPVPPVIGPFDGSRVRLAVLISMAVCIAMIVFSSCFCKYKHC 180
QY 181 KSISGRGRNRLDEQDEAFIPVGESLKDLIDQSQSSGSGGLPLLQRTIAKQIQMVRQV 240
DB 181 KSISGRGRNRLDEQDEAFIPVGESLKDLIDQSQSSGSGGLPLLQRTIAKQIQMVRQV 240
QY 241 GKGRYGEVMMGKWRGKAVKVFPTTEBASWPRETEIYQTVLMRHNILGFTAADIKGTG 300
DB 241 GKGRYGEVMMGKWRGKAVKVFPTTEBASWPRETEIYQTVLMRHNILGFTAADIKGTG 300
QY 301 SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAISAAACGLCHLHTEIYGTQGPAAIAH 360
DB 301 SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAISAAACGLCHLHTEIYGTQGPAAIAH 360
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DB 361 RDLKSKNLIKKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDESLSKN 420
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DB 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEEYQLPYNNMVPSPDPSYEDMRVVCVKRLR 480
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RESULT 2

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US-09-874-628-2
; Sequence 2, Application US/09874628
; Patent No. 6610513
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, John
; CELESTE, Anthony J.
; THIES, R. Scott
; YAMAJI, No. 6610513oru
; TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute Inc.- Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/874,628
; FILING DATE: 05-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/123,934
; FILING DATE: 17-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 876 1170
; TELEFAX: 617 876 5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-874-628-2
Query Match 100.0%; Score 2838; DB 2; Length 532;
Best Local Similarity 100.0%; Pred. No. 8.6e-261;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTQLYTYIRLLGACLIIFISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLAPEDTLPLFLK 60
DB 1 MTQLYTYIRLLGACLIIFISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLAPEDTLPLFLK 60
QY 61 CYCSGHCPCDDAINTTCITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKSPKAQLRR 120
DB 61 CYCSGHCPCDDAINTTCITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKSPKAQLRR 120
QY 121 TIECCRTNLCNQYLQPTLPVPPVIGPFDGSRVRLAVLISMAVCIAMIVFSSCFCKYKHC 180
DB 121 TIECCRTNLCNQYLQPTLPVPPVIGPFDGSRVRLAVLISMAVCIAMIVFSSCFCKYKHC 180
QY 181 KSISGRGRNRLDEQDEAFIPVGESLKDLIDQSQSSGSGGLPLLQRTIAKQIQMVRQV 240
DB 181 KSISGRGRNRLDEQDEAFIPVGESLKDLIDQSQSSGSGGLPLLQRTIAKQIQMVRQV 240
QY 241 GKGRYGEVMMGKWRGKAVKVFPTTEBASWPRETEIYQTVLMRHNILGFTAADIKGTG 300
DB 241 GKGRYGEVMMGKWRGKAVKVFPTTEBASWPRETEIYQTVLMRHNILGFTAADIKGTG 300
QY 301 SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAISAAACGLCHLHTEIYGTQGPAAIAH 360
DB 301 SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAISAAACGLCHLHTEIYGTQGPAAIAH 360
QY 361 RDLKSKNLIKKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDESLSKN 420
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DB 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEEYQLPYNNMVPSPDPSYEDMRVVCVKRLR 480
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RESULT 3
PCT-US94-10080-2
; Sequence 2, Application PC/TUS9410080
; GENERAL INFORMATION:
; APPLICANT: GENETICS INSTITUTE, INC.
; TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute Inc.- Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10080
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/123,934
; FILING DATE: 17-SEP-1993
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5203-PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8260
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-10080-2

Query Match 100.0%; Score 2838; DB 4; Length 532;
Best Local Similarity 100.0%; Pred. No. 8.6e-261;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMSDVKQKPKNGVTLAPEDTLPFLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMSDVKQKPKNGVTLAPEDTLPFLK 60

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Db 121 TIECRTLNCQYLOLTPPPVIGPFDGSRVRLAVLISMVAVCIAMIVFSSFCYKHYC 180

Qy 181 KSISSRGYNRDLQDEAFIPVGSLSKDLIDQSSGSGSLPLVLRHENILGFIAADIKGTG 240
Db 181 KSISSRGYNRDLQDEAFIPVGSLSKDLIDQSSGSGSLPLVLRHENILGFIAADIKGTG 240

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Db 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSACGLCHLHTEIYGTQKPAIAH 360

Qy 361 RDLKSKNILKKGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDESLSKN 420
Db 361 RDLKSKNILKKGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDESLSKN 420

Qy 421 HFQPYINADIYSFGLIIEWARRCITGIVVEEYQLPYNNVPDPSYEDMRVVCVKRLR 480
Db 421 HFQPYINADIYSFGLIIEWARRCITGIVVEEYQLPYNNVPDPSYEDMRVVCVKRLR 480

Qy 481 PIVSNRWNSECLRAVLKMSCEWHPNAPRLTALRIKKTAKWVSSQDVKI 532
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RESULT 4
US-09-382-256-14
Sequence 14, Application US/09382256A
Patent No. 6207814
GENERAL INFORMATION:
APPLICANT: MIYAZONO, Kohei
TEN DIKE, Peter
FRANZEN, Petra
YAMASHITA, Hidetoshi
HELDIN, Carl-Henrik
TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS
HAVING SERINE THREONINE KINASE DOMAINS,
AND THEIR USE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.

STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/382,256A
FILING DATE: 24-Aug-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: No. 6207814ember 17, 1993
APPLICATION NUMBER: GB 9224057.1
FILING DATE: No. 6207814ember 17, 1992
APPLICATION NUMBER: GB 9304677.9
FILING DATE: March 8, 1993
APPLICATION NUMBER: GB 9304680.3
FILING DATE: March 8, 1993
APPLICATION NUMBER: 9311047.6
FILING DATE: May 28, 1993
APPLICATION NUMBER: 9313763.6
FILING DATE: July 2, 1993
APPLICATION NUMBER: 9316099.2
FILING DATE: August 3, 1993
APPLICATION NUMBER: 321344.5
FILING DATE: October 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 6207814man D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5298.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-382-256-14

Query Match 99.5%; Score 2823; DB 2; Length 532;
Best Local Similarity 98.9%; Pred. No. 2.3e-259;
Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMSDVKQKPKNGVTLAPEDTLPFLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMSDVKQKPKNGVTLAPEDTLPFLK 60

Qy 61 CYCSGHCPCDDAINNCTITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
Db 61 CYCSGHCPCDDAINNCTITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120

Qy 121 TIECRTLNCQYLOLTPPPVIGPFDGSRVRLAVLISMVAVCIAMIVFSSFCYKHYC 180
Db 121 TIECRTLNCQYLOLTPPPVIGPFDGSRVRLAVLISMVAVCIAMIVFSSFCYKHYC 180

Qy 181 KSISSRGYNRDLQDEAFIPVGSLSKDLIDQSSGSGSLPLVLRHENILGFIAADIKGTG 240
Db 181 KSISSRGYNRDLQDEAFIPVGSLSKDLIDQSSGSGSLPLVLRHENILGFIAADIKGTG 240

Qy 241 GKGRYGEVMMGKWRGEKVAVKVFPTTEASWFRTEIYQTVLMRHNILGFIAADIKGTG 300
Db 241 GKGRYGEVMMGKWRGEKVAVKVFPTTEASWFRTEIYQTVLMRHNILGFIAADIKGTG 300

Qy 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSACGLCHLHTEIYGTQKPAIAH 360

Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAYSAAACGLCHLHTEIYGTQGPAAIAH 360
Qy 361 RDLKSKNLIKKGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDESLSKN 420
Db 361 RDLKSKNLIKKGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDESLSKN 420
Qy 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEEYQLPYNNVPSDPSYEDMRVVCVKRLR 480
Db 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEEYQLPYNNVPSDPSYEDMRVVCVKRLR 480
Qy 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532

RESULT 5

US-08-158-735A-4
; Sequence 4, Application US/08158735A
; Patent No. 6248554
; GENERAL INFORMATION:
; APPLICANT: COOK, JONATHAN S.
; APPLICANT: CORREA, PAUL E.
; APPLICANT: KOENIG, BETH B.
; APPLICANT: ROSENBAUM, JAN S.
; APPLICANT: TING, JERRY
; TITLE OF INVENTION: DNA SEQUENCE CODING FOR A BMP RECEPTOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE PROCTER & GAMBLE COMPANY
; STREET: 11810 EAST MIAMI RIVER ROAD
; CITY: ROSS
; STATE: OH
; COUNTRY: USA
; ZIP: 45061
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/158,735A
; FILING DATE: 24-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CORSTANJE, BRAHM J.
; REGISTRATION NUMBER: 34,804
; REFERENCE/DOCKET NUMBER: 5088
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (513) 627-2858
; TELEFAX: (513) 627-0260
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-158-735A-4

Query Match 99.5%; Score 2823; DB 2; Length 532;
Best Local Similarity 98.9%; Pred. No. 2.3e-259;
Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTQLYTYIRLLGACLPFIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPAPEDTLPLFLK 60
Db 1 MTQLYTYIRLLGACLPFIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPAPEDTLPLFLK 60
Qy 61 CYCSGHCPDANNTCTINGHCFAIIEEDDQGETTLTSCMKYEGSDFOCKDSPKAQLRR 120
Db 61 CYCSGHCPDANNTCTINGHCFAIIEEDDQGETTLTSCMKYEGSDFOCKDSPKAQLRR 120
Qy 121 TIECCTNLNCYLOPTLPVPVIGPFFDGSVRWLAVLISMVAVIAMVIFSSCFVCYKHYC 180
Db 121 TIECCTNLNCYLOPTLPVPVIGPFFDGSIRWLVLISMVAVIAMVIFSSCFVCYKHYC 180

Qy 181 KSISRGYNNRDLBODEAFIPVGBESLKULIDQSQSSGSGGLPLLVTQRTIAKQIQMVRQV 240
Db 181 KSISRGYNNRDLBODEAFIPVGBESLKULIDQSQSSGSGGLPLLVTQRTIAKQIQMVRQV 240
Qy 241 KGGRYGEVMMGKRGKAVKVVFFTEEASWPRETEIYQTVLMRHENILGFTAADIKGKG 300
Db 241 KGGRYGEVMMGKRGKAVKVVFFTEEASWPRETEIYQTVLMRHENILGFTAADIKGKG 300
Qy 301 SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAYSAAACGLCHLHTEIYGTQGPAAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAYSAAACGLCHLHTEIYGTQGPAAIAH 360
Qy 361 RDLKSKNLIKKGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDESLSKN 420
Db 361 RDLKSKNLIKKGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDESLSKN 420
Qy 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEEYQLPYNNVPSDPSYEDMRVVCVKRLR 480
Db 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEEYQLPYNNVPSDPSYEDMRVVCVKRLR 480
Qy 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532

RESULT 6

US-09-395-115-14
; Sequence 14, Application US/09395115
; Patent No. 6271365
; GENERAL INFORMATION:
; APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
; APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
; TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/395,115
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,265
; FILING DATE: 30-October-1995
; APPLICATION NUMBER: PCT/GB93/02367
; FILING DATE: 17-No. 6271365ember-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9224057.1
; FILING DATE: 17-No. 6271365ember-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9304677.9
; FILING DATE: 8-March-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9304680.3
; FILING DATE: 8-March-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9311047.6
; FILING DATE: 28-May-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9313763.6
; FILING DATE: 2-July-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9136099.2

;
; FILING DATE: 3-August-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9321344.5
; FILING DATE: 15-October-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohlel, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: LUD 5298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-395-115-14

Query Match 99.5%; Score 2823; DB 2; Length 532;
Best Local Similarity 98.9%; Pred. No. 2.3e-259;
Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTOLYTYIRLLGACLFIIISHVQGNLDSMLHGTGKMSDLDQKKPENGVTLPEDTLPFLK 60
DB 1 MTOLYTYIRLLGACLFIIISHVQGNLDSMLHGTGKMSDLDQKKPENGVTLPEDTLPFLK 60

QY 61 CYCSGHCPCDDAINTTCITNGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
DB 61 CYCSGHCPCDDAINTTCITNGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120

QY 121 TIECCRTNLCNOYLQPTLPVWIGPFDDGSVRWLAVLISMAVCIVAMIVPSSCFCKYKHC 180
DB 121 TIECCRTNLCNOYLQPTLPVWIGPFDDGSVRWLAVLISMAVCIVAMIVPSSCFCKYKHC 180

QY 181 KSISRGYRNRDLEQDEAFIPVGESLKDLIDQSQSGSGGLPLLQRTIAKQIQMVRQV 240
DB 181 KSISRGYRNRDLEQDEAFIPVGESLKDLIDQSQSGSGGLPLLQRTIAKQIQMVRQV 240

QY 241 GKGRYGEVWVGKRGKAVKVFPTTEASWFRTEIYQTVLMRHNILGFIAADIKGTG 300
DB 241 GKGRYGEVWVGKRGKAVKVFPTTEASWFRTEIYQTVLMRHNILGFIAADIKGTG 300

QY 301 SWTQLYLIIDYHENGSLYDFLKCATLDTRALLKLAISACGLCHLHTEIYGTGKPAIAH 360
DB 301 SWTQLYLIIDYHENGSLYDFLKCATLDTRALLKLAISACGLCHLHTEIYGTGKPAIAH 360

QY 361 RDLKSNILIKKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
DB 361 RDLKSNILIKKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420

QY 421 HFQPYIMADIIYSFGLIIWEMARRCITGGIVEEQYLPYNNVPSDDPSYEDMREVVCKRLR 480
DB 421 HFQPYIMADIIYSFGLIIWEMARRCITGGIVEEQYLPYNNVPSDDPSYEDMREVVCKRLR 480

QY 481 PIVSNRWNSECLRAVLKLMSECAWNPASRLTALRIKKTAKWVESQDVKI 532
DB 481 PIVSNRWNSECLRAVLKLMSECAWNPASRLTALRIKKTAKWVESQDVKI 532

RESULT 7
US-08-334-179A-12
; Sequence 12, Application US/08334179A
; Patent No. 6306622
; GENERAL INFORMATION:
; APPLICANT: ROSENBAUM, JAN S.
; APPLICANT: NOHNO, TSUTOMU
; TITLE OF INVENTION: CDNA ENCODING A BMP TYPE II RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE PROCTER AND GAMBLE COMPANY
; STREET: 11810 EAST MIAMI RIVER ROAD
; CITY: ROSS

;
; STATE: OH
; COUNTRY: US
; ZIP: 45061
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.30, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/334,179A
; FILING DATE: 04-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CORSTANJE, BRAHM J.
; REGISTRATION NUMBER: 34,804
; REFERENCE/DOCKET NUMBER: 5473
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 513-627-2858
; TELEFAX: 513-627-0260
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-334-179A-12

Query Match 99.5%; Score 2823; DB 2; Length 532;
Best Local Similarity 98.9%; Pred. No. 2.3e-259;
Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTOLYTYIRLLGACLFIIISHVQGNLDSMLHGTGKMSDLDQKKPENGVTLPEDTLPFLK 60
DB 1 MTOLYTYIRLLGACLFIIISHVQGNLDSMLHGTGKMSDLDQKKPENGVTLPEDTLPFLK 60

QY 61 CYCSGHCPCDDAINTTCITNGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
DB 61 CYCSGHCPCDDAINTTCITNGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120

QY 121 TIECCRTNLCNOYLQPTLPVWIGPFDDGSVRWLAVLISMAVCIVAMIVPSSCFCKYKHC 180
DB 121 TIECCRTNLCNOYLQPTLPVWIGPFDDGSVRWLAVLISMAVCIVAMIVPSSCFCKYKHC 180

QY 181 KSISRGYRNRDLEQDEAFIPVGESLKDLIDQSQSGSGGLPLLQRTIAKQIQMVRQV 240
DB 181 KSISRGYRNRDLEQDEAFIPVGESLKDLIDQSQSGSGGLPLLQRTIAKQIQMVRQV 240

QY 241 GKGRYGEVWVGKRGKAVKVFPTTEASWFRTEIYQTVLMRHNILGFIAADIKGTG 300
DB 241 GKGRYGEVWVGKRGKAVKVFPTTEASWFRTEIYQTVLMRHNILGFIAADIKGTG 300

QY 301 SWTQLYLIIDYHENGSLYDFLKCATLDTRALLKLAISACGLCHLHTEIYGTGKPAIAH 360
DB 301 SWTQLYLIIDYHENGSLYDFLKCATLDTRALLKLAISACGLCHLHTEIYGTGKPAIAH 360

QY 361 RDLKSNILIKKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
DB 361 RDLKSNILIKKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420

QY 421 HFQPYIMADIIYSFGLIIWEMARRCITGGIVEEQYLPYNNVPSDDPSYEDMREVVCKRLR 480
DB 421 HFQPYIMADIIYSFGLIIWEMARRCITGGIVEEQYLPYNNVPSDDPSYEDMREVVCKRLR 480

QY 481 PIVSNRWNSECLRAVLKLMSECAWNPASRLTALRIKKTAKWVESQDVKI 532
DB 481 PIVSNRWNSECLRAVLKLMSECAWNPASRLTALRIKKTAKWVESQDVKI 532

RESULT 8
US-08-436-265-14
; Sequence 14, Application US/08436265
; Patent No. 6316217
; GENERAL INFORMATION:

APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-October-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. 6316217ember-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6316217ember-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304680.3
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9311047.6
FILING DATE: 28-May-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9136099.2
FILING DATE: 3-August-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-October-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kohlei, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD 5298
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-265-14

Query Match 99.5%; Score 2823; DB 2; Length 532;
Best Local Similarity 98.9%; Pred. No. 2.3e-259;
Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTQLVYIRLLGACFLIISHVQGNLDSMLHGTGMSKSDVDQKKPENGVTLPAPEDTLPLK 60
DB 1 MTQLVYIRLLGACFLIISHVQGNLDSMLHGTGMSKSDLDQKKPENGVTLPAPEDTLPLK 60
QY 61 CYCSGHCDDAINNTCITNGHCFALIEDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRR 120
DB 61 CYCSGHCDDAINNTCITNGHCFALIEDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRR 120
QY 121 TTECRRTNLCNQYLOPTLPVVGPPFDGSRWLAVLISMVAVCIAMIVFSSCFCKHYC 180

DB 121 TTECRRTNLCNQYLOPTLPVVGPPFDGSRWLAVLISMVAVCIAMIVFSSCFCKHYC 180
QY 181 KSISRGYNRDLQDEAFIPVGSLSKDLIDQSSGSGGLPLLIVQRTIAKQIQMVRQV 240
DB 181 KSISRGYNRDLQDEAFIPVGSLSKDLIDQSSGSGGLPLLIVQRTIAKQIQMVRQV 240
QY 241 GKGRYGEVMMGKWRGEKVAVKVFVFTTEEASFRETEIYQTVLMRHNILGFTAAADIKGTG 300
DB 241 GKGRYGEVMMGKWRGEKVAVKVFVFTTEEASFRETEIYQTVLMRHNILGFTAAADIKGTG 300
QY 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSAAACGLHLHTEIYGTQGRPAIAH 360
DB 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSAAACGLHLHTEIYGTQGRPAIAH 360
QY 361 RDLKSKNLIKKGSCCCTIADLGLAVKFNSTNEVDIPLNTRVGTGRRYMAPEVLDLSLKN 420
DB 361 RDLKSKNLIKKGSCCCTIADLGLAVKFNSTNEVDIPLNTRVGTGRRYMAPEVLDLSLKN 420
QY 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEYQLPYNNMVPSPDSYEDMRVVCVKRLR 480
DB 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEYQLPYNNMVPSPDSYEDMRVVCVKRLR 480
QY 481 PIVSNRWNDSDECLRAVLKLMSECHWHPASRLTALRIKKTAKMVESQDVKI 532
DB 481 PIVSNRWNDSDECLRAVLKLMSECHWHPASRLTALRIKKTAKMVESQDVKI 532

RESULT 9
US-09-679-187-14
Sequence 14, Application US/09679187
Patent No. 6331621
GENERAL INFORMATION:
APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/679,187
FILING DATE: 03-OCT-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-October-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. 6331621ember-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6331621ember-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304680.3
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9311047.6
FILING DATE: 28-May-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 9136099.2
; FILING DATE: 3-August-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9231344.5
; FILING DATE: 15-October-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohlei, Vlnet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: LUD 5298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-679-187-14

Query Match          99.5%; Score 2823; DB 2; Length 532;
Best Local Similarity 98.9%; Pred. No. 2.3e-259;
Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGKMSDVKDQKPKENGVTTLAPEDTLPFLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGKMSDVKDQKPKENGVTTLAPEDTLPFLK 60
Qy 61 CYCSGCHPDDAINTCTINCHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKQALRR 120
Db 61 CYCSGCHPDDAINTCTINCHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKQALRR 120
Qy 121 TIECCRTNLCNQYLQPTLPVWIGPFFDGSVRWLAVLISMAVCIVAMIVFSSCFYKHYC 180
Db 121 TIECCRTNLCNQYLQPTLPVWIGPFFDGSIRWLVLISMAVCIVAMIVFSSCFYKHYC 180
Qy 181 KSISGRYNRDLQDEAFIPVGESLKDLIDQSQSGSGSGLPLLQRTIAKIQMVQRV 240
Db 181 KSISGRYNRDLQDEAFIPVGESLKDLIDQSQSGSGSGLPLLQRTIAKIQMVQRV 240
Qy 241 GKGRYGEVWVGKRGKGEKAVKVPFTTEASWPRETEIYQTVLMRHNILGFIAADIKGTG 300
Db 241 GKGRYGEVWVGKRGKGEKAVKVPFTTEASWPRETEIYQTVLMRHNILGFIAADIKGTG 300
Qy 301 SWTQLYLIIDYHENGSLYDFLKCATLDTRALLKLAISAACGLCHLHTEIYGTGCKPAIAH 360
Db 301 SWTQLYLIIDYHENGSLYDFLKCATLDTRALLKLAISAACGLCHLHTEIYGTGCKPAIAH 360
Qy 361 RDLKSKNLIKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDESLSKN 420
Db 361 RDLKSKNLIKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDESLSKN 420
Qy 421 HFQPYIMADIYSFGLIIEWEMARCCITGGIVEEYQLPYNNVPSPDPSYEDMREVVCKRLR 480
Db 421 HFQPYIMADIYSFGLIIEWEMARCCITGGIVEEYQLPYNNVPSPDPSYEDMREVVCKRLR 480
Qy 481 PIVSNRWNSECLRAVLKLMSECAWHPASRLTALRIKKTAKWVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAWHPASRLTALRIKKTAKWVESQDVKI 532

RESULT 10
US-09-267-963D-14
; Sequence 14, Application US/09267963D
; Patent No. 6692925
; GENERAL INFORMATION:
; APPLICANT: MIYAZONO, Kohei
; APPLICANT: IMAMURA, Takeshe
; APPLICANT: DEN DIJKE, Peter
; TITLE OF INVENTION: PROTEINS HAVING SERINE/THREONINE KINASE DOMAINS, CORRESPONDING
; FILE REFERENCE: LUD 5539.1 CIP
; CURRENT APPLICATION NUMBER: US/09/267,963D
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; CURRENT FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/GB93/02367
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: US 09/039,177
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-267-963D-14

Query Match          99.5%; Score 2823; DB 2; Length 532;
Best Local Similarity 98.9%; Pred. No. 2.3e-259;
Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGKMSDVKDQKPKENGVTTLAPEDTLPFLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGKMSDVKDQKPKENGVTTLAPEDTLPFLK 60
Qy 61 CYCSGCHPDDAINTCTINCHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKQALRR 120
Db 61 CYCSGCHPDDAINTCTINCHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKQALRR 120
Qy 121 TIECCRTNLCNQYLQPTLPVWIGPFFDGSVRWLAVLISMAVCIVAMIVFSSCFYKHYC 180
Db 121 TIECCRTNLCNQYLQPTLPVWIGPFFDGSIRWLVLISMAVCIVAMIVFSSCFYKHYC 180
Qy 181 KSISGRYNRDLQDEAFIPVGESLKDLIDQSQSGSGSGLPLLQRTIAKIQMVQRV 240
Db 181 KSISGRYNRDLQDEAFIPVGESLKDLIDQSQSGSGSGLPLLQRTIAKIQMVQRV 240
Qy 241 GKGRYGEVWVGKRGKGEKAVKVPFTTEASWPRETEIYQTVLMRHNILGFIAADIKGTG 300
Db 241 GKGRYGEVWVGKRGKGEKAVKVPFTTEASWPRETEIYQTVLMRHNILGFIAADIKGTG 300
Qy 301 SWTQLYLIIDYHENGSLYDFLKCATLDTRALLKLAISAACGLCHLHTEIYGTGCKPAIAH 360
Db 301 SWTQLYLIIDYHENGSLYDFLKCATLDTRALLKLAISAACGLCHLHTEIYGTGCKPAIAH 360
Qy 361 RDLKSKNLIKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDESLSKN 420
Db 361 RDLKSKNLIKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDESLSKN 420
Qy 421 HFQPYIMADIYSFGLIIEWEMARCCITGGIVEEYQLPYNNVPSPDPSYEDMREVVCKRLR 480
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Qy 481 PIVSNRWNSECLRAVLKLMSECAWHPASRLTALRIKKTAKWVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAWHPASRLTALRIKKTAKWVESQDVKI 532

RESULT 11
US-08-481-337A-6
; Sequence 6, Application US/08481337A
; Patent No. 5863738
; GENERAL INFORMATION:
; APPLICANT: TEN DIJKE, Peter
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: MIYAZONO, Kohei
; APPLICANT: SAMPATH, Kuber T.
; TITLE OF INVENTION: Morphogenic Protein-Specific Cell
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,337A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, Thomas C.
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: CRP-097CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-481-337A-6

Query Match 97.6%; Score 2769; DB 1; Length 532;
Best Local Similarity 97.2%; Pred. No. 3.1e-254;
Matches 517; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MTQLYTYIRLLGACLIIFSHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPAPEDTLPLFK 60
DB 1 MTQLYTYIRLLGAYLIIFSRVQGNLDSMLHGTGMKSDQKKSNGVTLPAPEDTLPLFK 60
QY 61 CYCSGHCPCDDAINNNTCITNGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
DB 61 CYCSGHCPCDDAINNNTCITNGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
QY 121 TIECCRTNLCNQYLOPTLPVPIVGFPGSGVRLAVLISMVAVCIAMIVFSSCFCKYKHC 180
DB 121 TIECCRTNLCNQYLOPTLPVPIVGFPGSGVRLAVLISMVAVCIAMIVFSSCFCKYKHC 180
QY 121 TIECCRTNLCNQYLOPTLPVPIVGFPGSGVRLAVLISMVAVCIAMIVFSSCFCKYKHC 180
DB 121 TIECCRTNLCNQYLOPTLPVPIVGFPGSGVRLAVLISMVAVCIAMIVFSSCFCKYKHC 180
QY 181 KSISSRGYNRDLEODEAFIPVGESLKDLIDQSQSGSGGLPLLAVQRTIAKQIOMVROV 240
DB 181 KSISSRGYNRDLEODEAFIPVGESLKDLIDQSQSGSGGLPLLAVQRTIAKQIOMVROV 240
QY 181 KSISSRRYNRDLEODEAFIPVGESLKDLIDQSQSGSGGLPLLAVQRTIAKQIOMVROV 240
DB 181 KSISSRRYNRDLEODEAFIPVGESLKDLIDQSQSGSGGLPLLAVQRTIAKQIOMVROV 240
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DB 241 GKGRYGEVNMKGWGEKAVKVFVFTTEASWFRTEIYQTVLMRHENILGFTAADIKGTG 300
QY 301 SWTQLYLTIDYHENGSLYDFLKCATLDTALLKLAYSACGLCHLHTEIYGTQGPATAH 360
DB 301 SWTQLYLTIDYHENGSLYDFLKCATLDTALLKLAYSACGLCHLHTEIYGTQGPATAH 360
QY 361 RDLKSKNILLIKNGSCCIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSLN 420
DB 361 RDLKSKNILLIKNGSCCIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSLN 420
QY 421 HFQPYIMADYISFGLIIEWMARRCITGGIVEYQIPLPYNMVPSDPSYEDMRVVCVKRLR 480
DB 421 HFQPYIMADYISFGLIIEWMARRCITGGIVEYQIPLPYNMVPSDPSYEDMRVVCVKRLR 480
QY 481 PIVSNRWNSDECLRAVLKLMSECAWNPASRLTALRIKTLAKMYESQDVKI 532
DB 481 PIVSNRWNSDECLRAVLKLMSECAWNPASRLTALRIKTLAKMYESQDVKI 532

RESULT 12
US-09-382-256-6
; Sequence 6, Application US/09382256A
; Patent No. 6207814
; GENERAL INFORMATION:
; APPLICANT: MIVAZONO, Kohei
; TEN DIJKE, Peter
; FRANZEN, Petra

```

```

;
; YAMASHITA, Hidetoshi
; HELDIN, Carl-Henrik
; TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS
; HAVING SERINE THREONINE KINASE DOMAINS,
; AND THEIR USE
;
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/382,256A
; FILING DATE: 24-Aug-1999
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/02367
; FILING DATE: No. 6207814ember 17, 1993
; APPLICATION NUMBER: GB 9224057.1
; FILING DATE: No. 6207814ember 17, 1992
; APPLICATION NUMBER: GB 9304677.9
; FILING DATE: March 8, 1993
; APPLICATION NUMBER: GB 9304680.3
; FILING DATE: March 8, 1993
; APPLICATION NUMBER: 9311047.6
; FILING DATE: May 28, 1993
; APPLICATION NUMBER: 9313763.6
; FILING DATE: July 2, 1993
; APPLICATION NUMBER: 9316099.2
; FILING DATE: August 3, 1993
; APPLICATION NUMBER: 321344.5
; FILING DATE: October 15, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6207814man D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5298.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
;
US-09-382-256-6

Query Match 97.6%; Score 2769; DB 2; Length 532;
Best Local Similarity 97.2%; Pred. No. 3.1e-254;
Matches 517; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MTQLYTYIRLLGACLIIFSHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPAPEDTLPLFK 60
DB 1 MTQLYTYIRLLGAYLIIFSRVQGNLDSMLHGTGMKSDQKKSNGVTLPAPEDTLPLFK 60
QY 61 CYCSGHCPCDDAINNNTCITNGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
DB 61 CYCSGHCPCDDAINNNTCITNGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
QY 121 TIECCRTNLCNQYLOPTLPVPIVGFPGSGVRLAVLISMVAVCIAMIVFSSCFCKYKHC 180
DB 121 TIECCRTNLCNQYLOPTLPVPIVGFPGSGVRLAVLISMVAVCIAMIVFSSCFCKYKHC 180
QY 181 KSISSRGYNRDLEODEAFIPVGESLKDLIDQSQSGSGGLPLLAVQRTIAKQIOMVROV 240
DB 181 KSISSRGYNRDLEODEAFIPVGESLKDLIDQSQSGSGGLPLLAVQRTIAKQIOMVROV 240

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Db 181 KSISRRRNRDLQDEAFIPVGBSLKDLIDQSSGSGSLPVLVQRTIAKIQIMVRQV 240
Qy 241 GKGRYGEVWVGKRGKAVKVFVFTTEASWFRTEIYQTVLMRHNILGFIAADIKGTG 300
Db 241 GKGRYGEVWVGKRGKAVKVFVFTTEASWFRTEIYQTVLMRHNILGFIAADIKGTG 300
Qy 301 SWTQLYLITDYHENGSLYDFLKCATLDTLRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTLRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Qy 361 RDLKSKNILIKKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGRTRRYMAPEVLDLSKN 420
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Db 421 HFQPYIMADIYSFGLIIMEMARRCITGGIVEEYQLPYNNMVPSPSYEDMRVVCVKRLR 480
Qy 481 PIVSNRWNSECLRAVLKLMSECAWHPASRLTALRIKKTAKWVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAWHPASRLTALRIKKTAKWVESQDVKI 532

RESULT 13
US-09-395-115-6
; Sequence 6, Application US/09395115
; Patent No. 6271365
; GENERAL INFORMATION:
; APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
; APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/395,115
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,265
; FILING DATE: 30-October-1995
; APPLICATION NUMBER: PCT/GB93/02367
; FILING DATE: 17-No. 6271365ember-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9224057.1
; FILING DATE: 17-No. 6271365ember-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9304677.9
; FILING DATE: 8-March-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9304680.3
; FILING DATE: 8-March-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9311047.6
; FILING DATE: 28-May-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9313763.6
; FILING DATE: 2-July-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9136099.2
; FILING DATE: 3-August-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9321344.5

; FILING DATE: 15-October-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohlei, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: LUD 5298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-395-115-6

Query Match 97.6%; Score 2769; DB 2; Length 532;
Best Local Similarity 97.2%; Pred. No. 3.1e-254;
Matches 517; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MTQLYTYIRLLGACFLFIISHVQGNLDSMLHGTGMKSDVDOKKPPENGVTILAPEDTLPLFK 60
Db 1 MTQLYTYIRLLGAYLFIISRQGNLDSMLHGTGMKSDSDQKKSENGVTILAPEDTLPLFK 60
Qy 61 CYCSGHCPCDDAINTTCITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
Db 61 CYCSGHCPCDDAINTTCITNGHCFALIEEDDQGETTLASGCMKYEGSDFOCKDSPKAQLRR 120
Qy 121 TTECCRTNLCNQYLOPTLPVVI GPPFDGSRVLA VLIISMAVCIVAMI VPSFCFCYKHYC 180
Db 121 TTECCRTNLCNQYLOPTLPVVI GPPFDGSRVLA VLIISMAVCIVAMI VPSFCFCYKHYC 180
Qy 181 KSISRRGRNDRLEDEAFIPVGESLKDLIDQSSGSGSLPVLVQRTIAKIQIMVRQV 240
Db 181 KSISRRGRNDRLEDEAFIPVGESLKDLIDQSSGSGSLPVLVQRTIAKIQIMVRQV 240
Qy 241 GKGRYGEVWVGKRGKAVKVFVFTTEASWFRTEIYQTVLMRHNILGFIAADIKGTG 300
Db 241 GKGRYGEVWVGKRGKAVKVFVFTTEASWFRTEIYQTVLMRHNILGFIAADIKGTG 300
Qy 301 SWTQLYLITDYHENGSLYDFLKCATLDTLRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTLRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Qy 361 RDLKSKNILIKKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGRTRRYMAPEVLDLSKN 420
Db 361 RDLKSKNILIKKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGRTRRYMAPEVLDLSKN 420
Qy 421 HFQPYIMADIYSFGLIIMEMARRCITGGIVEEYQLPYNNMVPSPSYEDMRVVCVKRLR 480
Db 421 HFQPYIMADIYSFGLIIMEMARRCITGGIVEEYQLPYNNMVPSPSYEDMRVVCVKRLR 480
Qy 481 PIVSNRWNSECLRAVLKLMSECAWHPASRLTALRIKKTAKWVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAWHPASRLTALRIKKTAKWVESQDVKI 532

RESULT 14
US-08-436-265-6
; Sequence 6, Application US/08436265
; Patent No. 6316217
; GENERAL INFORMATION:
; APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
; APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022

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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
APPLICANT: Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/679,187
FILING DATE: 03-OCT-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-October-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. 6331621ember-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6331621ember-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304680.3
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9311047.6
FILING DATE: 28-May-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9136099.2
FILING DATE: 3-August-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-October-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kohlei, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD 5298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-265-6

Query Match
Best Local Similarity 97.2%; Score 2769; DB 2; Length 532;
Matches 517; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MTQLVYIIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPLK 60
DB 1 MTQLVYIIRLLGAYLFIISRVQGNLDSMLHGTGMKSDSDQKKSENGVTLPEDTLPLK 60
QY 61 CYCSGHCPCPDANNTCITNGHCFIIEBDDQGETTLTSCMKYEGSDFOCKDSPKAQLRR 120
DB 61 CYCSGHCPCPDANNTCITNGHCFIIEBDDQGETTLTSCMKYEGSDFOCKDSPKAQLRR 120
QY 121 TTECRTLNCNQLPTLPVVPVFFDGSVRLAVLISMVCIIVAMIVFSSCFCKHYC 180
DB 121 TTECRTLNCNQLPTLPVVPVFFDGSIRLWLLISMVCIIVAMIVFSSCFCKHYC 180
QY 181 KSISRRGRNRLDEQDEAFIPVGESLKOLIDQSQSGSGGLPLLQVRTIAKIQIMVRQV 240
DB 181 KSISRRGRNRLDEQDEAFIPVGESLKOLIDQSQSGSGGLPLLQVRTIAKIQIMVRQV 240
QY 241 GKGRYGVMMGKRGKAVKAVKFFFTTEASWFRTEIYQTVLMRHNILGFTAAIDKGTG 300
DB 241 GKGRYGVMMGKRGKAVKAVKFFFTTEASWFRTEIYQTVLMRHNILGFTAAIDKGTG 300
QY 301 SWTQLYLIIDYHENGSLVDFLKCATLDRALLKLAYSAAACGLCHLHTEIYGTQGRPAIAH 360
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TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-679-187-6

Query Match 97.6%; Score 2769; DB 2; Length 532;
Best Local Similarity 97.2%; Pred. No. 3.1e-254;
Matches 517; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MTQLYTYIRLGLACLIIFISHVGGQNLDSMLHGTGKMSDVQKDPENGVTTLAPEDTLPFLK 60
Db |||||
1 MTQLYTYIRLGLAVLIIFSRVGGQNLDSMLHGTGKMSDVQKDPENGVTTLAPEDTLPFLK 60
Qy 61 CYCSGHCPDDAINNNTCTNGHCFALIEEDDQGETTLTSGCMKYEGSPQCKDSPKAQLRR 120
Db |||||
61 CYCSGHCPDDAINNNTCTNGHCFALIEEDDQGETTLTSGCMKYEGSPQCKDSPKAQLRR 120
Qy 121 TIECRTLNCQYLOPTLPVVGIPFPGDSVRLAVLISMAVCIAMIVFSSCFYKHC 180
Db |||||
121 TIECRTLNCQYLOPTLPVVGIPFPGDSVRLAVLISMAVCIAMIVFSSCFYKHC 180
Qy 181 KSISRRGRYNRDLQDEAFIPVGESLKDLDQSSGSGGLPLLQVORTIAKQIQMVRQV 240
Db |||||
181 KSISRRGRYNRDLQDEAFIPVGESLKDLDQSSGSGGLPLLQVORTIAKQIQMVRQV 240
Qy 241 GKGRYGEVWVGKMRGEKAVKVPFTTEASWFRTEIYQTVLMHENILGFIAADIKGTG 300
Db |||||
241 GKGRYGEVWVGKMRGEKAVKVPFTTEASWFRTEIYQTVLMHENILGFIAADIKGTG 300
Qy 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSACGLCHLHTEIYGTQKPAIAH 360
Db |||||
301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAYSACGLCHLHTEIYGTQKPAIAH 360
Qy 361 RDLKSKNILIKONGSCCIIADLGLAVKFNSTNEVDIPINTRVGTTRRYMAPEVLDES LKN 420
Db |||||
361 RDLKSKNILIKONGSCCIIADLGLAVKFNSTNEVDIPINTRVGTTRRYMAPEVLDES LKN 420
Qy 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYNNMVPSPSYEDMRVVCVKRLR 480
Db |||||
421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYNNMVPSPSYEDMRVVCVKRLR 480
Qy 481 PIVSNRWNSECLRAVLKLMSECAWHPASRLTALRIKKTIAKMWESQDVKI 532
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Job time : 47 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 06:11:50 ; Search time 166 Seconds
(without alignments)
1339.067 Million cell updates/sec

Title: US-10-600-645-2
Perfect score: 2838
Sequence: 1 MTQLTYIRLLGACLFIIISH.....TALRIKTKLAKMVESQDVKI 532

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pap:
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pap:
4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pap:
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pap:
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2838	100.0	532	4	US-10-463-190-105
3	2838	100.0	532	4	US-10-463-190-106
4	2838	100.0	532	4	US-10-463-190-107
5	2838	100.0	532	4	US-10-463-190-110
6	2838	100.0	532	4	US-10-600-645-2
7	2838	100.0	532	5	US-10-868-497-74
8	2838	100.0	532	5	US-10-868-497-75
9	2838	100.0	532	5	US-10-868-497-76
10	2838	100.0	532	5	US-10-868-497-79
11	2823	99.5	532	3	US-09-903-068-14
12	2823	99.5	532	3	US-10-739-413-14
13	2769	97.6	532	3	US-09-903-068-6
14	2769	97.6	532	3	US-09-982-543A-6
15	2769	97.6	532	4	US-10-153-217-2
16	2769	97.6	532	4	US-10-286-152A-38
17	2769	97.6	532	4	US-10-463-190-102
18	2769	97.6	532	5	US-10-739-413-6
19	2769	97.6	532	5	US-10-868-497-71
20	2769	97.6	532	5	US-10-492-380-38
21	2769	97.6	532	5	US-10-745-237-308
22	2769	97.6	532	6	US-11-098-889-6
23	2769	97.6	532	5	US-10-450-763-53229
24	2653	93.5	532	5	US-10-450-763-53236
25	2635.5	92.9	532	5	US-10-128-558-172
26	2604.5	91.8	637	5	US-10-128-558-173
27	2129.5	75.0	564	5	US-10-450-763-53235

28	1950.5	68.7	502	4	US-10-169-051-2	Sequence 2, Appli
29	1946.5	68.6	502	4	US-10-169-051-4	Sequence 4, Appli
30	1941	68.4	502	4	US-10-044-716-14	Sequence 14, Appl
31	1941	68.4	502	4	US-10-286-152A-40	Sequence 40, Appl
32	1941	68.4	502	4	US-10-139-814-14	Sequence 14, Appl
33	1941	68.4	502	4	US-10-341-220-112	Sequence 112, App
34	1941	68.4	502	4	US-10-295-027-68	Sequence 68, Appl
35	1941	68.4	502	4	US-10-295-027-789	Sequence 789, App
36	1941	68.4	502	4	US-10-295-027-837	Sequence 837, App
37	1941	68.4	502	4	US-10-295-027-881	Sequence 881, App
38	1941	68.4	502	4	US-10-173-999-64	Sequence 64, Appl
39	1941	68.4	502	4	US-10-463-190-103	Sequence 103, App
40	1941	68.4	502	4	US-10-463-190-104	Sequence 104, App
41	1941	68.4	502	4	US-10-463-190-108	Sequence 108, App
42	1941	68.4	502	4	US-10-463-190-109	Sequence 109, App
43	1941	68.4	502	4	US-10-058-270A-6	Sequence 6, Appli
44	1941	68.4	502	4	US-10-692-824-14	Sequence 14, Appl
45	1941	68.4	502	5	US-10-872-972-112	Sequence 112, App

ALIGNMENTS

RESULT 1
US-09-874-628-2
; Sequence 2, Application US/09874628
; Patent No. US20020137133A1
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, John
; CELESTES, Anthony J.
; THIES, R. Scott
; YAMAJI, No. US20020137133A1oru
; TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute Inc.- Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/874,628
; FILING DATE: 05-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/123,934
; FILING DATE: 17-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, Steven R
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 876 1170
; TELEFAX: 617 876 5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-874-628-2

Query Match 100.0%; Score 2838; DB 3; Length 532;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MTOLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDOKKPNGVTLAPEDTLPLFK 60
Db 1 MTOLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDOKKPNGVTLAPEDTLPLFK 60
Qy 61 CYCSGHCPCDDAINNCTITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
Db 61 CYCSGHCPCDDAINNCTITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
Qy 121 TIECCTNLCNQYLOPTLPPVIGPFDGSRVRLAVLISMAVCIAMIVFSSCFCKYKHC 180
Db 121 TIECCTNLCNQYLOPTLPPVIGPFDGSRVRLAVLISMAVCIAMIVFSSCFCKYKHC 180
Qy 181 KSISRGYRNRLDEODEAFIPVGESLKDLDIOSOSSGSGGLPLLQVORTIAKQIOMVRQV 240
Db 181 KSISRGYRNRLDEODEAFIPVGESLKDLDIOSOSSGSGGLPLLQVORTIAKQIOMVRQV 240
Qy 241 GKGRGYEVMGKRGKEKVAVKVFFFTTEEASWFRETEIYQTVLMRHNILGFTAAADIKGTG 300
Db 241 GKGRGYEVMGKRGKEKVAVKVFFFTTEEASWFRETEIYQTVLMRHNILGFTAAADIKGTG 300
Qy 301 SWTQLYLITDYHENGSLYDFLKCATLDTTRALLKLAYSAAACGLCHLHTEIYGTQGPATAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTTRALLKLAYSAAACGLCHLHTEIYGTQGPATAH 360
Qy 361 RDLKSKNLIKNGSCCIIADGLAVKFNSDTNEVDIPLNTRVGTTRYNAPEVLDESLSKN 420
Db 361 RDLKSKNLIKNGSCCIIADGLAVKFNSDTNEVDIPLNTRVGTTRYNAPEVLDESLSKN 420
Qy 421 HFQPYIMADIYSGFLIIWEMARRCITGGIVEEYQLPYYNMVPSDPSYEDMREVVCVKRLR 480
Db 421 HFQPYIMADIYSGFLIIWEMARRCITGGIVEEYQLPYYNMVPSDPSYEDMREVVCVKRLR 480
Qy 481 PIVSNRWNSDECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRWNSDECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
RESULT 2
US-10-463-190-105
; Sequence 105, Application US/10463190
; Publication No. US2004000935A1
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary E.
; APPLICANT: Galas, David J.
; APPLICANT: Kovacevich, Brian
; APPLICANT: Mulligan, John T.
; APPLICANT: Paeper, Bryan W.
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Winkler, David G.
; TITLE OF INVENTION: COMPOSITIONS AND MEHTODS FOR
; TITLE OF INVENTION: INCREASING BONE MINERALIZATION
; FILE REFERENCE: 240083.508C2
; CURRENT APPLICATION NUMBER: US/10/463,190
; CURRENT FILING DATE: 2003-06-16
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 105
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-463-190-105
Query Match 100.0%; Score 2838; DB 4; Length 532;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MTOLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDOKKPNGVTLAPEDTLPLFK 60
Db 1 MTOLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDOKKPNGVTLAPEDTLPLFK 60
Qy 61 CYCSGHCPCDDAINNCTITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
Db 61 CYCSGHCPCDDAINNCTITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
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Qy 121 TIECCTNLCNQYLOPTLPPVIGPFDGSRVRLAVLISMAVCIAMIVFSSCFCKYKHC 180
Db 121 TIECCTNLCNQYLOPTLPPVIGPFDGSRVRLAVLISMAVCIAMIVFSSCFCKYKHC 180
Qy 181 KSISRGYRNRLDEODEAFIPVGESLKDLDIOSOSSGSGGLPLLQVORTIAKQIOMVRQV 240
Db 181 KSISRGYRNRLDEODEAFIPVGESLKDLDIOSOSSGSGGLPLLQVORTIAKQIOMVRQV 240
Qy 241 GKGRGYEVMGKRGKEKVAVKVFFFTTEEASWFRETEIYQTVLMRHNILGFTAAADIKGTG 300
Db 241 GKGRGYEVMGKRGKEKVAVKVFFFTTEEASWFRETEIYQTVLMRHNILGFTAAADIKGTG 300
Qy 301 SWTQLYLITDYHENGSLYDFLKCATLDTTRALLKLAYSAAACGLCHLHTEIYGTQGPATAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTTRALLKLAYSAAACGLCHLHTEIYGTQGPATAH 360
Qy 361 RDLKSKNLIKNGSCCIIADGLAVKFNSDTNEVDIPLNTRVGTTRYNAPEVLDESLSKN 420
Db 361 RDLKSKNLIKNGSCCIIADGLAVKFNSDTNEVDIPLNTRVGTTRYNAPEVLDESLSKN 420
Qy 421 HFQPYIMADIYSGFLIIWEMARRCITGGIVEEYQLPYYNMVPSDPSYEDMREVVCVKRLR 480
Db 421 HFQPYIMADIYSGFLIIWEMARRCITGGIVEEYQLPYYNMVPSDPSYEDMREVVCVKRLR 480
Qy 481 PIVSNRWNSDECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRWNSDECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
RESULT 3
US-10-463-190-106
; Sequence 106, Application US/10463190
; Publication No. US2004000935A1
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary E.
; APPLICANT: Galas, David J.
; APPLICANT: Kovacevich, Brian
; APPLICANT: Mulligan, John T.
; APPLICANT: Paeper, Bryan W.
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Winkler, David G.
; TITLE OF INVENTION: COMPOSITIONS AND MEHTODS FOR
; TITLE OF INVENTION: INCREASING BONE MINERALIZATION
; FILE REFERENCE: 240083.508C2
; CURRENT APPLICATION NUMBER: US/10/463,190
; CURRENT FILING DATE: 2003-06-16
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 106
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-463-190-106
Query Match 100.0%; Score 2838; DB 4; Length 532;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MTOLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDOKKPNGVTLAPEDTLPLFK 60
Db 1 MTOLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDOKKPNGVTLAPEDTLPLFK 60
Qy 61 CYCSGHCPCDDAINNCTITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
Db 61 CYCSGHCPCDDAINNCTITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
Qy 121 TIECCTNLCNQYLOPTLPPVIGPFDGSRVRLAVLISMAVCIAMIVFSSCFCKYKHC 180
Db 121 TIECCTNLCNQYLOPTLPPVIGPFDGSRVRLAVLISMAVCIAMIVFSSCFCKYKHC 180
Qy 181 KSISRGYRNRLDEODEAFIPVGESLKDLDIOSOSSGSGGLPLLQVORTIAKQIOMVRQV 240
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Db 181 KSISRRGRNDRLEQDEAFIPVGSGLKDLIDQSSGSGSGLPLLVORTIAKIQMVRQV 240
Qy 241 GKGRYGEVMMGKRGKAVKVPFFTEEASWFRTEIYQTVLMRHNILGFIAADIKGTG 300
Db 241 GKGRYGEVMMGKRGKAVKVPFFTEEASWFRTEIYQTVLMRHNILGFIAADIKGTG 300
Qy 301 SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAISAACGLCHLHTEIYGTQKPAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAISAACGLCHLHTEIYGTQKPAIAH 360
Qy 361 RDLKSKNILIKKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSLKN 420
Db 361 RDLKSKNILIKKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSLKN 420
Qy 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEEYQLPYNNMVPSPSDPSYEDMREVVCVKRLR 480
Db 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEEYQLPYNNMVPSPSDPSYEDMREVVCVKRLR 480
Qy 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532

RESULT 4
US-10-463-190-107
; Sequence 107, Application US/10463190
; Publication No. US20040009535A1
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary E.
; APPLICANT: Galas, David J.
; APPLICANT: Kovacevich, Brian
; APPLICANT: Mulligan, John T.
; APPLICANT: Paepet, Bryan W.
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Winkler, David G.
; TITLE OF INVENTION: COMPOSITIONS AND MEHTODS FOR
; FILE REFERENCE: 240083.508C2
; CURRENT APPLICATION NUMBER: US/10/463,190
; CURRENT FILING DATE: 2003-06-16
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-463-190-107

Query Match 100.0%; Score 2838; DB 4; Length 532;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPFLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPFLK 60
Qy 61 CYCSGHCPDDAINTCTINGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLR 120
Db 61 CYCSGHCPDDAINTCTINGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLR 120
Qy 121 TIECCRTNLNQYLQPTLPVWIGPFDGSRVWLAVLISMAVCIVAMIVFSSCFYKHYC 180
Db 121 TIECCRTNLNQYLQPTLPVWIGPFDGSRVWLAVLISMAVCIVAMIVFSSCFYKHYC 180
Qy 181 KSISRRGRNDRLEQDEAFIPVGSGLKDLIDQSSGSGSGLPLLVORTIAKIQMVRQV 240
Db 181 KSISRRGRNDRLEQDEAFIPVGSGLKDLIDQSSGSGSGLPLLVORTIAKIQMVRQV 240
Qy 241 GKGRYGEVMMGKRGKAVKVPFFTEEASWFRTEIYQTVLMRHNILGFIAADIKGTG 300
Db 241 GKGRYGEVMMGKRGKAVKVPFFTEEASWFRTEIYQTVLMRHNILGFIAADIKGTG 300
Qy 301 SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAISAACGLCHLHTEIYGTQKPAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAISAACGLCHLHTEIYGTQKPAIAH 360
Qy 361 RDLKSKNILIKKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSLKN 420
Db 361 RDLKSKNILIKKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSLKN 420
Qy 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEEYQLPYNNMVPSPSDPSYEDMREVVCVKRLR 480
Db 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEEYQLPYNNMVPSPSDPSYEDMREVVCVKRLR 480
Qy 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
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Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAISAACGLCHLHTEIYGTQKPAIAH 360
Qy 361 RDLKSKNILIKKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSLKN 420
Db 361 RDLKSKNILIKKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSLKN 420
Qy 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEEYQLPYNNMVPSPSDPSYEDMREVVCVKRLR 480
Db 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEEYQLPYNNMVPSPSDPSYEDMREVVCVKRLR 480
Qy 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532

RESULT 5
US-10-463-190-110
; Sequence 110, Application US/10463190
; Publication No. US20040009535A1
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary E.
; APPLICANT: Galas, David J.
; APPLICANT: Kovacevich, Brian
; APPLICANT: Mulligan, John T.
; APPLICANT: Paepet, Bryan W.
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Winkler, David G.
; TITLE OF INVENTION: COMPOSITIONS AND MEHTODS FOR
; FILE REFERENCE: 240083.508C2
; CURRENT APPLICATION NUMBER: US/10/463,190
; CURRENT FILING DATE: 2003-06-16
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-463-190-110

Query Match 100.0%; Score 2838; DB 4; Length 532;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPFLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPFLK 60
Qy 61 CYCSGHCPDDAINTCTINGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLR 120
Db 61 CYCSGHCPDDAINTCTINGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLR 120
Qy 121 TIECCRTNLNQYLQPTLPVWIGPFDGSRVWLAVLISMAVCIVAMIVFSSCFYKHYC 180
Db 121 TIECCRTNLNQYLQPTLPVWIGPFDGSRVWLAVLISMAVCIVAMIVFSSCFYKHYC 180
Qy 181 KSISRRGRNDRLEQDEAFIPVGSGLKDLIDQSSGSGSGLPLLVORTIAKIQMVRQV 240
Db 181 KSISRRGRNDRLEQDEAFIPVGSGLKDLIDQSSGSGSGLPLLVORTIAKIQMVRQV 240
Qy 241 GKGRYGEVMMGKRGKAVKVPFFTEEASWFRTEIYQTVLMRHNILGFIAADIKGTG 300
Db 241 GKGRYGEVMMGKRGKAVKVPFFTEEASWFRTEIYQTVLMRHNILGFIAADIKGTG 300
Qy 301 SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAISAACGLCHLHTEIYGTQKPAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTALLKLAISAACGLCHLHTEIYGTQKPAIAH 360
Qy 361 RDLKSKNILIKKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSLKN 420
Db 361 RDLKSKNILIKKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSLKN 420
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421	Qy	HFQPYIMADISFGLLIWMEMARRCITGGIVEEYQLPYNNMVPSPDPSPDYEDREVVVCVKRLR	480
421	Db	HFQPYIMADISFGLLIWMEMARRCITGGIVEEYQLPYNNMVPSPDPSPDYEDREVVVCVKRLR	480
481	Qy	PVSNRNWNSDECLRAVLKIMSECWAHPASRLTALRIKKTAKKWSQDVYKI	532
481	Db	PVSNRNWNSDECLRAVLKIMSECWAHPASRLTALRIKKTAKKWSQDVYKI	532

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Dd	181	KSISRRGRNRDLEQDEAFIPVGESIKDLIDQSSGSSGSLPLLIVORTAKQIQMVQRQV	240
Qy	241	KGGRYGEVVMGKWRGKVAVKVFPTTTEASWPRETEIYQTVLMRHENILGFIAADIKGTG	300
Dd	241	KGGRYGEVVMGKWRGKVAVKVFPTTTEASWPRETEIYQTVLMRHENILGFIAADIKGTG	300
Qy	301	SWTQLYLIITDYHENGSLYDFLKCATIDTRALLKLAYSAAACGLCHLHTEIYGTQGKPAIAH	360
Dd	301	SWTQLYLIITDYHENGSLYDFLKCATIDTRALLKLAYSAAACGLCHLHTEIYGTQGKPAIAH	360
Qy	361	RDLKSKNLIILKNGSCCIADGLAVKFNSTDNEVDPLNTRVGRTRRYMAPEVLDLSLKN	420
Dd	361	RDLKSKNLIILKNGSCCIADGLAVKFNSTDNEVDPLNTRVGRTRRYMAPEVLDLSLKN	420
Qy	421	HFQPYIMADIYSFGLIIEWEMARRCITGGIVEEYQLPYYNMVPDPSYEDMREVVVCVKRLR	480
Dd	421	HFQPYIMADIYSFGLIIEWEMARRCITGGIVEEYQLPYYNMVPDPSYEDMREVVVCVKRLR	480
Qy	481	PIVSNRWNSECLRAVLKLMSECAWNPASRLTALRIKKTAKMVEVSQDVKI	532
Dd	481	PIVSNRWNSECLRAVLKLMSECAWNPASRLTALRIKKTAKMVEVSQDVKI	532
RESULT 7			
US-10-868-497-74			
; Sequence 74, Application US/10868497			
; Publication No. US20050106683A1			
; GENERAL INFORMATION:			
; APPLICANT: Winkler, David G.			
; APPLICANT: Shi, Jiye			
; APPLICANT: Latham, John			
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR SCLEROSTIN AND			
; TITLE OF INVENTION: METHODS FOR INCREASING BONE MINERALIZATION			
; FILE REFERENCE: 60117-128			
; CURRENT APPLICATION NUMBER: US/10/868,497			
; CURRENT FILING DATE: 2004-06-15			
; NUMBER OF SEQ ID NOS: 112			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 74			
; LENGTH: 532			
; TYPE: PRT			
; ORGANISM: Rattus sp.			
US-10-868-497-74			

Query Match	100.0%;	Score 2838;	DB 5;	Length 532;
Best Local Similarity	100.0%;	Pred. No. 1e-243;		
Matches 532; Conservative	0;	Mismatches 0;	Indels 0;	Gaps. 0;
Qy	1	MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTMGKSDVDQKPKENGVTTLAPEDTLPPLK	60	
Db	1	MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTMGKSDVDQKPKENGVTTLAPEDTLPPLK	60	
Qy	61	CYSGHCPDDAINNTCITNGHCFALIEEDDQGETTTLTSGCMKYEGSDFQCKSPKAQLRR	120	
Db	61	CYSGHCPDDAINNTCITNGHCFALIEEDDQGETTTLTSGCMKYEGSDFQCKSPKAQLRR	120	
Qy	121	TTECCRTNLNCQYLOPTLPWVIGPFFDGSVRMLAVLISMAVCIVAMIVSSCFCYKHVC	180	
Db	121	TTECCRTNLNCQYLOPTLPWVIGPFFDGSVRMLAVLISMAVCIVAMIVSSCFCYKHVC	180	
Qy	181	KSISRRGRYNRDLDEQDEAFIPVGESLKDLLDQSGSGSGGLPLLVTAKQIQMVRQV	240	
Db	181	KSISRRGRYNRDLDEQDEAFIPVGESLKDLLDQSGSGSGGLPLLVTAKQIQMVRQV	240	
Qy	241	GKGRYGEVMMGKWRGEKVAVKVFTTTEASWPRETEIYQTVLMRHNILGFIADIKGTG	300	
Db	241	GKGRYGEVMMGKWRGEKVAVKVFTTTEASWPRETEIYQTVLMRHNILGFIADIKGTG	300	
Qy	301	SWTQLYLIITDYHENGSLYDFLKCATLDTRALLKLAYSAAAGLCHLHTEIYCTOCKPATAH	360	
Db	301	SWTQLYLIITDYHENGSLYDFLKCATLDTRALLKLAYSAAAGLCHLHTEIYCTOCKPATAH	360	
Qy	361	RDLKSNKILIKKNGSCCIIADLGLAVKFNSDTNEVDIPLNTRVGTGRTTMYMAPEVLDES	420	

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Db 361 RDLKSNLILKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
Qy 421 HFQPYIMADISFGLIIEWARRCITGGIVEEYQLPYNNVPSPSYEDMREVVCVKRLR 480
Db 421 HFQPYIMADISFGLIIEWARRCITGGIVEEYQLPYNNVPSPSYEDMREVVCVKRLR 480
Qy 481 PIVSNRNSDECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRNSDECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532

RESULT 8
US-10-868-497-75
; Sequence 75, Application US/10868497
; Publication No. US20050106683A1
; GENERAL INFORMATION:
; APPLICANT: Winkler, David G.
; APPLICANT: Shi, Jiye
; APPLICANT: Latham, John
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR SCLEROSTIN AND
; TITLE OF INVENTION: METHODS FOR INCREASING BONE MINERALIZATION
; FILE REFERENCE: 60117-128
; CURRENT APPLICATION NUMBER: US/10/868,497
; CURRENT FILING DATE: 2004-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-868-497-75

Query Match 100.0%; Score 2838; DB 5; Length 532;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDOKKPPENGVTILAPEDTLPFLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDOKKPPENGVTILAPEDTLPFLK 60
Qy 61 CYCSGHCPDDAINNTCITNGHCFALIEEDDQGETTLTSGCMKYEYSGDFQCKDSPKAQLRR 120
Db 61 CYCSGHCPDDAINNTCITNGHCFALIEEDDQGETTLTSGCMKYEYSGDFQCKDSPKAQLRR 120
Qy 121 TIECCRTNLCNOYLOPTLPVWIGPFDGSRVRLAVLISMAVCIVAMIVFSSCFYKHYC 180
Db 121 TIECCRTNLCNOYLOPTLPVWIGPFDGSRVRLAVLISMAVCIVAMIVFSSCFYKHYC 180
Qy 181 KSISSRGYNRDLQDEAFIPVGESLKDLIDQSSGSGGLPLLQRTIAKQIQMVROV 240
Db 181 KSISSRGYNRDLQDEAFIPVGESLKDLIDQSSGSGGLPLLQRTIAKQIQMVROV 240
Qy 241 GKGRYGEVWMGKRGKAVKVFPTTEASWPRETEIYQTVLMRHNILGFTAADIKGTG 300
Db 241 GKGRYGEVWMGKRGKAVKVFPTTEASWPRETEIYQTVLMRHNILGFTAADIKGTG 300
Qy 301 SWTQLYLTIDYHENGSLYDFLKCATLDTRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Db 301 SWTQLYLTIDYHENGSLYDFLKCATLDTRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Qy 361 RDLKSNLILKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
Db 361 RDLKSNLILKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
Qy 421 HFQPYIMADISFGLIIEWARRCITGGIVEEYQLPYNNVPSPSYEDMREVVCVKRLR 480
Db 421 HFQPYIMADISFGLIIEWARRCITGGIVEEYQLPYNNVPSPSYEDMREVVCVKRLR 480
Qy 481 PIVSNRNSDECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRNSDECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
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Query Match 100.0%; Score 2838; DB 5; Length 532;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDOKKPPENGVTILAPEDTLPFLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDOKKPPENGVTILAPEDTLPFLK 60
Qy 61 CYCSGHCPDDAINNTCITNGHCFALIEEDDQGETTLTSGCMKYEYSGDFQCKDSPKAQLRR 120
Db 61 CYCSGHCPDDAINNTCITNGHCFALIEEDDQGETTLTSGCMKYEYSGDFQCKDSPKAQLRR 120
Qy 121 TIECCRTNLCNOYLOPTLPVWIGPFDGSRVRLAVLISMAVCIVAMIVFSSCFYKHYC 180
Db 121 TIECCRTNLCNOYLOPTLPVWIGPFDGSRVRLAVLISMAVCIVAMIVFSSCFYKHYC 180
Qy 181 KSISSRGYNRDLQDEAFIPVGESLKDLIDQSSGSGGLPLLQRTIAKQIQMVROV 240
Db 181 KSISSRGYNRDLQDEAFIPVGESLKDLIDQSSGSGGLPLLQRTIAKQIQMVROV 240
Qy 241 GKGRYGEVWMGKRGKAVKVFPTTEASWPRETEIYQTVLMRHNILGFTAADIKGTG 300
Db 241 GKGRYGEVWMGKRGKAVKVFPTTEASWPRETEIYQTVLMRHNILGFTAADIKGTG 300
Qy 301 SWTQLYLTIDYHENGSLYDFLKCATLDTRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Db 301 SWTQLYLTIDYHENGSLYDFLKCATLDTRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Qy 361 RDLKSNLILKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
Db 361 RDLKSNLILKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
Qy 421 HFQPYIMADISFGLIIEWARRCITGGIVEEYQLPYNNVPSPSYEDMREVVCVKRLR 480
Db 421 HFQPYIMADISFGLIIEWARRCITGGIVEEYQLPYNNVPSPSYEDMREVVCVKRLR 480
Qy 481 PIVSNRNSDECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRNSDECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
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RESULT 9
US-10-868-497-76
; Sequence 76, Application US/10868497
; Publication No. US20050106683A1
; GENERAL INFORMATION:
; APPLICANT: Winkler, David G.
; APPLICANT: Shi, Jiye
; APPLICANT: Latham, John
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR SCLEROSTIN AND
; TITLE OF INVENTION: METHODS FOR INCREASING BONE MINERALIZATION
; FILE REFERENCE: 60117-128
; CURRENT APPLICATION NUMBER: US/10/868,497
; CURRENT FILING DATE: 2004-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-868-497-76

Query Match 100.0%; Score 2838; DB 5; Length 532;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDOKKPPENGVTILAPEDTLPFLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDOKKPPENGVTILAPEDTLPFLK 60
Qy 61 CYCSGHCPDDAINNTCITNGHCFALIEEDDQGETTLTSGCMKYEYSGDFQCKDSPKAQLRR 120
Db 61 CYCSGHCPDDAINNTCITNGHCFALIEEDDQGETTLTSGCMKYEYSGDFQCKDSPKAQLRR 120
Qy 121 TIECCRTNLCNOYLOPTLPVWIGPFDGSRVRLAVLISMAVCIVAMIVFSSCFYKHYC 180
Db 121 TIECCRTNLCNOYLOPTLPVWIGPFDGSRVRLAVLISMAVCIVAMIVFSSCFYKHYC 180
Qy 181 KSISSRGYNRDLQDEAFIPVGESLKDLIDQSSGSGGLPLLQRTIAKQIQMVROV 240
Db 181 KSISSRGYNRDLQDEAFIPVGESLKDLIDQSSGSGGLPLLQRTIAKQIQMVROV 240
Qy 241 GKGRYGEVWMGKRGKAVKVFPTTEASWPRETEIYQTVLMRHNILGFTAADIKGTG 300
Db 241 GKGRYGEVWMGKRGKAVKVFPTTEASWPRETEIYQTVLMRHNILGFTAADIKGTG 300
Qy 301 SWTQLYLTIDYHENGSLYDFLKCATLDTRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Db 301 SWTQLYLTIDYHENGSLYDFLKCATLDTRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Qy 361 RDLKSNLILKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
Db 361 RDLKSNLILKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
Qy 421 HFQPYIMADISFGLIIEWARRCITGGIVEEYQLPYNNVPSPSYEDMREVVCVKRLR 480
Db 421 HFQPYIMADISFGLIIEWARRCITGGIVEEYQLPYNNVPSPSYEDMREVVCVKRLR 480
Qy 481 PIVSNRNSDECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRNSDECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
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RESULT 10
US-10-868-497-79
; Sequence 79, Application US/10868497
; Publication No. US20050106683A1
; GENERAL INFORMATION:
; APPLICANT: Winkler, David G.
; APPLICANT: Shi, Jiye
; APPLICANT: Latham, John
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR SCLEROSTIN AND
; TITLE OF INVENTION: METHODS FOR INCREASING BONE MINERALIZATION
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; FILE REFERENCE: 60117-128
; CURRENT APPLICATION NUMBER: US/10/868,497
; CURRENT FILING DATE: 2004-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-868-497-79

Query Match      100.0%; Score 2838; DB 5; Length 532;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGKMSVDQKKPENGVTLPAPEDTLPLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGKMSVDQKKPENGVTLPAPEDTLPLK 60

Qy 61 CYCSGHCPCDDAINNTCTINGHCFALIEBDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRR 120
Db 61 CYCSGHCPCDDAINNTCTINGHCFALIEBDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRR 120

Qy 121 TIECCRTNLCNQYLOPTLPVPIVGFPGDSVRLAVLISMAVICIVAMIVFSSCFCKHYC 180
Db 121 TIECCRTNLCNQYLOPTLPVPIVGFPGDSVRLAVLISMAVICIVAMIVFSSCFCKHYC 180

Qy 181 KSISRGYRNRLDEDEAFIPVGESLKDLDQSSGSGSLPLLVQRTIAKIQMVQV 240
Db 181 KSISRGYRNRLDEDEAFIPVGESLKDLDQSSGSGSLPLLVQRTIAKIQMVQV 240

Qy 241 GKRGYGEVWVGKRGKAVKVVFFTTBEASWFRTEIYQTVLMRHENILGFIADIKGTG 300
Db 241 GKRGYGEVWVGKRGKAVKVVFFTTBEASWFRTEIYQTVLMRHENILGFIADIKGTG 300

Qy 301 SWTQLYLTIDYHENGSLYDFLKCATLDTRALLLKLAISAACGLCHLHTEIYGTQKPAIAH 360
Db 301 SWTQLYLTIDYHENGSLYDFLKCATLDTRALLLKLAISAACGLCHLHTEIYGTQKPAIAH 360

Qy 361 RDLKSKNILIKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTGRRYMAPEVLDLSKN 420
Db 361 RDLKSKNILIKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTGRRYMAPEVLDLSKN 420

Qy 421 HFQPYIMADIYSFGLIIEWEMARRCTIGGIVEYQLPYNNMVPSPDSYEDMREVVCVKRLR 480
Db 421 HFQPYIMADIYSFGLIIEWEMARRCTIGGIVEYQLPYNNMVPSPDSYEDMREVVCVKRLR 480

Qy 481 PIVSNRWNSDCLRAVLKLMSECAHNPASRLTALRIKTKLAKMVESQDVKI 532
Db 481 PIVSNRWNSDCLRAVLKLMSECAHNPASRLTALRIKTKLAKMVESQDVKI 532

RESULT 11
US-09-903-068-14
; Sequence 14, Application US/09903068
; Patent No. US20020123139A1
; GENERAL INFORMATION:
; APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
; Franzen, Petra; Yamashita, Hidetoshi;
; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
; Having Serine Threonine Kinase Domains And Their Use
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/903,068
; FILING DATE: 11-Jul-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/679,187
; FILING DATE: <unknown>
; APPLICATION NUMBER: PCT/GB93/02367
; FILING DATE: 17-No. US20020123139A1ember-1993
; APPLICATION NUMBER: 9224057.1
; FILING DATE: 17-No. US20020123139A1ember-1992
; APPLICATION NUMBER: 9304677.9
; FILING DATE: 8-March-1993
; APPLICATION NUMBER: 9304680.3
; FILING DATE: 8-March-1993
; APPLICATION NUMBER: 9311047.6
; FILING DATE: 28-May-1993
; APPLICATION NUMBER: 9313763.6
; FILING DATE: 2-July-1993
; APPLICATION NUMBER: 9136099.2
; FILING DATE: 3-August-1993
; APPLICATION NUMBER: 9321344.5
; FILING DATE: 15-October-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohlei, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: LUD 5298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-903-068-14

Query Match      99.5%; Score 2823; DB 3; Length 532;
Best Local Similarity 98.9%; Pred. No. 2.2e-242;
Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGKMSVDQKKPENGVTLPAPEDTLPLK 60
Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGKMSVDQKKPENGVTLPAPEDTLPLK 60

Qy 61 CYCSGHCPCDDAINNTCTINGHCFALIEBDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRR 120
Db 61 CYCSGHCPCDDAINNTCTINGHCFALIEBDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRR 120

Qy 121 TIECCRTNLCNQYLOPTLPVPIVGFPGDSVRLAVLISMAVICIVAMIVFSSCFCKHYC 180
Db 121 TIECCRTNLCNQYLOPTLPVPIVGFPGDSVRLAVLISMAVICIVAMIVFSSCFCKHYC 180

Qy 181 KSISRGYRNRLDEDEAFIPVGESLKDLDQSSGSGSLPLLVQRTIAKIQMVQV 240
Db 181 KSISRGYRNRLDEDEAFIPVGESLKDLDQSSGSGSLPLLVQRTIAKIQMVQV 240

Qy 241 GKRGYGEVWVGKRGKAVKVVFFTTBEASWFRTEIYQTVLMRHENILGFIADIKGTG 300
Db 241 GKRGYGEVWVGKRGKAVKVVFFTTBEASWFRTEIYQTVLMRHENILGFIADIKGTG 300

Qy 301 SWTQLYLTIDYHENGSLYDFLKCATLDTRALLLKLAISAACGLCHLHTEIYGTQKPAIAH 360
Db 301 SWTQLYLTIDYHENGSLYDFLKCATLDTRALLLKLAISAACGLCHLHTEIYGTQKPAIAH 360

Qy 361 RDLKSKNILIKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTGRRYMAPEVLDLSKN 420
Db 361 RDLKSKNILIKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTGRRYMAPEVLDLSKN 420

Qy 421 HFQPYIMADIYSFGLIIEWEMARRCTIGGIVEYQLPYNNMVPSPDSYEDMREVVCVKRLR 480
Db 421 HFQPYIMADIYSFGLIIEWEMARRCTIGGIVEYQLPYNNMVPSPDSYEDMREVVCVKRLR 480
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Qy 481 PIVSNRWNDECLRAVLKLMSECAHNPASRLTALRIKKTAKWVESQDVKI 532
Db 481 PIVSNRWNDECLRAVLKLMSECAHNPASRLTALRIKKTAKWVESQDVKI 532

RESULT 12
US-10-739-413-14
; Sequence 14, Application US/10739413
; Publication No. US20050048607A1
; GENERAL INFORMATION:
; APPLICANT: MIYAZONO, Kohei
; APPLICANT: IMAMURA, Takeshe
; APPLICANT: DEN DIJKE, Peter
; TITLE OF INVENTION: PROTEINS HAVING SERINE/THREONINE KINASE DOMAINS, CORRESPONDING
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND THEIR USE
; FILE REFERENCE: LUD 5539.1 CIP
; CURRENT APPLICATION NUMBER: US/10/739, 413
; PRIOR FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US/09/267,963
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/GB93/02367
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: US 09/039,177
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-739-413-14

Query Match 99.5%; Score 2823; DB 5; Length 532;
Best Local Similarity 98.9%; Pred. No. 2.2e-242;
Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTQLYTYIRLLGACFLIISHVQGNLDSMLHGTGMSKSDVDQKPKENGVTLPEDTLPFLK 60
Db 1 MTQLYTYIRLLGACFLIISHVQGNLDSMLHGTGMSKSDVDQKPKENGVTLPEDTLPFLK 60

Qy 61 CYCSGHCPCDDAINTTCITNGHCFALIEEDDQGETTLTSCGMKYEGSDFQCKSPKQALRR 120
Db 61 CYCSGHCPCDDAINTTCITNGHCFALIEEDDQGETTLTSCGMKYEGSDFQCKSPKQALRR 120

Qy 121 TIECCRTNLCNOYLQPTLPVWIGPFDGSRVRLAVLISMAVCIVAMIVFSSCFCKHYC 180
Db 121 TIECCRTNLCNOYLQPTLPVWIGPFDGSRVRLAVLISMAVCIVAMIVFSSCFCKHYC 180

Qy 181 KSISSRGYNRDLQDEAFIPVGSLSKDLIDQSSGSGSLPLLVQRTIAQIQMVROV 240
Db 181 KSISSRGYNRDLQDEAFIPVGSLSKDLIDQSSGSGSLPLLVQRTIAQIQMVROV 240

Qy 241 GKGRYGEVMWGKRGKAVKVFPTTEASWFRTEIYQTVLMRHNILGFAADIKGTG 300
Db 241 GKGRYGEVMWGKRGKAVKVFPTTEASWFRTEIYQTVLMRHNILGFAADIKGTG 300

Qy 301 SWTQLYLTIDYHENGSLYFLKCATLDTALLKLAYSACGLCHLHTEIYGTQKPAIAH 360
Db 301 SWTQLYLTIDYHENGSLYFLKCATLDTALLKLAYSACGLCHLHTEIYGTQKPAIAH 360

Qy 361 RDLKSNKILIKKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVCTTRYMAPEVLDLSKN 420
Db 361 RDLKSNKILIKKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVCTTRYMAPEVLDLSKN 420

Qy 421 HFQPYIMADISFGLIIEWEMARCIITGGIVEEYQLPYNNVPSDPSYEDMRVVCVKRLR 480
Db 421 HFQPYIMADISFGLIIEWEMARCIITGGIVEEYQLPYNNVPSDPSYEDMRVVCVKRLR 480

Qy 481 PIVSNRWNDECLRAVLKLMSECAHNPASRLTALRIKKTAKWVESQDVKI 532
Db 481 PIVSNRWNDECLRAVLKLMSECAHNPASRLTALRIKKTAKWVESQDVKI 532

RESULT 13
US-09-903-068-6
; Sequence 6, Application US/09903068
; Patent No. US20020123139A1
; GENERAL INFORMATION:
; APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
; Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
; Having Serine Threonine Kinase Domains And Their Use
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/903,068
; FILING DATE: 11-Jul-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/679,187
; FILING DATE: <Unknown>
; APPLICATION NUMBER: PCT/GB93/02367
; FILING DATE: 17-No. US20020123139A1ember-1993
; APPLICATION NUMBER: 9224057.1
; FILING DATE: 17-No. US20020123139A1ember-1992
; APPLICATION NUMBER: 9304677.9
; FILING DATE: 8-March-1993
; APPLICATION NUMBER: 9304680.3
; FILING DATE: 8-March-1993
; APPLICATION NUMBER: 9311047.6
; FILING DATE: 28-May-1993
; APPLICATION NUMBER: 9313763.6
; FILING DATE: 2-July-1993
; APPLICATION NUMBER: 9336099.2
; FILING DATE: 3-August-1993
; APPLICATION NUMBER: 9321344.5
; FILING DATE: 15-October-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohlei, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: LUD 5298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-903-068-6

Query Match 97.6%; Score 2769; DB 3; Length 532;
Best Local Similarity 97.2%; Pred. No. 1.4e-237;
Matches 517; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MTQLYTYIRLLGACFLIISHVQGNLDSMLHGTGMSKSDVDQKPKENGVTLPEDTLPFLK 60
Db 1 MTQLYTYIRLLGACFLIISHVQGNLDSMLHGTGMSKSDVDQKPKENGVTLPEDTLPFLK 60

Qy 61 CYCSGHCPCDDAINTTCITNGHCFALIEEDDQGETTLTSCGMKYEGSDFQCKSPKQALRR 120
Db 61 CYCSGHCPCDDAINTTCITNGHCFALIEEDDQGETTLTSCGMKYEGSDFQCKSPKQALRR 120

Qy 121 TIECCRTNLCNOYLQPTLPVWIGPFDGSRVRLAVLISMAVCIVAMIVFSSCFCKHYC 180

Db 121 TIECCTNLCNQYLQPTLPVVGFFDGSIRWLVLISMVACIIAMIFSSCFCKHYC 180
Qy 181 KSISRRGRNRLDEQDEAFIPVGESLKDLIDQSQSSGSGGLPLLVQRTIAKIQIMVRQV 240
Db 181 KSISRRRRNRLDEQDEAFIPVGESLKDLIDQSQSSGSGGLPLLVQRTIAKIQIMVRQV 240
Qy 241 GKGRYGEVMMGKWRGEKAVKVFVFTTEASWFRTEIYQTVLMRHNILGFTAAIDKGTG 300
Db 241 GKGRYGEVMMGKWRGEKAVKVFVFTTEASWFRTEIYQTVLMRHNILGFTAAIDKGTG 300
Qy 301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Qy 361 RDLKSKNLIKKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDSELSKN 420
Db 361 RDLKSKNLIKKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDSELSKN 420
Qy 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEYQLPYYNMVPSDPSYEDMREVVCVKRLR 480
Db 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEYQLPYYNMVPSDPSYEDMREVVCVKRLR 480
Qy 481 PIVSNRNSDECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRNSDECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532

RESULT 14
US-09-982-543A-6
; Sequence 6, Application US/09982543A
; Patent No. US20020155500A1
; GENERAL INFORMATION:
; APPLICANT: Dijke, P.
; APPLICANT: Miyazano, K.
; APPLICANT: Sampath, K.
; APPLICANT: Heldin, C.
; TITLE OF INVENTION: MORPHOGENIC PROTEIN-SPECIFIC CELL SURFACE RECEPTORS AND USES
; FILE REFERENCE: THEREFOR
; CURRENT APPLICATION NUMBER: US/09/982,543A
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 08/448,371
; PRIOR FILING DATE: 1995-06-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-982-543A-6

Query Match 97.6%; Score 2769; DB 3; Length 532;
Best Local Similarity 97.2%; Pred. No. 1.4e-237;
Matches 517; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
Qy 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVT LAPEDTLPLFK 60
Db 1 MTQLYTYIRLLGAYLFIISRVOGNLDSMLHGTGMKSDSDQKSENGVT LAPEDTLPLFK 60
Qy 61 CYCSGHCPCDDAINNTCTINGHCFAIIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
Db 61 CYCSGHCPCDDAINNTCTINGHCFAIIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
Qy 121 TIECCTNLCNQYLQPTLPVVGFFDGSVRWLAVLISMVACIIVAMIVFSSCFCKHYC 180
Db 121 TIECCTNLCNQYLQPTLPVVGFFDGSIRWLVLISMVACIIAMIFSSCFCKHYC 180
Qy 181 KSISRRGRNRLDEQDEAFIPVGESLKDLIDQSQSSGSGGLPLLVQRTIAKIQIMVRQV 240
Db 181 KSISRRRRNRLDEQDEAFIPVGESLKDLIDQSQSSGSGGLPLLVQRTIAKIQIMVRQV 240
Qy 241 GKGRYGEVMMGKWRGEKAVKVFVFTTEASWFRTEIYQTVLMRHNILGFTAAIDKGTG 300
Db 241 GKGRYGEVMMGKWRGEKAVKVFVFTTEASWFRTEIYQTVLMRHNILGFTAAIDKGTG 300

Db 241 GKGRYGEVMMGKWRGEKAVKVFVFTTEASWFRTEIYQTVLMRHNILGFTAAIDKGTG 300
Qy 301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Qy 361 RDLKSKNLIKKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDSELSKN 420
Db 361 RDLKSKNLIKKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDSELSKN 420
Qy 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEYQLPYYNMVPSDPSYEDMREVVCVKRLR 480
Db 421 HFQPYIMADIYSFGLIIEWEMARRCITGGIVEYQLPYYNMVPSDPSYEDMREVVCVKRLR 480
Qy 481 PIVSNRNSDECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532
Db 481 PIVSNRNSDECLRAVLKLMSECAHNPASRLTALRIKKTAKMVESQDVKI 532

RESULT 15
US-10-153-217-2
; Sequence 2, Application US/10153217
; Publication No. US20030072758A1
; GENERAL INFORMATION:
; APPLICANT: HOWE, JAMES R.
; TITLE OF INVENTION: BMPRIA INVOLVEMENT IN JUVENILE POLYPOSIS
; FILE REFERENCE: IOWA:037US
; CURRENT APPLICATION NUMBER: US/10/153,217
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: 60/292,691
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-153-217-2

Query Match 97.6%; Score 2769; DB 4; Length 532;
Best Local Similarity 97.2%; Pred. No. 1.4e-237;
Matches 517; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
Qy 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVT LAPEDTLPLFK 60
Db 1 MTQLYTYIRLLGAYLFIISRVOGNLDSMLHGTGMKSDSDQKSENGVT LAPEDTLPLFK 60
Qy 61 CYCSGHCPCDDAINNTCTINGHCFAIIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
Db 61 CYCSGHCPCDDAINNTCTINGHCFAIIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
Qy 121 TIECCTNLCNQYLQPTLPVVGFFDGSVRWLAVLISMVACIIVAMIVFSSCFCKHYC 180
Db 121 TIECCTNLCNQYLQPTLPVVGFFDGSIRWLVLISMVACIIVAMIVFSSCFCKHYC 180
Qy 181 KSISRRGRNRLDEQDEAFIPVGESLKDLIDQSQSSGSGGLPLLVQRTIAKIQIMVRQV 240
Db 181 KSISRRRRNRLDEQDEAFIPVGESLKDLIDQSQSSGSGGLPLLVQRTIAKIQIMVRQV 240
Qy 241 GKGRYGEVMMGKWRGEKAVKVFVFTTEASWFRTEIYQTVLMRHNILGFTAAIDKGTG 300
Db 241 GKGRYGEVMMGKWRGEKAVKVFVFTTEASWFRTEIYQTVLMRHNILGFTAAIDKGTG 300
Qy 301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Db 301 SWTQLYLITDYHENGSLYDFLKCATLDTRALLKLAYSAAACGLCHLHTEIYGTQKPAIAH 360
Qy 361 RDLKSKNLIKKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDSELSKN 420
Db 361 RDLKSKNLIKKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDSELSKN 420

Qy 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYNNMVPSPDPSYEDMREVVCVKRLR 480
Db 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYNNMVPSPDPSYEDMREVVCVKRLR 480
Qy 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKWVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKKTAKWVESQDVKI 532

Search completed: December 3, 2005, 06:25:48
Job time : 168 secs

us-10-600-645-2.rapbm

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 06:12:35 ; Search time 11 Seconds
(without alignments)
231.581 Million cell updates/sec

Title: US-10-600-645-2

Perfect score: 2838

Sequence: 1 MTQLYTYIRLLGACLFISH.....TALRIKTKLAKMVESQDVKI 532

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	561.5	19.8	567	6	US-10-420-192-8
2	287	10.1	450	7	US-11-109-156-21
3	248	8.7	835	7	US-11-186-283-2
4	242	8.5	835	7	US-11-186-283-8
5	241.5	8.5	456	7	US-11-021-441-18
6	241.5	8.5	1035	7	US-11-021-441-4
7	238	8.4	648	7	US-11-109-156-17
8	230.5	8.1	460	6	US-10-990-276-1
9	230	8.1	459	6	US-10-990-276-3
10	228.5	8.1	984	7	US-11-113-424-60
11	225	7.9	995	7	US-11-113-424-62
12	224	7.9	479	7	US-11-021-441-20
13	222	7.8	490	7	US-11-021-441-26
14	222	7.8	497	7	US-11-021-441-22
15	222	7.8	497	7	US-11-021-441-24
16	222	7.8	985	7	US-11-113-424-61
17	219	7.7	256	7	US-11-113-424-183
18	212.5	7.5	987	6	US-10-949-720-395
19	212.5	7.5	990	6	US-10-821-234-1201
20	211	7.4	998	6	US-10-510-524-1
21	210	7.4	983	7	US-11-113-424-59
22	207.5	7.3	1142	7	US-11-109-156-22
23	206.5	7.3	1005	7	US-11-113-424-63
24	203.5	7.2	656	6	US-10-821-234-1121
25	199	7.0	379	7	US-11-109-156-16

26	193	6.8	344	7	US-11-109-156-13	Sequence 13, Appli
27	186.5	6.6	1311	6	US-10-509-422-5	Sequence 5, Appli
28	184.5	6.5	543	6	US-10-821-234-1158	Sequence 1158, Ap
29	183.5	6.5	654	7	US-11-046-668-4	Sequence 4, Appli
30	183.5	6.5	683	7	US-11-046-668-2	Sequence 2, Appli
31	179.5	6.3	403	7	US-11-109-156-12	Sequence 12, Appli
32	178	6.3	297	7	US-11-109-156-11	Sequence 11, Appli
33	178	6.3	898	7	US-11-099-691-7	Sequence 7, Appli
34	174.5	6.1	664	6	US-10-485-517-308	Sequence 308, App
35	174.5	6.1	1035	7	US-11-113-424-20	Sequence 20, Appli
36	174.5	6.1	1052	7	US-11-113-424-22	Sequence 22, Appli
37	171	6.0	588	6	US-10-821-234-1137	Sequence 1137, Ap
38	166	5.8	480	7	US-11-109-156-18	Sequence 18, Appli
39	165.5	5.8	833	6	US-10-667-295-102	Sequence 102, App
40	165.5	5.8	839	6	US-10-667-295-101	Sequence 101, App
41	165.5	5.8	1196	6	US-10-667-295-100	Sequence 100, App
42	163.5	5.8	1255	7	US-11-022-562-213	Sequence 213, App
43	162	5.7	348	6	US-10-661-426-9	Sequence 9, Appli
44	162	5.7	348	6	US-10-661-426-14	Sequence 14, Appli
45	161.5	5.7	1338	6	US-10-821-234-1622	Sequence 1622, Ap

ALIGNMENTS

RESULT 1
US-10-420-192-8
; Sequence 8, Application US/10420192
; Publication No. US20050260579A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Xiao-Fan
; APPLICANT: Weinberg, Robert A.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: TGF-Beta Type Receptor cDNAs Encoded Products and Uses
; FILE REFERENCE: 0399.1086-022
; CURRENT APPLICATION NUMBER: US/10/420,192
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US 09/584,929
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 08/446,936
; PRIOR FILING DATE: 1995-05-23
; PRIOR APPLICATION NUMBER: US 08/311,703
; PRIOR FILING DATE: 1994-09-23
; PRIOR APPLICATION NUMBER: US 07/786,063
; PRIOR FILING DATE: 1991-10-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; TYPE: PRT
; LENGTH: 567
; ORGANISM: genomic
US-10-420-192-8

Query Match	19.8%;	Score 561.5;	DB 6;	Length 567;
Best Local Similarity	29.1%;	Pred. No. 8.5e+46;		
Matches 144;	Conservative 104;	Mismatches 195;	Indels 51;	Gaps 13;
QY	63	CSGHCPDAINNTCTINGH-CFAIIEEDDQGGTTLTSGC--MKYEGSDPCKD--SPKQAQ	117	
Db	67	CMNSC--SITICEKPEQVCVAVVRKNDN-ITLETVCNDPKLPVHDFILEDAASPCKI	122	
QY	118	LRRTE-----CCTNLCNOYL-----OPTLPVVGIPFGDSVRLAVLISM	160	
Db	123	MKEKKKPGETTFMPCSSCDNDNIFSEYNTSNPDLLLVI-----QVTGISLLPPL	176	
QY	161	AVCIAMIVFESSCFCKYCKYKISSRGRVNRDL--QDEAFIPVGESLKDLDQSSGSS	218	
Db	177	GVAISVIIIF-----YCYVRNRQOKLSSTWETGTRKLMFESEHCAIILEDORSDL	228	
QY	219	SGSLPLLQVORTIAKIQMVVRQVKGKRYGEVMMKWRG-----EKVAVKVFFTTEASWF	272	

Db	229	STCANNINHNTELLPIELDTLVGKGRFAEYVYKAKLKQNTSEQFETVAVKIFPYEEYASWK	288
Qy	273	RETEIYQTVLMRHNELGFIADIKGTGSWTQLYLITDYHENGSLYDFLCLKCATLDTLRALL	332
Db	289	TEKDIFSDINLKHENILOFLTAERKTELKGQYWLITAFHAKGNLQEYLTRHVISWEDLR	348
Qy	333	KLAYSAAACGLCHLHTEIYGTQKGP--ATAHRDLKSKNLIILKNGSCCIADLGLAVKFNSD	390
Db	349	KLGSLSLARGIAHLHSD-HTPCGRPKMPIVHRDLKSKNLIILKNDLTLCCCLCDFGLSLURLDPT	407
Qy	391	TNEVDIPLNTRVGTRRYNAPEVDESLSKNHPQPYIMADYIFGLIIEWMARSCITGGIV	450
Db	408	LSVDDLANSQGVGTARYNAPEVLESRMLENAAESFKQTDVYSMALVLWEMTSRCNAVGEV	467
Qy	451	EYEQLPYYNMPSPDSYEDREVCVKRLRPVSNRNSDECLRAVLKLMSCWAHNPA	510
Db	468	KDYEPFGSKVREHPCVSCVMKDNVLDRGRPEIPSPFLNHQGIQMVCTLTTECDWDHDEA	527
Qy	511	RLTALRIKTKTAKM	524
Db	528	RLTAOCVAERFSEL	541

	US-11-109-156-21	
	; Sequence 21, Application US/11109156	
	; Publication No. US20050250144A1	
	; GENERAL INFORMATION:	
	; APPLICANT: Toshio Ota	
	; APPLICANT: Takao Isogai	
	; APPLICANT: Tetsuo Nishikawa	
	; APPLICANT: Koji Hayashi	
	; APPLICANT: Kaoru Otsuka	
	; APPLICANT: Jun-Ichi Yamamoto	
	; APPLICANT: Shizuko Ishii	
	; APPLICANT: Tomoyasu Sugiyama	
	; APPLICANT: Ai Wakamatsu	
	; APPLICANT: Keiichi Nagai	
	; APPLICANT: Tetsuji Otsuki	
	; APPLICANT: Shin-Ichi Funahashi	
	; APPLICANT: Chiaki Senoo	
	; APPLICANT: Jun-Ichi Nezu	
	; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN	
	; FILE REFERENCE: 06501-089002	
	; CURRENT APPLICATION NUMBER: US/11/109,156	
	; CURRENT FILING DATE: 2005-04-19	
	; PRIOR APPLICATION NUMBER: US/10/060,065	
	; PRIOR FILING DATE: 2002-01-29	
	; PRIOR APPLICATION NUMBER: PCT/JPO0/05061	
	; PRIOR FILING DATE: 2000-07-28	
	; PRIOR APPLICATION NUMBER: US 60/159,590	
	; PRIOR FILING DATE: 1999-10-18	
	; PRIOR APPLICATION NUMBER: US 60/183,322	
	; PRIOR FILING DATE: 2000-02-17	

	RESULT 2	
	US-11-186-283-2	
	; Sequence 2, Application US/11186283	
	; Publication No. US2005025520A1	
	; GENERAL INFORMATION:	
	; APPLICANT: Raju, Jeyaseelan	
	; TITLE OF INVENTION: NOVEL CARK PROTEIN AND NUCLEIC ACID MOLECULES AND USES	
	; FILE REFERENCE: MNI-068CP2	
	; CURRENT APPLICATION NUMBER: US/11/186,283	
	; CURRENT FILING DATE: 2005-07-21	
	; PRIOR APPLICATION NUMBER: US/10/626,173	
	; PRIOR FILING DATE: 2003-07-24	
	; PRIOR APPLICATION NUMBER: US/09/947,199A	
	; PRIOR FILING DATE: 2001-09-05	
	; PRIOR APPLICATION NUMBER: US 60/111,938	
	; PRIOR FILING DATE: 1998-12-11	
	; PRIOR APPLICATION NUMBER: US 09/291,839	
	; PRIOR FILING DATE: 1999-04-14	
	; PRIOR APPLICATION NUMBER: US 09/458,457	
	; PRIOR FILING DATE: 1999-12-10	
	; NUMBER OF SEQ ID NOS: 9	
	; SOFTWARE: Patentin Ver. 2.0	
	; SEQ ID NO 2	
	; LENGTH: 835	
	; TYPE: PRP	
	; ORGANISM: Homo sapiens	
	US-11-186-283-2	

Matches	87; Conservative	67; Mismatches	116; Indels	72; Gaps	14;
Qy	204	ESLKLDIDOSQSGSGSL-----PLLVORTIA-----	KQIQMVRQVQKGRY	245	
Db	147	ENLMQLVEHYTSDADGLCTRLIIPKVMEGTVAADFEYRSGWALNNKELKLLQTIGKGEF	206		
Qy	246	GEYVMGKWRGEKVAVKVFFFTTEESAFRETEIYQTVLMRHNILGFIAADIKGTGSWTQL	305		
Db	207	GDVWLGDYRGNKVAVKCIKNDATAQAFLAEASVMTQL-RHSNLVQLLVIVEEKG--L	262		
Qy	306	YLITDTHENGSLYDFLKC-----ATLDTRALLLKLAYSAAAGLCHLUHTEIYGTQGKPAATAHRD	362		
Db	263	YIVTEYMAKGSVDYLRSRGRSVLGGDCLLKFSLD-----VCEAMEYLEGNN-----FVHRD	314		
Qy	363	LKSKNLIILKNGSCCTADIGLAVKFNSDINEVDIPLNTRVGTTRYNAPEVLDESLSKNHF	422		
Db	315	LAARNVLVSDNNVAKVSDFDGLTKEASTQDTGKLPV-----KWTAPEALREKKFST--	365		
Qy	423	QPYIMADIYSFGLIIWEMARRCITGIVEEYQLPYPYNNVPSDPSYEDMREVVVCVKRLRPI	482		
Db	366	----KSDVMSFGILLWE-----IYSGFRVPY----PRIP-----LKDVV-----PR	398		
Qy	483	VSNRWNDSDE---CLRAVLKLMSCWAHNPNASRLTALRIKKTLL	521		
Db	399	VEKGYKMDADPGCPPPAVYEVNKCNCWHLDAAMRPSFLQLRQOL	440		

Query Match 10.1%; Score 287; DB 7; Length 450;
Best Local Similarity 25.4%; Pred. No. 7.1e-20;

Db 569 DVAKGMEYLHNL---TQ---PIIHRDLNSHNILLYEDGHAVVADFGES-REFLOSLEDN- 620
Qy 397 PLNTRVGTTRYMAPEVLDESLSKNHFQPYIMADIYSFGLIIEWMARRCITGGIVEEYQLP 456
Db 621 -MTKQPGNLRWMAPEVFTQCTRYT-----IKADVFSYALCLWEI-----LTG-----EIP 664
Qy 457 YNMV-----SDPSYEDMREWCVKRLRPV-----NRWNS-----DECLRAVLKLMSECV 504
Db 665 FAHLKPAAAAADMAVHHIRPPIGYSIPKPISSLLIRGNWACBGRPEFSEVVMKL-EECL 723
Qy 505 AH-----NPAS 510
Db 724 CNIELMSPAS 733

RESULT 4
US-11-186-283-8
; Sequence 8, Application US/11186283
; Publication No. US2005025520A1
; GENERAL INFORMATION:
; APPLICANT: Raju, Jeyaseelan
; TITLE OF INVENTION: NOVEL CARP PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MNI-068CP2
; CURRENT APPLICATION NUMBER: US/11/186,283
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/626,173
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: US/09/947,199A
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/111,938
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 09/291,839
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/458,457
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 835
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-186-283-8

Query Match 8.5%; Score 242; DB 7; Length 835;
Best Local Similarity 26.0%; Pred.No. 3.2e-15;
Matches 98; Conservative 65; Mismatches 112; Indels 102; Gaps 21;
Qy 189 YNRDLEQDEAFIPVGSLSKDLIDQSOSGSGSL-----PLLVQRTIAK----- 232
Db 404 YKRQEE-----LPCNE-----YSQPGDGSYVSPSLGKIKSWTKKADVLLRLAEL 452
Qy 233 -----QIQMROVGRGVEVMGKRWKGEKAVK-----VFTTEASWF-RETEI 277
Db 453 PSRFLQLSEIEFHEIIGSGSGFKVYKGRNKIVAIKRYRANTYCSKSDVDMFCREVSI 512
Qy 278 YQTVLMRHNILGFIAADIKGTGWTQLYLITDYHENGSLYDFL--KCATLDTALLKLA 335
Db 513 --LCQLNHPCVQVQVGCALDDP---SQFAIVTYIGSGSLFLLHQBQKRLDLQSKLIITA 567
Qy 336 YSAACGLCHLHTEIYQTKPAIAHRDLKSKNLIKNGSCCIAADLGLAVKFNSTNVEVD 395
Db 568 VDVAKGMEYLHSL--TQ---PIIHRDLNSHNILLYEDGHAVVADFGES-REFLOSLEDN 620
Qy 396 IPLNTRVGTTRYMAPEVLDESLSKNHFQPYIMADIYSFGLIIEWMARRCITGGIVEEYQL 455
Db 621 ---MTKQPGNLRWMAPEVFTQCTRYT-----IKADVFSYSLCLWEL-----LTG-----EI 663
Qy 456 PYNMV-----SDPSYEDMREWCVKRLRPV-----NRWNS-----DECL 493
Db 664 PPAHLKPAAAAADMAVHHIRPPIGYSIPKPISSLLIRGNWACBGRPEFSEVVMKLEBCL 723

Qy 494 RAVLKLMSCEWAhNPAS 510
Db 724 CNV-ELMS-----PAS 733
RESULT 5
US-11-021-441-18
; Sequence 18, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKI, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 282172003900
; CURRENT APPLICATION NUMBER: US/11/021,441
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/616,750
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/615,287
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US 60/599,377
; PRIOR FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: PCT/US2004/23881
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US 10/883,599
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/556,744
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-441-18

Query Match 8.5%; Score 241.5; DB 7; Length 456;
Best Local Similarity 24.4%; Pred.No. 1.5e-15;
Matches 97; Conservative 70; Mismatches 156; Indels 75; Gaps 18;
Qy 154 LAVLSMAVCIVAMIVFSSCFYKHYCKSISSRGYNRDLQO--DEAFIPVGSLSKDL-- 209
Db 15 LAVIGGVAVGVLLLVLAGVGFIIH-----RRRNQARQSPEDVYFSKSEQLKPLKT 67
Qy 210 -IDQSQSSGSGSLPLVQRTIAKQIQMROVGRGVEVMG--KWRGKAVAVKYVFTT 266
Db 68 YVDPTHYEDPNQAVLKFTTEIHPSCVTRQKVIGAGEFGEVYKGLTKTSSGKKEVPVAIKT 127
Qy 267 EASWFRTEIYQTVLMRHNILGFIA---ADIKGT-GSWTQLYLITDYHENGSLYDFL 321
Db 128 LKAGY---TEKQVDFLGEAGIMGQFSHHNIIRLEGVISKYKPMIITEYMGALDKFL 184
Qy 322 --KCATLDTALLKLAYSNACGLCHLHTEIYQTKPAIAHRDLKSKNLIKNGSCCIA 379
Db 185 REKGEFSLVQLVGMRLGRTAGMKYLANNNY-----VHRDLAARNILVNSLVCKVVS 236
Qy 380 DLGLAVKFNSD-----TNEVDIPLNTRVGTTRYMAPEVLDESLSKNHFQPYIMA-DIYS 432
Db 237 DFGLSRVLEDDPEATYTTSGGKIPI-----RWTAPEAIS-----YRKFTSADSVMS 282
Qy 433 FGLIIEWMARRCITGGIVEEYQLYPNMVPSPDSYEDMREWCVKRL-RPIVSNRWNSDE 491
Db 283 FGIWMVEV---MTYG-----ERYWEL----SNHEVMKAIINDGFRLLPTM-----D 321
Qy 492 CLRAVLKLMSCEWAhNPASRLTALRIKKTAKWVESQD 529
Db 322 CPSAIYQLMMQCMQOERARRPKFADIVSLDKLIRAPD 359

RESULT 6
US-11-021-441-4
; Publication 4, Application US/11021441
; Publication NO. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKY, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 282172003900
; CURRENT APPLICATION NUMBER: US/11/021,441
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/616,750
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/615,287
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US 60/599,377
; PRIOR FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: PCT/US2004/23881
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US 10/883,599
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/556,744
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1035
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein
US-11-021-441-4

Query Match 8.5%; Score 241.5; DB 7; Length 1035;
Best Local Similarity 24.4%; Pred. No. 4.8e-15;
Matches 97; Conservative 70; Mismatches 156; Indels 75; Gaps 18;

Qy 154 LAVLISMVAVICVAMIVFSCFCYKHYCKYSISRGYRNDRLEQ--DEAFIPVGESLKDL-- 209
Db LAVIGVAVGVVLLVLVAGVGFFH-----RRRNQARQSPEDVYFSKQKPLKT 646

Qy 210 -IDQSQSSGSGGLPVLVQRTIAKQIQMVQVQKGRYGEVWMG--KWRGEKVAVKVFVTT 266
Db YVDPHTYEDPNQAVLKFTEIHPSCVTRQKQVIGAGEFGEVYKGLKTSKGKKEVPVAIKT 706

Qy 267 EASWFRTEIYQTVLMRHENILGFIA----ADIKGT-GSWTQLYLITDYHENGSLYDPL 321
Db LKAGY---TEKQVDFLGBAGIMGQFSSHNIIRLEGVISKYKPMIITEYMENGALDKPL 763

Qy 322 --KCATLDRALLKLAYSAAACGLCHLHTEIYGTQKPAIAHRLDKSKNLIKNGSCCIA 379
Db REKDEGFSVLQVGLRGIAAGKYLANNY-----VHRDLAARILVNLSLVCKVS 815

Qy 380 DLGLAVKFNDS-----TNEVDIPLNTRVGTTRYMAPEVLDSELSKNHFQPYIMA-DIYS 432
Db DFLSLRVLEDDPEATYTTSGGKIPI-----RWTAPPAIS-----YRKFTSASDWS 861

Qy 433 FGLLIWEMARRCITGGIVVEYQOLPYNNVMPSPDSYEDMRREVVCVRL-RPIVSNRWNSDE 491
Db FGIWMEV-----MTYG-----BRPYWEL-----SNHEVMKAINDGFRLPTPM-----D 900

Qy 492 CLRAVLKLMSECAHNPASRLTALRIKKTAKWVESQD 529
Db CPFAIYQLMMQCQOERARRPKFADIVSILDKLIRAPD 938

RESULT 7
US-11-109-156-17
; Sequence 17, Application US/11109156

Publication No. US20050250144A1
; GENERAL INFORMATION:
; APPLICANT: Toshio Ota
; APPLICANT: Takao Isogai
; APPLICANT: Tetsuo Nishikawa
; APPLICANT: Koji Hayashi
; APPLICANT: Kaoru Otsuka
; APPLICANT: Jun-ichi Yamamoto
; APPLICANT: Shizuko Ishii
; APPLICANT: Tomoyasu Sugiyama
; APPLICANT: Ai Wakamatsu
; APPLICANT: Keiichi Nagai
; APPLICANT: Tetsuji Otsuki
; APPLICANT: Shin-ichi Funahashi
; APPLICANT: Chiaki Senoo
; APPLICANT: Jun-ichi Nezu
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
; TITLE OF INVENTION: PHOSPHATASE
; FILE REFERENCE: 06501-099002
; CURRENT APPLICATION NUMBER: US/11/109,156
; CURRENT FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: US/10/060,065
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05061
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 17
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-109-156-17

Query Match 8.4%; Score 238; DB 7; Length 648;
Best Local Similarity 29.2%; Pred. No. 5.3e-15;
Matches 84; Conservative 56; Mismatches 88; Indels 60; Gaps 18;

Qy 231 AKQIQMVQVQKGRYGEVWMGKWRGEKVAVKVF-----TTEASWFRTEIYQTVLMRHE 286
Db ASEVMLSTRIGSGSGFTYKYGKWHGD-VAVKILKVVDPTPEQQAFR-NEVAVLKRTRHV 403

Qy 287 NIL---GFIAADIKGTGSGWTQLYLITDYHENGSLYDLKCATLDR---ALLKLAYSAA 339
Db NILFMGWTMD-----NLAIVTQMGESSLYKHLH--VQETKFMQFQIDIRQTA 453

Qy 340 CGLCHLHTEIYGTQKPAIAHRLDKSKNLIKNGSCCIAADGLA-VKFN-SDTNVEVDIP 397
Db QGMDYLHAK-----NIIHRDMKSNNI FLHEGLTVKIGDFGLATVKSRSQSQVEQP 505

Qy 398 LNRVGTTRYMAPEVLDSELSKNHFQPYIMADIYFGLIIEWEMARRCITGGIVVEYQOLPY 457
Db ---TGSVLWMAPEVI-RMQDNNPFS--FQSDVYSYGVLYVEL-----MTG-----ELPY 548

Qy 458 YNMVSPDSPSYEDMRREVVCVKR--LRPIVSNRWNSDECLRAVLKLMSEC 503
Db SHINNRD-----QIIFWVGRGYASPDLSKLYKN--CPKMKRLVADC 588

RESULT 8
US-10-990-276-1
; Sequence 1, Application US/10990276

[illegible]

```

; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 984
; TYPE: PRP
; ORGANISM: Rattus norvegicus
US-11-113-424-60

Query Match      8.1%; Score 228.5; DB 7; Length 984;
Best Local Similarity 20.9%; Pred.No. 7.7e-14;
Matches 102; Conservative 74; Mismatches 144; Indels 169; Gaps 22;

QY      82 CFAIIEEDQGEGTTLTSGCMKYEGSDFOCKDPSKAQLRRITTECRNLGNQYLQPLPPV 141
        ||| :||| :
Db       522 CFQTLLDDDY-----KSELRQL-----539

QY      142 VIGPFDFGDSVRWLAVLISMAVCIVAMIVFSSCFXYKHCKYSISSRGYRNRLDEQDEAFIP 201
        ||| |
Db       540 ---PIATGSA-----AAGVFVVVSIVAISTVC-----SRKPAYSKEAVVYSDKI---579

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202	Qy	VGESLKDLIQSSSGSGS-GLPLVLQ-----RTIAKOI-----QMVQVQVKGR 244
		: : : : : : : : : : : : : : :
580	Db	-----QHYSTGRGSPGMKIYIDPFTVEDPNEAVREFAKEIDVSVFKVIEEVIGAGE 629
		: : : : : : : : : : : : : : :
245	Qy	YGEVVMGKWR--GEK--VAVKV-----PFTTEEASWERETEYQTVLMRHENILGFIAD 295
		: : : : : : : : : : : : : : :
630	Db	FGEVYKGRUKLPFGKEEIVAKTKAGYSEKQRDFLSEASINGO--FDHPNIIIRLEGV 687
		: : : : : : : : : : : : : : :
296	Qy	IKGTGSWTQYLITDYHENGSLYDFLK--CATLDTRALLKLAYSAAAGCLHLHTEIYGTQ 353
		: : : : : : : : : : : : : : :
688	Db	TKS-----RPVMIITEFMENGALDSFLRQNDQFTVIQVGMRLGIAAGMKYIASENNY--- 740
		: : : : : : : : : : : : : : :
354	Qy	GKPAIAHRDLKSKNLIKNGSGCCIALGLAVKFNSTNEVDIPLNTRVGTR--RYMAP 410
		: : : : : : : : : : : : : : :
741	Db	-----VHRDLAARNILVNSNLVCKVSDPGLSRYLQDDTS--DPTYTSSLGGKIPVRWTAP 793
		: : : : : : : : : : : : : : :
411	Qy	EVLDESLSKNHFQPYIMA-DIYSGLIWE-----MARRCITGGIVEEYOLPY 458
		: : : : : : : : : : : : : : :
794	Db	EAI-----AYRKFTSASDWYSGYVWVWVMSFGERPYWDMNQDVINAISODYRLP-- 844
		: : : : : : : : : : : : : : :
459	Qy	NNVPSPDPSYEDMREYVVCVKRLRPIVSNRWNDSDECLRAVLKLMSECWAHNPASRLTALRIK 518
		: : : : : : : : : : : : : : :
845	Db	--PPMD-----CPAALHQLMLDCQKQKORNSRPFPAEIV 875
		: : : : : : : : : : : : : : :
519	Qy	KTAKKVES 527
		: : : : : : : : : : : : : : :
876	Db	NTLDKMRN 884
		: : : : : : : : : : : : : : :

```

RESULT 11
US-11-113-424-62
; Sequence 62, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gargolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 995
; TYPE: PRT
; ORGANISM: Gallus gallus
US-11-113-424-62

RESULT 12
US-11-021-441-20
; Sequence 20, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKY, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 282172003900
; CURRENT APPLICATION NUMBER: US/11/021,441
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/616,750
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/615,287
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US 60/599,377
; PRIOR FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: PCT/US2004/23881
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US 10/883,599
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/556,744
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein
US-11-021-441-20

```

Qy		200	IPVGESUKDLIDQSQSSGSG-----SGLPLLVO-----RTIAKIQIM-----VRQV- 240
Db		585	-----EYTDKLQHVTSGHMTGPMKIYIDPFTYEDPNEAVREPAKEIDISCVKIEQVI 636
Qy		241	GKGREYGWVG--KWGEK-----VAVKVP---PTTEEASWPTEIYQTVLM---RHENIL 289
Db		637	GAGEFGEVCGHLKPKGREIFAIKTKSGYTEKQ-----RRDFLSEASIMGQFDHPNVI 692
Qy		290	GFTAADIKGTGSWTQLVLIIDYHENGSLYDFLK--CATLDTRALLKLAYSAAACGLCHLT 347
Db		693	HLEGVTKS-----SPVMIIETFMENGSLDSFLRQNDQOFTVIQVGMRLGIAAGMKYLAD 748
Qy		348	EIYGTQGPALAHRLDKSNLIIKNGSCCIADIGLAVKFNSDTNEVDIPLNTRVGTR-- 405
Db		749	MNY-----VHRDLAARNILVNSNLVKVSDFGLSRFLEDDTS--DPTYTALSUGGKPI 798
Qy		406	-RYMAPEVLDESLSKNHFQPIMA-DIYSFGLLITWEMARRCITGGIVBEYQOLPYYNMVP 463
Db		799	IRWTAPEAI-----QYRKPTSASDVMSYGIWNVE-----VMSGEPYPWDMTNQ 842
Qy		464	DPSYEDRMVVVCVKRLRPVNSRNWSD-----ECLRAVLKJMCSECAWHNPASRLTALR 516
Db		843	D-----VINATEODYRLPPMDPCPNALHQMLMLDCWKORHNRPKFGQ 884
Qy		517	IKKTAKOVES 527
Db		885	IYNTLDKWIEN 895

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RESULT 12
US-11-021-441-20
; Sequence 20, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKY, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 282172003900
; CURRENT APPLICATION NUMBER: US/11/021.441
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/616,750
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/615,287
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US 60/599,377
; PRIOR FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: PCT/US2004/23881
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US 10/883,599
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/556,744
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein
US-11-021-441-20

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Db 56 KH--ADLEHRRRNQARQSPEDVYFSKSQLKPLKTYVDPHTYEDPNQAVLKFTTEIHP 113
QY 232 KOIQMVROVQGRYGEVWVG--KWRGKAVKVFVFTTEASWFRTEIYQTVLMRHNIL 289
Db 114 SCVTRQKVGAGFGEVYKGMKLTSSOKKEVPVAIKTKAGY---TEKQRVDFLGEAGIM 170
QY 290 GFIA----ADIKGT-GSWTQLYLITDYHENGSLYDFL--KCATLDRALLKLAYSAAACGL 342
Db 171 GQFSHHNIIRLEGVISKPMIITEYMGALDKFLREKDGESFVLQVLGMLRGIAAGM 230
QY 343 CHLHTEYGTQGRPAIAHRLKSKNLIKNGSCCTADLGLAVKFNDS-----TNEVDI 396
Db 231 KYLANMNY-----VHRLAARNILVNSLVCKVDFGLSRVLEDDPEATYTTSGGKI 282
QY 397 PLNTRVGTTRYMAPEVLDESLSKNHFQYIMA-DIYSFGLIIEWEMARRCITGIVEYQOL 455
Db 283 PI-----RWTAPEAIS-----YRKFTSASDVMSFGIWMVEV-----MTYG-----ER 319
QY 456 PYNMVPSDPSYDMREVVCVKRL-RPIVSNRNWNSDECLRAVLKLMSECAHNPASRLTA 514
Db 320 PYWEL-----SNHEVMKAINDFRLPTPM-----DCPSAIYQLMMQWQQRARRPKF 367
QY 515 LRIKTKLAKMVESQD 529
Db 368 ADIVSILDKLIRAPD 382

RESULT 13
US-11-021-441-22
; Sequence 26, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKY, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
; FILE REFERENCE: 282172003900
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/616,750
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/615,287
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US 60/599,377
; PRIOR FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: PCT/US2004/23881
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US 10/883,599
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/556,744
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein
US-11-021-441-22

Query Match 7.8%; Score 222; DB 7; Length 490;
Best Local Similarity 24.3%; Pred. No. 1.2e-13;
Matches 89; Conservative 63; Mismatches 146; Indels 68; Gaps 17;
QY 186 RGRYNRDLEQ--DEAFIPVGESLKDL---IDQSQSSGSGGLPLLIVQRTIAQIQMVROV 240
Db 64 RRRKNQARQSPEDVYFSKSQLKPLKTYVDPHTYEDPNQAVLKFTTEIHPSCVTRQKVI 123
QY 241 KGGRYGEVWVG--KWRGKAVKVFVFTTEASWFRTEIYQTVLMRHNILGFIA----A 294

Db 124 GAGEFGEVYKGMKLTSSGKKEVPVAIKTKAGY---TEKQRVDFLGEAGIMQFSHHNI 180
QY 295 DIKGT-GSWTQLYLITDYHENGSLYDFL--KCATLDRALLKLAYSAAACGLCHLHTEIYG 351
Db 181 RLEGVISKYKPMIITEYMGALDKFLREKDGESFVLQVLGMLRGIAAGMKYLANMNY- 239
QY 352 TQCKPAIAHRLKSKNLIKNGSCCTADLGLAVKFNDS-----TNEVDIPLNTRVGTG 405
Db 240 -----VHRDLAARNILVNSLVCKVDFGLSRVLEDDPEATYTTSGGKIPI----- 285
QY 406 RYMAPEVLDESLSKNHFQYIMA-DIYSFGLIIEWEMARRCITGIVEYQOLPYNMVPSD 464
Db 286 RWTAPEAIS-----YRKFTSASDVMSFGIWMVEV-----MTYG-----ERPWE 325
QY 465 PSYEDMREVVCVKRL-RPIVSNRNWNSDECLRAVLKLMSECAHNPASRLTALRIKTKLAK 523
Db 326 SNHEVMKAINDFRLPTPM-----DCPSAIYQLMMQWQQRARRPKFADIVSILDK 377
QY 524 MVESQD 529
Db 378 LIRAPD 383

RESULT 14
US-11-021-441-22
; Sequence 22, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKY, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
; FILE REFERENCE: 282172003900
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/616,750
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/615,287
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US 60/599,377
; PRIOR FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: PCT/US2004/23881
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US 10/883,599
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/556,744
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein
US-11-021-441-22

Query Match 7.8%; Score 222; DB 7; Length 497;
Best Local Similarity 24.3%; Pred. No. 1.2e-13;
Matches 89; Conservative 63; Mismatches 146; Indels 68; Gaps 17;
QY 186 RGRYNRDLEQ--DEAFIPVGESLKDL---IDQSQSSGSGGLPLLIVQRTIAQIQMVROV 240
Db 71 RRRKNQARQSPEDVYFSKSQLKPLKTYVDPHTYEDPNQAVLKFTTEIHPSCVTRQKVI 130
QY 241 KGGRYGEVWVG--KWRGKAVKVFVFTTEASWFRTEIYQTVLMRHNILGFIA----A 294
Db 131 GAGEFGEVYKGMKLTSSGKKEVPVAIKTKAGY---TEKQRVDFLGEAGIMQFSHHNI 187

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 06:01:23 ; Search time 40 Seconds
(without alignments)
1279.683 Million cell updates/sec

Title: US-10-600-645-2

Perfect score: 2838

Sequence: 1 MTQLYTYIRLLGACLFIIISH.....TALRIKTKLAKMVESQDVKI 532

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2838	100.0	532	2 JC2387	bone morphogenetic
2	2823	99.5	532	2 A56238	bone morphogenetic
3	2769	97.6	532	2 I37163	ALK-3 - human
4	2223	78.3	527	2 A54985	BMP receptor precu
5	1934.5	68.2	502	2 JC2491	serine/threonine k
6	1933.5	68.1	502	2 A53444	activin receptor-1
7	1926	67.9	502	2 A56683	receptor protein k
8	1274	44.9	503	2 JC2061	transforming growt
9	1274	44.9	509	2 I45713	Dpp receptor TKV,
10	1268	44.7	499	2 JC2062	transforming growt
11	1268	44.7	503	2 A49432	activin receptor-1
12	1208.5	42.6	440	2 A56693	receptor protein k
13	1204.5	42.4	509	2 A45992	activin A receptor
14	1198	42.2	601	2 A55921	serine/threonine k
15	1194	42.1	509	2 A49664	activin type I rec
16	1190.5	41.9	509	2 I59576	transforming growt
17	1184	41.7	505	2 I38959	activin A receptor
18	1180	41.6	505	2 I53417	type I serine-thre
19	1114	39.3	503	2 A49431	activin/TGF-beta-1
20	1093	38.5	502	2 JC4337	activin receptor l
21	1080	38.1	502	2 I48241	ALK-1 - mouse
22	1050	37.0	570	2 I45712	Dpp receptor SAX p
23	1047	36.9	476	2 I80182	activin type I rec
24	896	31.6	487	2 I80183	activin type I rec
25	754	26.6	247	2 FC4260	activin type I rec
26	751.5	26.5	636	2 T15734	hypothetical prote
27	686	24.2	514	2 JQ1317	activin receptor p
28	674.5	23.8	512	2 S21171	activin receptor S
29	665	23.4	513	2 A39896	activin receptor p

RESULT 1

JC2387

bone morphogenetic protein type IA receptor precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Oct-2004

C;Accession: JC2387

R;Takeda, K.; Oida, S.; Ichijo, H.; Iimura, T.; Maruoka, Y.; Amagasa, T.; Sasaki, S.

Biochem. Biophys. Res. Commun. 204, 203-209, 1994

A;Title: Molecular cloning of rat bone morphogenetic protein (BMP) type IA receptor and

A;Reference number: JC2387; MUID:95032096; PMID:7945360

A;Accession: JC2387

A;Molecule type: mRNA

A;Residues: 1-532 <TAK>

A;Cross-references: UNIPROT:Q64308; UNIPARC:UPT000008BA68; DBJ:D38082; NID:gl398909; P

C;Keywords: ATP; glycoprotein; receptor; transmembrane protein

F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-527/Product: bone morphogenetic protein type IA receptor #status predicted <BMP>

F;153-175/Domain: transmembrane #status predicted <TM>

F;232-528/Domain: protein kinase homology <KIN>

F;236-527/Region: kinase domain

F;240-248/Region: protein kinase ATP-binding motif

F;73/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 2838; DB 2; Length 532;

Best Local Similarity 100.0%; Pred. No. 8.7e-145;

Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMSKSDVDQKPKENGVTLPAPDTPFLK 60

Db 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTGMSKSDVDQKPKENGVTLPAPDTPFLK 60

QY 61 CYCSGHCPCPDANNTCITNGHCFATIEEDDQGETTLTSGCMKYEGSDFQCKSPKQLR 120

Db 61 CYCSGHCPCPDANNTCITNGHCFATIEEDDQGETTLTSGCMKYEGSDFQCKSPKQLR 120

QY 121 TIECCRTNLCNQYLQPTLPVVGPPFDGSRVRLAVLISMAVCIVAMIVSSFCYKHYC 180

Db 121 TIECCRTNLCNQYLQPTLPVVGPPFDGSRVRLAVLISMAVCIVAMIVSSFCYKHYC 180

QY 181 KSISSRGRNRLDQDEARFIPVGESLKDLDQSSGSGSGLPLLVORTIAKQIQWROV 240

Db 181 KSISSRGRNRLDQDEARFIPVGESLKDLDQSSGSGSGLPLLVORTIAKQIQWROV 240

QY 241 GKRGYGEVVMGKRGKAVKVFVFTTEASWPRETEIYQTVLMRHNILGFIAADIKGTG 300

Db 241 GKRGYGEVVMGKRGKAVKVFVFTTEASWPRETEIYQTVLMRHNILGFIAADIKGTG 300

QY 301 SWTQLYLIIDYHENGSLYDFLKCATLDTALLKLAYSACGLCHLHTEIYGTGCKPAIAH 360

Db 301 SWTQLYLIIDYHENGSLYDFLKCATLDTALLKLAYSACGLCHLHTEIYGTGCKPAIAH 360

QY 361 RDLKSKNILLKNGSCCIIADLGLAVKFNSDTNEVDIPLNTRVTRTRYMAPEVLDLSKN 420

ALIGNMENTS

Db 361 RDLKSKNLIKKNGSCCIADLGLAVKFNSDTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
QY 421 HFQPYIMADIYFGLIIWEMARRCITGGIVEYQLPYNNMVPSPSYEDMRVVCVKRLR 480
Db 421 HFQPYIMADIYFGLIIWEMARRCITGGIVEYQLPYNNMVPSPSYEDMRVVCVKRLR 480
QY 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKTKLAKMVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKTKLAKMVESQDVKI 532
RESULT 2
A56238
bone morphogenetic protein receptor BRK-1 precursor - mouse
N:Alternate names: ALK-3 protein; BMP receptor
C:Species: Mus musculus (house mouse)
C:Date: 03-Oct-1995 #sequence revision 03-Oct-1995 #text_change 31-Dec-2004
C:Accession: A56238; B56238; S40158; I48242; I49543
R:Koenig, B.B.; Cook, J.S.; Wolsing, D.H.; Ting, J.; Tiesman, J.P.; Correa, P.E.; Olson, M.O. Cell. Biol. 14, 5961-5974, 1994
A:Title: Characterization and cloning of a receptor for BMP-2 and BMP-4 from NIH 3T3 cell
A:Reference number: A56238; MUID:94344106; PMID:8065329
A:Accession: A56238
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-532 <KOE>
A:Cross-references: UNIPROT:P36895; UNIPARC:UPI000000B293; GB:U04672; NID:G538362; PIDN:
A:Accession: B56238
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-431, 'VSNSQVPVK' <K02>
A:Cross-references: UNIPARC:UPI000000B293; GB:U04673; NID:G538364; PIDN:AAA21515.1; PID:
A>Note: neither protein nor nucleotide sequence is given; it is unclear whether this cld
R:Miyazono, K.; Moren, A.; Grimsby, S.; Ichijo, H.; Heldin, C.; ten Dijke, P.
submitted to the EMBL Data Library, June 1993
A:Description: ALK-3 and ALK-6: the closely related members in the serine/threonine kin
A:Reference number: S40158
A:Accession: S40158
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-532 <MY>
A:Cross-references: UNIPARC:UPI000000B293; EMBL:Z23154; NID:G437868; PIDN:CAA80678.1; PI
R:Dewulf, N.; Verschueren, K.; Lonnoy, O.; Moren, A.; Grimsby, S.; Vande Spieghele, K.; Mi
Endocrinology 136, 2652-2663, 1995
A:Title: Distinct spatial and temporal expression patterns of two type I receptors for b
A:Reference number: I48241; MUID:95269711; PMID:7750489
A:Accession: I48242
A>Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-532 <RES>
A:Cross-references: UNIPARC:UPI000000B293; EMBL:Z23154; NID:G437868; PIDN:CAA80678.1; PI
R:Suzuki, A.; Thies, R.S.; Yamaji, N.; Song, J.J.; Wozney, J.; Murakami, K.; Kung, H.
Proc. Natl. Acad. Sci. U.S.A. 91, 10255-10259, 1994
A:Title: A truncated bone morphogenetic protein receptor affects dorsal-ventral patterni
A:Reference number: I49543; MUID:195024092; PMID:7937936
A:Accession: I49543
A>Status: translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-532 <RE2>
A:Cross-references: UNIPARC:UPI000000B293; GB:D16250; NID:G577633; PIDN:BA003769.1; PID:
C:Keywords: ATP; phosphotransferase; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:232-528/Domain: protein kinase homology <KIN>
F:240-248/Region: protein kinase ATP-binding motif
Query Match 99.5%; Score 2823; DB 2; Length 532;
Best Local Similarity 98.9%; Pred. No. 5.5e-144;
Matches 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 1 MTQLYTYIRLLGACLIIFISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPFLK 60
Db 1 MTQLYTYIRLLGACLIIFISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPFLK 60

QY 61 CYCSGHCPPDDAINNTCIINGHCFALIEBDDOGETTTLTSGCMKYEGSDFOCKSPKAQLRR 120
Db 61 CYCSGHCPPDDAINNTCIINGHCFALIEBDDOGETTTLTSGCMKYEGSDFOCKSPKAQLRR 120
QY 121 TIECCRTNLCNOYLOPTLPVVGIPFGDSVRWLAVLISMAVCIVAMIVFSSCFCKVHC 180
Db 121 TIECCRTNLCNOYLOPTLPVVGIPFGDSVRWLAVLISMAVCIVAMIVFSSCFCKVHC 180
QY 181 KSISRRGRNDRLEODEAFIPVGESLKDIDQSQSSGSGGLPLLQVORTIAQIQMVROV 240
Db 181 KSISRRGRNDRLEODEAFIPVGESLKDIDQSQSSGSGGLPLLQVORTIAQIQMVROV 240
QY 241 KGGRYGEVVMGKWRGEKVAVKVFPTTEBASWPRETEIYQTVLMRHENILGFTAADIKGTG 300
Db 241 KGGRYGEVVMGKWRGEKVAVKVFPTTEBASWPRETEIYQTVLMRHENILGFTAADIKGTG 300
QY 301 SWTQLYLITDTHENGSLYDFLKCATLDRALLKLAYSAAAGLCHLHTEIYGTQGPAPIAH 360
Db 301 SWTQLYLITDTHENGSLYDFLKCATLDRALLKLAYSAAAGLCHLHTEIYGTQGPAPIAH 360
QY 361 RDLKSKNLIKKNGSCCIADLGLAVKFNSDTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
Db 361 RDLKSKNLIKKNGSCCIADLGLAVKFNSDTNEVDIPLNTRVGTTRYMAPEVLDLSKN 420
QY 421 HFQPYIMADIYFGLIIWEMARRCITGGIVEYQLPYNNMVPSPSYEDMRVVCVKRLR 480
Db 421 HFQPYIMADIYFGLIIWEMARRCITGGIVEYQLPYNNMVPSPSYEDMRVVCVKRLR 480
QY 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKTKLAKMVESQDVKI 532
Db 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKTKLAKMVESQDVKI 532
RESULT 3
I37163
ALK-3 - human
C:Species: Homo sapiens (man)
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Oct-2004
C:Accession: I37163; S37183
R:ten Dijke, P.; Ichijo, H.; Franzen, P.; Schulz, P.; Saras, J.; Toyoshima, H.; Heldin, C.
Oncogene 8, 2879-2887, 1993
A:Title: Activin receptor-like kinases: a novel subclass of cell-surface receptors with
A:Reference number: I37161; MUID:93390967; PMID:8397373
A:Accession: I37163
A>Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-532 <RES>
A:Cross-references: UNIPROT:P36894; UNIPARC:UPI000011D628; EMBL:Z22535; NID:G402186; PI
C:Keywords: ATP
F:232-528/Domain: protein kinase homology <KIN>
F:240-248/Region: protein kinase ATP-binding motif
Query Match 97.6%; Score 2769; DB 2; Length 532;
Best Local Similarity 97.2%; Pred. No. 4.2e-141;
Matches 517; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
QY 1 MTQLYTYIRLLGACLIIFISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPFLK 60
Db 1 MTQLYTYIRLLGACLIIFISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPFLK 60
QY 61 CYCSGHCPPDDAINNTCIINGHCFALIEBDDOGETTTLTSGCMKYEGSDFOCKSPKAQLRR 120
Db 61 CYCSGHCPPDDAINNTCIINGHCFALIEBDDOGETTTLTSGCMKYEGSDFOCKSPKAQLRR 120
QY 121 TIECCRTNLCNOYLOPTLPVVGIPFGDSVRWLAVLISMAVCIVAMIVFSSCFCKVHC 180
Db 121 TIECCRTNLCNOYLOPTLPVVGIPFGDSVRWLAVLISMAVCIVAMIVFSSCFCKVHC 180
QY 181 KSISRRGRNDRLEODEAFIPVGESLKDIDQSQSSGSGGLPLLQVORTIAQIQMVROV 240
Db 181 KSISRRGRNDRLEODEAFIPVGESLKDIDQSQSSGSGGLPLLQVORTIAQIQMVROV 240

QY 241 CGRGYGEVMGKRGKGVAVKVFTEEASWFRTEIYQTVLMRHNILGFIADIKGTG 300
DB 241 CGRGYGEVMGKRGKGVAVKVFTEEASWFRTEIYQTVLMRHNILGFIADIKGTG 300
QY 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAISAACGLCHLHTEIYGTQKPAIAH 360
DB 301 SWTQLYLITDYHENGSLYDFLKCATLDRALLKLAISAACGLCHLHTEIYGTQKPAIAH 360
QY 361 RDLKSKNLIKKNKSGCCCIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSKN 420
DB 361 RDLKSKNLIKKNKSGCCCIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSKN 420
QY 421 HFQPIYIADIVSFGLLIWMARRCITGIVEEYQLPYNNVPSPSYEDMRVVCVKRLR 480
DB 421 HFQPIYIADIVSFGLLIWMARRCITGIVEEYQLPYNNVPSPSYEDMRVVCVKRLR 480
QY 481 PIVSNRNSDECLRAVLKIMSECAHNPASRLTALRIKKTAKWVESQDVKI 532
DB 481 PIVSNRNSDECLRAVLKIMSECAHNPASRLTALRIKKTAKWVESQDVKI 532

RESULT 4
A:54985
C:Species: precursor - African clawed frog
C:Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 31-Dec-2004
C:Accession: A54985
R:Graff, J.M.; Thies, R.S.; Song, J.J.; Celeste, A.J.; Melton, D.A.
Cell 79, 169-179, 1994
A:Title: Studies with a Xenopus BMP receptor suggest that ventral mesoderm-inducing sign
A:Reference number: A54985; MUID:9500777; PMID:7522972
A:Accession: A54985
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-527 <GRA>
A:Cross-references: UNIPROT:Q91578; UNIPARC:UPI00000FD12B; GB:U16654; NID:G609353; PIDN:
C:Keywords: ATP
F:227-523/Domain: protein kinase homology <KIN>
F:235-243/Region: protein kinase ATP-binding motif

Query Match 78.3%; Score 2223; DB 2; Length 527;
Best Local Similarity 80.0%; Pred. No. 6.3e-112;
Matches 423; Conservative 44; Mismatches 52; Indels 10; Gaps 5;

QY 7 YIRLLGACFLIISHVQGNLDSMLHGTGMSKSDVDOKKPENGVTLAPEDTLPLFLKVCYCSGH 66
DB 6 FIACFGALLLVI-HTQGDFFNLPLPHRTGKMSNDPKKQENGVTLAPEDTLPLFLNCYCSGY 64
QY 67 CPDDAINNTCITNGHCFPAIIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAOLRRITIECCR 126
DB 65 CPQNAVNTCITNGOCFAMIEEDDHGDIILTSGCMKNEGSDFOCKDSPKALSRTIECCR 124
QY 127 TNLNQNLYQTLPPVITGPFDDG--SVRLAVLISMAVCIVMIVF--SSCFCKHYCKSI 183
DB 125 TDFCNRLDLEPLSPKI----SDGEYALRFFALIIISLVCLILIVGFTLIITWIKH--KLH 178
QY 184 SSRGRYNRDLQDEAFIPVGSLSKLIIDQSQSGSGGLPLLVQRTIAKQIOMVRQVKG 243
DB 179 SQRLMYNRNLDPPDAFIPAGESLALDIDISQSSGSGGLPLLVQRTIAKQIOMVRQIGKG 238
QY 244 RYGEVMGKWRGKGVAVKVFTEEASWFRTEIYQTVLMRHNILGFIADIKGTGSWT 303
DB 239 RYGEVMGKWRGKGVAVKVFTEEASWFRTEIYQTVLMRHNILGFIADIKGTGSWT 298
QY 304 QLYLITDYHENGSLYDFLKCATLDRALLKLAISAACGLCHLHTEIYGTQKPAIAHRL 363
DB 299 QMYLITEYHENGSLYDFLKCTTLDRSLLKLAISAACGLCHLHTEIYGTQKPAIAHRL 358
QY 364 KSKNLIKKNKSGCCCIADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSKNHFQ 423
DB 359 KSKNLIKKNWTCICADLGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSKNHFQ 418
QY 424 PYIMADIYSFGLIIMWARRCITGIVEEYQLPYNNVPSPSYEDMRVVCVKRLRPV 483

DB 419 AYIMADIYSFGLIIMWARRCITGIVEEYQLPYNNVPSPSYEDMRVVCVKRLRPV 478
QY 484 SNRWNSDECLRAVLKIMSECAHNPASRLTALRIKKTAKWVESQDVKI 532
DB 479 SNRWNSDECLRAVLKIMAECAHNPASRLTALRIKKTAKWVESQDVKI 527

RESULT 5
JC2491
serine/threonine kinase receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Apr-1995 #sequence_revision 26-May-1995 #text_change 05-Oct-2004
C:Accession: JC2491
R:Yamaji, N.; Celeste, A.J.; Thies, R.S.; Song, J.J.; Bernier, S.M.; Goltzman, D.; Lyon
Biochem. Biophys. Res. Commun. 205, 1944-1951, 1994
A:Title: A mammalian serine/threonine kinase receptor specifically binds BMP-2 and BMP-
A:Reference number: JC2491; MUID:95110346; PMID:7811286
A:Accession: JC2491
A:Molecule type: mRNA
A:Residues: 1-502 <YAM>
A:Cross-references: UNIPARC:UPI000008B8DE
C:Keywords: ATP; glycoprotein; transmembrane protein
F:127-148/Domain: transmembrane #status predicted <TM>
F:202-498/Domain: protein kinase homology <KIN>
F:210-218/Region: protein kinase ATP-binding motif
F:284,343,388/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 68.2%; Score 1934.5; DB 2; Length 502;
Best Local Similarity 72.1%; Pred. No. 1.6e-96;
Matches 364; Conservative 60; Mismatches 76; Indels 5; Gaps 5;

QY 29 MLHGTGMSKSDVDOKKPENGVTLAPEDTLPLFLKVCYCSGHCPDDAINNTCITNGHCFPAIIE 88
DB 2 LLRSSG-KLVNVTGKK-EDGEAPTARPKVLCKCHHHCPEDSVNNICSDTGYCFTMIE 59
QY 89 DQGETTLTSGCMKYEGSDFOCKDSPKAOLRRITIECC-RTNLNQNLYQTLPPVITGPF 147
DB 60 DSGTTPVTISGCLGEGSDFOCRDTPIPHQRISIECTERNECNKOLHPTLPKDRDFV 119
QY 148 DGSVRVLAVLISMAVCIVMIVFSSCFCKHYCKSISSRGRYNRDLQDEAFIPVGSLSK 207
DB 120 DGPFIHHKALLISVTVCSL-LLVLIILFCYFRY-KRQEARPRYSIGLEQDETIYPPGESLR 177
QY 208 DLIDQSQSGSGGLPLLVQRTIAKQIOMVRQVKGKRGYGEVMGKWRGKGVAVKVFTE 267
DB 178 DLIEQSQSGSGGLPLLVQRTIAKQIOMVRQVKGKRGYGEVMGKWRGKGVAVKVFTE 237
QY 268 EASWFRTEIYQTVLMRHNILGFIADIKGTGSWTQLYLITDYHENGSLYDFLKCATLD 327
DB 238 EASWFRTEIYQTVLMRHNILGFIADIKGTGSWTQLYLITDYHENGSLYDFLKCATLD 297
QY 328 TRALLKLAISAACGLCHLHTEIYGTQKPAIAHRLKSNILTKNKGSCCIADLGLAVKF 387
DB 298 AKSMLKLAISYSSVGLCHLHTEIFSTQKPAIAHRLKSNILKKNKGTCCIADLGLAVKF 357
QY 388 NSDTNEVDIPLNTRVGTTRRYMAPEVLDLSKNHFQPIYIMADIYSFGLIIMWARRCITG 447
DB 358 ISDTNEVDIPLNTRVGTTRRYMAPEVLDLSNTHFQSYIMADMWYSFGLIIMWARRCIVSG 417
QY 448 GIVEEYQLPYNNVPSPSYEDMRVVCVKRLRPVSNRWNSDECLRAVLKIMSECAH 507
DB 418 GIVEEYQLPYNNVPSPSYEDMRVVCVKRLRPVSNRWNSDECLRAVLKIMSECAH 477
QY 508 PASRLTALRIKKTAKWVESQDVKI 532
DB 478 PASRLTALRIKKTAKWVESQDIKL 502

RESULT 6
A53444
activin receptor-like kinase 6 precursor - mouse
C:Species: Mus musculus (house mouse)

C>Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 05-Oct-2004
C:Accession: A53444; S40159
R:ten Dijke, P.; Yamashita, H.; Ichijo, H.; Franzen, P.; Laiho, M.; Miyazono, K.; Heldin
Science 264, 101-104, 1994
A>Title: Characterization of type I receptors for transforming growth factor-beta and ac
A:Reference number: A53444; MUID:94188705; PMID:8140412
A:Accession: A53444
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-502 <TEN>
A:Cross-references: UNIPROT:P36898; UNIPARC:UPI00000417C; EMBL:Z23143; NID:G437870; PIDN:G437870; PIDN:
R:Miyazono, K.; Moren, A.; Grimsby, S.; Ichijo, H.; Heldin, C.; ten Dijke, P.
submitted to the EMBL Data Library, June 1993
A:Description: ALK-3 and ALK-6: the closely related members in the serine/threonine kin
A:Reference number: S40158
A:Accession: S40159
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-502 <MIY>
A:Cross-references: UNIPARC:UPI00000417C; EMBL:Z23143; NID:G437870; PIDN:CAA80674.1; PI
C:Superfamily: Serine/threonine-specific protein kinase, activin receptor II type; prote
C:Keywords: ATP; serine/threonine-specific protein kinase; transmembrane protein
F:202-498/Domain: protein kinase homology <KIN>
F:210-218/Region: protein kinase ATP-binding motif

Query Match 68.1%; Score 1933.5; DB 2; Length 502;
Best Local Similarity 72.1%; Pred. No. 1.8e-96;
Matches 364; Conservative 60; Mismatches 76; Indels 5; Gaps 5;

QY 29 MLHGTGMKDVQKKPENGVTIAPEDTLPFLKCYCSGHCPCDDAINNCTITNGHCFATIE 88
DB 2 LRRSSG-KLVNGTKK-EDGESTAPTRPKILCKCHHCHPCDSVNNICSTDGCTFMIEE 59

QY 89 DQGETTLTSGCMKYEGSFQCKDSPKAQLRTIECC-RTNLCNQYLQPTLPPVVGIPFF 147
DB 60 DDSGMPVVTSGCLGEGSDFQCRDTPIPHQRSEIECTQDYCNKHLHPTLPKXNRDFAEGNIHK 119

QY 148 DGSVRVLAVLSMAVCIVAMIVFSSCFCKYKCKSISSRGRVNRDLEQDEAFIPVGESLK 207
DB 120 DGPPIHKALLISVTVCSL-LLVLLIIFCYFRY-KRQEARPRYSIGLEQDITYPPGESLR 177

QY 208 DLIQDOSQSGSGGLPLLVORTIAKQIOMVROVGKRYGEVWGMKRGKVAVKVFFTE 267
DB 178 DLIQDOSQSGSGGLPLLVORTIAKQIOMVROVGKRYGEVWGMKRGKVAVKVFFTE 237

QY 268 EASWFRETEIYQTVLMRHNILGFTAAADIKGTGSMTQLYLITDYHENGSLYDLKCATLD 327
DB 238 EASWFRETEIYQTVLMRHNILGFTAAADIKGTGSMTQLYLITDYHENGSLYDLKSTTLD 297

QY 328 TRALLKLAYSACGLCHLHTEIYGTQKPAIAHRDLKSNKILIKNGSCCIADIGLAVKF 387
DB 298 AKSMLKLAYSVSSGLCHLHTEIYGTQKPAIAHRDLKSNKILIKNGTCCCIADIGLAVKF 357

QY 388 NSDTNEVDIPLNTRVGTTRYMAPEVLDESLSKNHFQPYIMADIYSFGLIIEWEMARRCITG 447
DB 358 ISDTNEVDIPLNTRVGTTRYMAPEVLDESLSKNHFQPYIMADIYSFGLIIEWEARRCVSG 417

QY 448 GIVEEYQLPYNNMVPSPSYEDMREVVCVKRLRPVSNRWNSECLRAVLKLMSECAW 507
DB 418 GIVEEYQLPYHDLVPSDPSYEDMREVVCVKRLRPSPFPNRSWSSDECLRQWGLMTECAQN 477

QY 508 PASRLTALRIKKTAKMWESQDVKI 532
DB 478 PASRLTALRVKKTAKMWESQDIKL 502

RESULT 7
A56683
receptor protein kinase RPK-1 precursor - chicken
C:Species: Gallus gallus (chicken)
C>Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 05-Oct-2004
C:Accession: A56683
R:Sumitomo, S.; Saito, T.; Nohno, T.

DNA Seq. 3, 297-302, 1993
A>Title: A new receptor protein kinase from chick embryo related to type II receptor fo
A:Reference number: A56683; MUID:94003400; PMID:8400359
A:Accession: A56683
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-502 <SUM>
A:Cross-references: UNIPROT:Q05438; UNIPARC:UPI0000126A3C; GB:D13432; NID:G222862; PIDN:
C:Superfamily: Serine/threonine-specific protein kinase, activin receptor II type; prote
C:Keywords: ATP; phosphotransferase; transmembrane protein
F:202-498/Domain: protein kinase homology <KIN>
F:210-218/Region: protein kinase ATP-binding motif

Query Match 67.9%; Score 1926; DB 2; Length 502;
Best Local Similarity 72.3%; Pred. No. 4.4e-96;
Matches 360; Conservative 59; Mismatches 75; Indels 4; Gaps 4;

QY 36 KSDVDQKKPENGVTIAPEDTLPFLKCYCSGHCPCDDAINNCTITNGHCFATIEEDDQGETT 95
DB 8 KLSMESRKEDSEGT-APAPPQKKUSCQHHCHPCDSVNSTCSTDGTCFTIIEEDSGGHL 66

QY 96 LTSGCMKYEGSDFQCKDSPKAQLRTIECCR-TNLCNQYLQPTLPPVVGIPFDFGSVRWL 154
DB 67 VTKGCLGLEGSDFOCRDTPIPHQRSEIECTQDYCNKHLHPTLPKXNRDFAEGNIHK 126

QY 155 AVLISMVAVCIAMIVFSSCFCKYKCKSISSRGRVNRDLEQDEAFIPVGESLKLDIQSQ 214
DB 127 ALLISVTVCSS-LLVLLIIFCYFRY-KRQEARPRYSIGLEQDITYPPGESLKLDIEQSQ 184

QY 215 SSGSGGLPLLVORTIAKQIOMVROVGKRYGEVWGMKRGKVAVKVFFTEEASWPRE 274
DB 195 SSGSGGLPLLVORTIAKQIOMVROVGKRYGEVWGMKRGKVAVKVFFTEEASWPRE 244

QY 275 TEIYQTVLMRHNILGFTAAADIKGTGSMTQLYLITDYHENGSLYDLKCATLDTALLKL 334
DB 245 TEIYQTVLMRHNILGFTAAADIKGTGSMTQLYLITDYHENGSLYDLKSTTLDTKGMLK 304

QY 335 AYSAACGLCHLHTEIYGTQKPAIAHRDLKSNKILIKNGSCCIADIGLAVKFNSTNEV 394
DB 305 AYSSVSGGLCHLHTEIYGTQKPAIAHRDLKSNKILIKNGTCCCIADIGLAVKFI 364

QY 395 DIPNTRVGTTRYMAPEVLDESLSKNHFQPYIMADIYSFGLIIEWEMARRCITGGIVEEQ 454
DB 365 DIPNTRVGTTRYMAPEVLDESLSKNHFQPYIMADIYSFGLIIEWEARRCVSGGIVEEQ 424

QY 455 LPYNNMVPSPSYEDMREVVCVKRLRPVSNRWNSECLRAVLKLMSECAWNPASRLTA 514
DB 425 LPYHDLVPSDPSYEDMREVVCVKRLRPSPFPNRSWSSDECLRQWGLMMECAWNPASRLTA 484

QY 515 LRIKKTAKMWESQDVKI 532
DB 485 LRVKKTAKMWESQDIKL 502

RESULT 8
JC2061
transforming growth factor beta receptor type I, ESK 2 precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 05-Oct-2004
C:Accession: JC2061
R:Tomoda, T.; Kudoh, T.; Noma, T.; Nakazawa, A.; Muramatsu, M.; Arai, K.
Biochem. Biophys. Res. Commun. 198, 1054-1062, 1994
A>Title: Molecular cloning of a mouse counterpart for human TGF-beta type I receptor.
A:Reference number: JC2061; MUID:94161714; PMID:8117261
A:Accession: JC2061
A:Molecule type: mRNA
A:Residues: 1-503 <TOM>
A:Cross-references: UNIPROT:Q64729; UNIPARC:UPI0000021038; GB:D28526; NID:G467521; PIDN:
C:Comment: This protein is the mouse counterpart for human transforming growth factor be
C:Keywords: ATP; glycoprotein; receptor; transmembrane protein
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-501/Product: transforming growth factor-beta type I receptor ESK 2 #status predict
F:126-147/Domain: transmembrane #status predicted <TM>

F;203-499/Domain: protein kinase homology <KIN>
F;211-219/Region: protein kinase ATP-binding motif
F;41/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 44.9%; Score 1274; DB 2; Length 503;
Best Local Similarity 51.4%; Pred. No. 3.1e-61;
Matches 263; Conservative 70; Mismatches 144; Indels 32; Gaps 10;

QY 42 KKPENGVTLAPEDTL-----PFLKCYCSGH-CPDDAINNTCITNGHCFALIEEDDQGETTL 96
DB 9 RRPQLLIVLVAATLLPGAKALQCF--HLCTKD--NFTCETDGLCFVSVTEITD-KVTH 63
QY 97 TSCMKY-----EGSDFQCKDSKPAQLRTIECCRNLCNQYLOPTLPPVVGPFDD--- 148
DB 64 NSMCIAEIDLPRDRPFVCAPSKGTAVTTTCNQDHCNKIELPT-----TGPFSEKQS 118
QY 149 ---GSYRWLAVLISMA--VCIVAMIVPSSFCFYKHYCKSISSRGYRNRLDEQAEFIPVG 203
DB 119 AGLGPVELAAVIAGPVCFVCIALLMLMVYIC---HNRTVIHHRVNEEDPSLDRPFISEG 174
QY 204 ESLKDLIDOSQSGSGGLPLLVORTIAQIQMVROVKGKRGVGMKGWGEKAVKVF 263
DB 175 TTLKDLIYDWTYSGSGGLPLLVORTIAQITIVLOESIGKRGFGEVWKGWGEVAVKIF 234
QY 264 FTTEASWPRETEIYQTVLMRHNILGFTAAIDKGTGTSWTQLYLTDYHENGSLYDFLKC 323
DB 235 SSREERSWPREAIEYQTVLMRHNILGFTAAIDKNGTWTQLWLVSDYHEHGLSPDYLNR 294
QY 324 ATLDTALLKLAYSACGLCHLHTEIYGTQGRPAIAHRDLKSNKILIKNGSGCCIALDGL 383
DB 295 YTVTEGMIKLALSTASGLAHLHMEIVGTQGRPAIAHRDLKSNKILIKNGSGCCIALDGL 354
QY 384 AVKFNSTDNEVDIPLNTRVTRYMAPEVLDESLSKNHFQPYIMADIYSGFLIEMARR 443
DB 355 AVRHDSATDITDIAPNHRVGTTRYMAPEVLDDISNMKHFESFRADVIAMGLVFWFIEARR 414
QY 444 CITGIVEEYQLPYNNVPSDESYEDMRVVCVKLRPIVSNRWNSECLRAVLKMSRC 503
DB 415 CSIGGIHEDYQLPYDLVPSDESYEDMRVVCVKLRPIVSNRWNSECLRAVLKMSRC 474
QY 504 WAHNPASRLTALRIKTLAKVSESQDVKI 532
DB 475 WYANGAARLTALRIKTLQSLQSQEGIKM 503

RESULT 9
I45713
Dpp receptor TKV, splice form 1 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 05-Oct-2004
C:Accession: I45713
R:Brummel, T.J.; Twombly, V.; Marques, G.; Wrana, J.L.; Newfeld, S.J.; Attisano, L.; Mas
Cell 78, 251-266, 1994
A>Title: Characterization and relationship of Dpp receptors encoded by the saxophone and
F;198-500/Domain: protein kinase homology <KIN>
A:Reference number: A54829; MUID:94320137; PMID:8044839
A:Accession: I45713
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-509 <RES>
A:Cross-references: UNIPROT:Q9SSI0; UNIPARC:UPI000002A1A5; EMBL:U11442; NID:G523341; PID
C:Genetics:
A:Gene: FlyBase:tkv; thickveins
A:Cross-references: FlyBase:FBgn0003716
C:Keywords: alternative splicing; ATP
F;206-214/Region: protein kinase homology <KIN>
F;206-214/Region: protein kinase ATP-binding motif

Query Match 44.9%; Score 1274; DB 2; Length 509;
Best Local Similarity 53.5%; Pred. No. 3.1e-61;
Matches 262; Conservative 63; Mismatches 133; Indels 32; Gaps 12;

QY 59 LKCYSGHCPDDAINNTCIT--NGHCFALIE---EDDQG---ETTLTSGCMKYE--GSDPQ 109
DB 59 LKCYSGHCPDDAINNTCIT--NGHCFALIE---EDDQG---ETTLTSGCMKYE--GSDPQ 109

DB 15 LTCYDGSQCPDVSNGTCETPRGSCFSVAQQLYDDETTGMYEERTYGCMPPEDENGGFLM 74
QY 110 CXDSPKAQLR-RTIECC-RTNLCNQYLOPTLPPVVGPFDD-----GSYRWLAVL--ISM 160
DB 75 CKVAAPVPHUGKNIIVCCDKEDFCNRDLYPTYPKLTTPAPDLPVSSSELHTLAVFGSIII 134
QY 161 AVCIVAMIVPSSFCFYKHYCKSISSRGYRNRLDEQAEFIPVGESLKDLIDOSQSGSGS; 220
DB 135 SLVSFWLIVASLCFTYKRR-EKLRQKPRILNSMCNSQL-----SPLSQAVE--QSSGSGS; 186
QY 221 GLPLLIVORTIAQIQMVROVKGKRGVGMKGWGEKAVKVFPTTEBASWPRETEIYQ 280
DB 187 GLPLLIVORTIAQIQMVRLVGRYGEVWLAKRDERVAVKFTPTTEBASWPRETEIYQ 246
QY 281 VLMRHNILGFTAAIDKGTGTSWTQLYLTDYHENGSLYDFLKCATLDTALLKLAYSAC 340
DB 247 VLMRHNILGFTAAIDKGTGTSWTQMLLTDYHENGSLYDLSMSVNPQKQLALASLAS; 306
QY 341 GLCHLHTEIYGTQGRPAIAHRDLKSNKILIKNGSGCCIALDGLAVKFNSTDNEVDIPLN 400
DB 307 GLAHLHDEIFGTGPKPAIAHRDLKSNKILIKNGSGCCIALDGLAVKFNSELDVIHIAQNP 366
QY 401 RVGTRYMAPEVLDESLSKNHFQPYIMADIYSGFLIEMARRCIT-----GGIVEEYQ 454
DB 367 RVGTRYMAPEVLSQLDPKQFEFVKRADMYSGVLVWEMTRRCYTPVSGTKTTTCEDYA 426
QY 455 LPYNNVPSDESYEDMRVVCVKLRPIVSNRWNSECLRAVLKMSCEWAHNPASRLTA 514
DB 427 LPYHDVPSDPTFEDHMAVVCVKGPRPPIPSRQWQEDDLATVSKIMQECWHNPPTVRLTA 486
QY 515 LRIKTLAKM 524
DB 487 LRVKTLGLRL 496

RESULT 10
JC2062
Transforming growth factor beta receptor type I precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 05-Oct-2004
C:Accession: JC2062
R:Suzuki, A.; Shioda, N.; Maeda, T.; Tada, M.; Ueno, N.
Biochem. Biophys. Res. Commun. 198, 1063-1069, 1994
A>Title: A mouse TGF-beta type I receptor that requires type II receptor for ligand bin
A:Reference number: JC2062; MUID:94161715; PMID:8117262
A:Accession: JC2062
A:Molecule type: mRNA
A:Residues: 1-499 <SUZ>
A:Cross-references: UNIPROT:Q64729; UNIPARC:UPI000016D072
C:Keywords: ATP; glycoprotein; growth factor receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-499/Product: transforming growth factor-beta type I receptor #status predicted <TNM>
F;122-145/Domain: transmembrane #status predicted <TM>
F;146-499/Domain: intracellular #status predicted <INK>
F;199-499/Domain: protein kinase homology <KIN>
F;207-215/Region: protein kinase ATP-binding motif
F;41/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 44.7%; Score 1268; DB 2; Length 499;
Best Local Similarity 51.4%; Pred. No. 6.3e-61;
Matches 261; Conservative 70; Mismatches 143; Indels 34; Gaps 9;

QY 42 KKPENGVTLAPEDTL-----PFLKCYCSGH-CPDDAINNTCITNGHCFALIEEDDQGETTL 96
DB 9 RRPQLLIVLVAATLLPGAKALQCF--HLCTKD--NFTCETDGLCFVSVTEITD-KVTH 63
QY 97 TSGCMKY-----EGSDFQCKDSKPAQLRRTIECCRNLCNQYLOPT-----LPPVWIG 144
DB 64 NSMCIAEIDLPRDRPFVCAPSKGTAVTTTCNQDHCNKIELPTTEKQSGAGLPVELA 123
QY 145 PFDGSGRWLAVLISMAVCIVAMIVPSSFCFYKHYCKSISSRGYRNRLDEQAEFIPVG 204
DB 124 AVIAGPVCF-----VCIALMLMVYIC---HNRTVIHHRVNEEDPSLDRPFISEGT 171

activin A receptor type I - human
N;Alternate names: activin A receptor type II-like kinase 2; ALK-2; serine/threonine kinase 2; ALK-2
C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence revision 03-May-1994 #text_change 31-Dec-2004
C;Accession: A45992; J37162; S37182
R;Matsuzaki, K.; Xu, J.; Wang, F.; McKeehan, W.L.; Krummen, L.; Kan, M.
J. Biol. Chem. 268, 12719-12723, 1993
A;Title: A widely expressed transmembrane serine/threonine kinase that does not bind actin
A;Reference number: A45992; MUID:93286114; PMID:8389764
A;Accession: A45992
A>Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-509 <MAT>
A;Cross-references: UNIPROT:Q04771; UNIPARC:UPT0000000163F; GB:L02911; NID:g338218; PIDN:
R;ten Dijke, P.; Ichijo, H.; Franzén, P.; Schulz, P.; Saras, J.; Toyoshima, H.; Heidlin,
Oncogene 8, 2879-2887, 1993
A;Title: Activin receptor-like kinases: a novel subclass of cell-surface receptors with
A;Reference number: J37161; MUID:93390967; PMID:8397373
A;Accession: J37162
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A;Residues: 1-509 <RES>
A;Cross-references: UNIPARC:UPT0000000163F; EMBL:Z22534; NID:g402184; PIDN:CAA80256.1; PT
C;Genetics:
A;Gene: GDB:ACVR1; ACVRLK2; SKR1; ALK2
A;Cross-references: GDB:216986; OMIM:601298
C;Keywords: ATP; serine/threonine-specific protein kinase; transmembrane protein
F;206-502/Domain: protein kinase homology <KIN>
F;214-222/Region: protein kinase ATP-binding motif

Query Match	42.4%	Score 1204.5	DB 2	Length 509
Best Local Similarity	48.6%	Pred. No. 1.6e-57		
Matches 253	Conservative 79	Mismatches 132	Indels 57	Gaps 14
QY	46	NGVTLP-----BDTLP-----FLKVCVSG-----HCPDDAINNCTCINGH	81	
DB	3	DGVNLPVLIMIALPSPSMEDEKPKVNPKULYMCVCGLSGCGNEDHCEGO-----Q	52	
QY	82	CFIAIIBEDDOGETTLTSGCMK--YEGSDFOCKDSPKAQLRRTIECCRTNLCNQYLQPTLPP	140	
DB	53	CFSSLSIND-GFHVYQKGFQVVEYQGWTKCTPSP--GQAVECCOGDWCNRNITQAQLP-	108	
QY	141	VWJGPPFDGS-----VRWLAVLISMAVCIVAMIVSSCFPCYKHYCKSISSRGYN-RDL	193	
DB	109	-TRGKSPFGTQNFHLEVGLIILSVFVAVCLLGLGVALRKPKR-----RNQERLNPRDV	162	
QY	194	EQD--BAFIP--VGES-LKDLIDOSSGSGGLPLLVORTIAKOIQMVQVCKGRYGEV	248	
DB	163	EYGTIEGLITTVNGDSTLADLLSHCSTSGSGGLPFLVQRTVARQITLLECVCVGRYGEV	222	
QY	249	WMGKWRGEKVAVKVFVFTTEEASMFRETEIYQTVLMRHENILGFIAADIKGTGSWTQLYLI	308	
DB	223	WRGSGQGNVAVXIFSSROEKSWFRETELYNTVLMRHENILGFIAADMTSRHSSTQWLII	282	
QY	309	TDHENGSLYDFLKCATLDTRALLKLAYSAAAGLCHLHTEIYCTQKPAIAHRDLKSKNI	368	
DB	283	THYHENGSLYDYLQTLTLDTVSCLVLSTIASGLAHLHIEIFGTQKPAIAHRDLKSKNI	342	
QY	369	LIKNGSCCIIADGLAVKFNSTDNEVDIPLNTRVGTTRYMAPRVDLSLKHQFQPIWA	428	
DB	343	LVKNGQCCIIADGLAVMHSQSTNQDVGNNPRVGTTRYMAPRVDLDTIQVCFDSYKRV	402	
QY	429	DIYSFGLIIWEMARRCITGGIVVEYQLPYNNMVPSPDSEYEDMRVVCVKRLRPVSNRNW	488	
DB	403	DIWAFGLVLWEVARRMVNSGIVEDYKPPFVYVVPNDPSPEDMRKVVQVQDQRENINRWF	462	
QY	489	SDECLRAVLKIMSECAHNPASBLTALRIKTLAKWVESQD	529	
DB	463	SDPTLTSKLAKMECHQWNPASBLTALRIKTLTKIDNSLD	503	

RESULT 14
A55921

serine/threonine kinase Atr-1 - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C>Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 31-Dec-2004
C:Accession: A55921
R:Wrana, J.L.; Tran, H.; Attieano, L.; Arora, K.; Childs, S.R.; Massague, J.; O'Connor, M. Cell. Biol. 14, 944-950, 1994
A:Title: Two distinct transmembrane serine/threonine kinases from *Drosophila melanogaster*
A:Reference number: A55921; MUID:94119112; PMID:8289834
A:Accession: A55921
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-601 <WRA>
A:Cross-references: UNIPROT:Q23975; UNIPARC:UPI000007A851; GB:U04692; NID:9436960; PIDN
C:Genetics:
A:Gene: FlyBase:babo
A:Cross-references: FlyBase:FBgn0011300
C:Keywords: ATP
F:301-597/Domain: protein kinase homology <KIN>
F:308-317/Region: protein kinase ATP-binding motif

	Query Match	42.2%	Score 1198;	DB 2;	Length 601;
	Best Local Similarity	46.3%	Pred. No. 4.1e-57;		
	Matches 237;	Conservative 83;	Mismatches 138;	Indels 54;	Gaps 10;
Qy	42	KKPENGVTLPADETLFLKCYKCGHCPDDAINNTCIINHGHCFALIEEDDQGGTTTUSGCM	101		
Db	121	KKPENKI-----KCHCD-TCKES--NNICETDGFCTSVKNSDGSIIISYSCH	166		
Qy	102	--KY---EGSDFOCKDSPKQALRRTTECCRTNLCNQ-----YLOPTLPVVGIP	145		
Db	167	VVKYNQKSPKSECLTSNERFDYRIDCKSDFCNKNNMKRIETDVPVPHRLT-----	220		
Qy	146	FPDGVRMLAVLISMAVCIVAMIVFSSCFYK---HYCKSISSRGYNRDLEQDEAFIPV	202		
Db	221	----SWEFVAIIIGATLFI-----CFTGTSTWYTCORRKMASGRTFAKEDSAYDPI	268		
Qy	203	---GSSLKDILIDOSOSSGSGGLPLLVORTIAKOIMVRQVGKRYGVEVMGKWRGEKVA	259		
Db	269	LNGNTTIHDIEMTTSGSGSAGLPLLVQSRARQVLCHVIGKRGFGEVWRGRNGENVA	328		
Qy	260	VKVFPTTEASWFRETEIYQTVLMRHENILGFTAAADIKGTGSWTQLYLITDYHENGSLYD	319		
Db	329	VKIFSSRECSWFREABIIYQTVLMRHENILGFTAAADNKDNGTWTQLWLVTDYHENGSLFD	388		
Qy	320	FLKCATLTDTRALLKLAYSACGLCHLHTEIYGTQGPAPAIARHDLKSNILIKONGSCCIA	379		
Db	389	YLTHPVDNTMLNWSLSIATGLAHLHMDIVGTGRGPAPAIARHDLKSNILVKSNLSCAIG	448		
Qy	380	DLGLAVKNSDNEVDIPIPLNTRVGTTRYMAPEVLDESLSKNHFQPIYIMADYISFGLIWE	439		
Db	449	DLGLAVRHVEKNSVDIPISTHVRVGTGRYMAPEVLDESMDQHPDSYKRAVYVAFGLIWE	508		
Qy	440	MARRCITGGIVEEYQLPYNNMVPSPDSYEDMRVVCVKRLRPVSNRWNSECLRAVLKL	499		
Db	509	IARRCNMGMIYDEYQLPYDVVQPDPISEMKKVCIEKCRPNIPNRWHASDVLHNMKV	568		
Qy	500	MSECHWNPASRLTALRIKTLAKMYESQDVK	531		
Db	569	MKECHYPNPVARTALRIKTLASIVEDKVK	600		

RESULT 15
A49664
activin type I receptor - rat
C:Species: *Rattus norvegicus* (Norway rat)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 31-Dec-2004
C:Accession: A49664
R:Tsuchida, K.K.T.; Vale, W.W.
Proc. Natl. Acad. Sci. U.S.A. 90, 11242-11246, 1993
A:Title: Cloning and characterization of a transmembrane serine kinase that acts as an
A:Reference number: A49664; MUID:94068580; PMID:8248234
A:Accession: A49664
A:Status: preliminary; translated from GB/EMBL/DBJ

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 06:00:33 ; Search time 235 Seconds
(without alignments)
1597.196 Million cell updates/sec

Title: US-10-600-645-2

Perfect score: 2838

Sequence: 1 MTQLTYTIRLLGACLFIIISH.....TALRIKTKLAKMVESQDVKI 532

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2838	100.0	532	2 Q64308_RAT	Q64308 rattus norv
2	2838	100.0	532	2 Q78EA7_MOUSE	Q78EA7 rattus sp.
3	2823	99.5	532	1 BMRIA_MOUSE	P36895 mus musculus
4	2823	99.5	532	2 Q53243_MOUSE	Q53243 mus musculus
5	2763	97.4	532	1 BMRIA_HUMAN	P36894 homo sapien
6	2616	92.2	500	2 Q60607_MOUSE	Q60607 mus musculus
7	2582.5	91.0	533	2 Q90754_CHICK	Q90754 gallus gall
8	2570.5	90.6	533	2 Q9PUF5_COTCO	Q9PUF5 coturnix co
9	2223	78.3	527	2 Q91578_XENLA	Q91578 xenopus lae
10	2222	78.3	527	2 Q42338_XENLA	Q42338 xenopus lae
11	2211	77.9	527	2 Q42339_XENLA	Q42339 xenopus lae
12	2109	74.3	527	2 Q93243_BRARE	Q93243 brachydanio
13	2107.5	74.3	499	2 Q4RG20_TETNG	Q4RG20 tetraodon n
14	2104.5	74.2	534	2 Q66HY1_BRARE	Q66HY1 brachydanio
15	1950.5	68.7	502	2 Q9BD14_SHEEP	Q9BD14 ovis aries
16	1944.5	68.5	502	2 Q95123_PIG	Q95123 sus scrofa
17	1941	68.4	502	1 BMRIA_HUMAN	Q00238 homo sapien
18	1934.5	68.2	502	2 Q9QVT7_MOUSE	Q9QVT7 rattus sp.
19	1933.5	68.1	502	1 BMRIA_MOUSE	P36898 mus musculus
20	1926.5	67.9	502	2 Q9PUF4_COTCO	Q9PUF4 coturnix co
21	1926	67.9	502	1 BMRIA_CHICK	Q05438 gallus gall
22	1918.5	67.6	502	2 Q4PRC1_CAPHI	Q4PRC1 capra hircu
23	1894	66.7	530	2 Q9W629_BRARE	Q9W629 brachydanio
24	1878	66.2	508	2 Q4SJF6_TETNG	Q4SJF6 tetraodon n
25	1631	57.5	479	2 Q4RT67_TETNG	Q4RT67 tetraodon n
26	1612	56.8	371	2 Q8SPU3_PIG	Q8SPU3 sus scrofa
27	1591.5	56.1	361	2 Q4Z1Q1_CAPHI	Q4Z1Q1 capra hircu
28	1383	48.7	237	2 Q569A5_RAT	Q569A5 rattus norv
29	1336	47.1	286	2 Q8SPU4_PIG	Q8SPU4 sus scrofa
30	1307.5	46.1	534	2 Q7YXAI_CRAGI	Q7YXAI crassostrea
31	1290	45.5	499	2 Q5CD19_PIG	Q5CD19 sus scrofa

RESULT 1

ID	Q64308_RAT	PRELIMINARY;	PRT;	532 AA.
AC	Q64308;			
DT	01-NOV-1996 (Tremblrel. 01, Created)			
DT	01-NOV-1996 (Tremblrel. 01, Last sequence update)			
DT	10-MAY-2005 (Tremblrel. 30, Last annotation update)			
DE	Bone morphogenetic protein type IA receptor precursor (Bone morphogenetic protein 4 receptor).			
DE	merphogenetic protein 4 receptor).			
GN	Name=ALUK-3;			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OC	Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=Wistar; TISSUE=Dental pulp;			
RX	MEDLINE=95032096; PubMed=7945360;			
RA	Takeda K., Oida S., Ichijo H., Iimura T., Maruoka Y., Amagasa T.,			
RA	Sasaki S.;			
RT	"Molecular cloning of rat bone morphogenetic protein (BMP) type IA receptor and its expression during ectopic bone formation induced by BMP*."			
RT	Biochem. Biophys. Res. Commun. 204:203-209(1994).			
RL	NUCLEOTIDE SEQUENCE.			
RN	[2]			
RP	STRAIN=Wistar; TISSUE=Brain;			
RC	Ikeda T., Takahashi H.;			
RA	"Expression pattern of bone morphogenetic protein 4 receptor in embryo and adult rat."			
RT	Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.			
CC	-I- SUBUNIT: Interacts with ALP1. Part of a complex consisting of ALP1, ACVR2, ACVR1B and MADH3 (By similarity).			
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).			
CC	-I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.			
DR	EMBL; D38082; BAA07275.1; -; mRNA.			
DR	EMBL; D17667; BAA04549.1; -; mRNA.			
DR	PIR; J2387; JC2387.			
DR	HSSP; P36894; 1ES7.			
DR	SMR; Q64308; 55-143.			
DR	Ensembl; ENSRNOG0000010814; Rattus norvegicus.			
DR	RGD; 70989; Bmpra.			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0005524; F:ATP binding; IEA.			
DR	GO; GO:0004872; F:receptor activity; IEA.			
DR	GO; GO:0005024; F:transforming growth factor beta receptor ac. . ; IEA.			
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.			
DR	GO; GO:0007178; P:transmembrane receptor protein serine/threo. . ; IEA.			
DR	InterPro; IPR000472; Activin_receptor.			
DR	InterPro; IPR000333; Actn_receptorII.			
DR	InterPro; IPR000719; Prot_kinase.			
DR	InterPro; IPR008271; Ser_thr_pkin_AS.			
DR	InterPro; IPR003605; TGFbetarecept_GS.			

32	1288.5	45.4	500	2 Q91595_XENLA	Q91595 xenopus lae
33	1288	45.4	503	2 Q5CD18_PIG	Q5CD18 sus scrofa
34	1287	45.3	499	2 Q5CD21_PIG	Q5CD21 sus scrofa
35	1285	45.3	503	2 Q5CD20_PIG	Q5CD20 sus scrofa
36	1283.5	45.2	548	2 Q7QGF7_ANOGA	Q7QGF7 anopheles g
37	1283.5	45.2	565	2 Q6PUB5_BOVIN	Q6PUB5 anopheles g
38	1280	45.1	499	2 Q46680_BOVIN	Q46680 bos taurus
39	1280	45.1	531	2 Q81PK9_DROME	Q81PK9 drosophila
40	1280	45.1	563	2 Q7JQ37_DROME	Q7JQ37 drosophila
41	1280	45.1	563	2 Q7KTP1_DROME	Q7KTP1 drosophila
42	1280	45.1	575	2 Q9VMT1_DROME	Q9VMT1 drosophila
43	1274	44.9	503	1 TGFRI_MOUSE	Q64729 mus musculu
44	1274	44.9	503	2 Q4FJL1_MOUSE	Q4FJL1 mus musculu
45	1274	44.9	509	2 Q95S10_DROME	Q95S10 drosophila

ALIGNMENTS

DR Pfam; PF01064; Activin_recp; 1.
 DR PFam; PF00069; Pkinase_1.
 DR PRINTS; PR00653; ACTIVIN2R.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00467; GS; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
 KW ATP-binding; Kinase; Nucleotide-Binding; Receptor;
 FT Serine/Threonine-protein kinase; Signal; Transferase; Transmembrane.
 FT SIGNAL 1 23 Potential.
 SQ SEQUENCE 532 AA; 59994 MW; 14ED4C03E2540A0C CRC64;

Query Match 100.0%; Score 2838; DB 2; Length 532;
 Best Local Similarity 100.0%; Pred. No. 9.3e-188;
 Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTQLYTYIRLLGACLIIFSHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPLFLK 60
 Db 1 MTQLYTYIRLLGACLIIFSHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPLFLK 60

QY 61 CYCSGHCPCDDAINNTCTITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
 Db 61 CYCSGHCPCDDAINNTCTITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120

QY 121 TIECCRTNLCNOYLOPTLPVVGPFDDGSVRWLAVLISMAVICIAMIIVFSSCFCKYHC 180
 Db 121 TIECCRTNLCNOYLOPTLPVVGPFDDGSVRWLAVLISMAVICIAMIIVFSSCFCKYHC 180

QY 181 KSISSRGYNRDLQDEAFIPVGESLKDLDOSQSGSGGLPLLVQRTIAKQIOMVRQV 240
 Db 181 KSISSRGYNRDLQDEAFIPVGESLKDLDOSQSGSGGLPLLVQRTIAKQIOMVRQV 240

QY 241 GKGRYGEVVMGKRGKAVKVFVFTTEASWFRTEIYQTVLMRHNILGFTAAIDKGTG 300
 Db 241 GKGRYGEVVMGKRGKAVKVFVFTTEASWFRTEIYQTVLMRHNILGFTAAIDKGTG 300

QY 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEYQLPYNNMVPSPSPSYEDMREVVCVKRLR 480
 Db 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEYQLPYNNMVPSPSPSYEDMREVVCVKRLR 480

QY 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKTLAKMVESQDVKI 532
 Db 481 PIVSNRWNSECLRAVLKLMSECAHNPASRLTALRIKTLAKMVESQDVKI 532

RESULT 2

Q78EA7_9MURI PRELIMINARY; PRT; 532 AA.
 AC Q78EA7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Bone morphogenetic protein type IA receptor.
 GN Name=Bmprla;
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=95204990; PubMed=7897267;
 RA Takeda K.;
 RT "Expression of serine/threonine kinase receptors during ectopic bone

RT formation induced by bone morphogenetic protein (BMP).";
 RL Kokubo Gakkai Zasshi 61:512-526(1994).
 CC -I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; S75359; AAB33865.1; -; mRNA.
 DR HSSP; P36897; 1B6C.
 DR SMR; Q78EA7; 55-143.
 DR RGD; 70989; Bmprla.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0005024; F:transforming growth factor beta receptor ac. .; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR GO; GO:0007178; P:transmembrane receptor protein serine/threo. .; IEA.
 DR InterPro; IPR000472; Activin_receptor.
 DR InterPro; IPR000333; Actn_receptorII.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR003605; TGFbetarecept_GS.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF01064; Activin_recp; 1.
 DR Pfam; PF00069; Pkinase; 1.
 DR PRINTS; PR00653; ACTIVIN2R.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00467; GS; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
 KW ATP-binding; Kinase; Nucleotide-Binding; Receptor;
 KW Serine/threonine-protein kinase; Transferase; Transmembrane.
 SQ SEQUENCE 532 AA; 59994 MW; 14ED4C03E2540A0C CRC64;

Query Match 100.0%; Score 2838; DB 2; Length 532;
 Best Local Similarity 100.0%; Pred. No. 9.3e-188;
 Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTQLYTYIRLLGACLIIFSHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPLFLK 60
 Db 1 MTQLYTYIRLLGACLIIFSHVQGNLDSMLHGTGMKSDVDQKKPENGVTLPEDTLPLFLK 60

QY 61 CYCSGHCPCDDAINNTCTITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120
 Db 61 CYCSGHCPCDDAINNTCTITNGHCFALIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRR 120

QY 121 TIECCRTNLCNOYLOPTLPVVGPFDDGSVRWLAVLISMAVICIAMIIVFSSCFCKYHC 180
 Db 121 TIECCRTNLCNOYLOPTLPVVGPFDDGSVRWLAVLISMAVICIAMIIVFSSCFCKYHC 180

QY 181 KSISSRGYNRDLQDEAFIPVGESLKDLDOSQSGSGGLPLLVQRTIAKQIOMVRQV 240
 Db 181 KSISSRGYNRDLQDEAFIPVGESLKDLDOSQSGSGGLPLLVQRTIAKQIOMVRQV 240

QY 241 GKGRYGEVVMGKRGKAVKVFVFTTEASWFRTEIYQTVLMRHNILGFTAAIDKGTG 300
 Db 241 GKGRYGEVVMGKRGKAVKVFVFTTEASWFRTEIYQTVLMRHNILGFTAAIDKGTG 300

QY 301 SWTQLYLTIDYHENGSLYDFLKCATLDRALLKLAYSACGLCHLHTEIYGTQGPATAH 360
 Db 301 SWTQLYLTIDYHENGSLYDFLKCATLDRALLKLAYSACGLCHLHTEIYGTQGPATAH 360

QY 361 RDLKSKNLIKKNGSCCIADGLAVKFNSTDNEVDIPLNTRVGTTRYNAPEVLDLSKN 420
 Db 361 RDLKSKNLIKKNGSCCIADGLAVKFNSTDNEVDIPLNTRVGTTRYNAPEVLDLSKN 420

QY 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEYQLPYNNMVPSPSPSYEDMREVVCVKRLR 480
 Db 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEYQLPYNNMVPSPSPSYEDMREVVCVKRLR 480

QY 481 PIVSNRWNSECLRAVLKLMSECAWNPASRLTALRIKKTAKWVESQDVKI 532
 |||||||
 DB 481 PIVSNRWNSECLRAVLKLMSECAWNPASRLTALRIKKTAKWVESQDVKI 532
 |||||||

RESULT 3
 ID BMR1A_MOUSE STANDARD; PRT; 532 AA.
 AC P36895;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DE Bone morphogenetic protein receptor type IA precursor (EC 2.7.1.37)
 DE (Serine/threonine-protein kinase receptor R5) (SKR5) (Activin
 DE receptor-like kinase 3) (ALK-3) (BMP-2/BMP-4 receptor).
 GN Names=Bmr1a; Synonyms=Acvrlk3, Bmpr;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Swiss; TISSUE=Embryo;
 RX MEDLINE=95269711; PubMed=7750489; DOI=10.1210/en.136.6.2652;
 RA Suzuki A., Thies R.S., Yamaji N., Song J.J., Wozney J., Murakami K.,
 RA Kung H.;
 RT "A truncated bone morphogenetic protein receptor affects dorsal-
 RT ventral patterning in the early *Xenopus* embryo";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:10255-10259(1994).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=95024092; PubMed=7937936;
 RA Suzuki A., Thies R.S., Yamaji N., Song J.J., Wozney J., Murakami K.,
 RA Kung H.;
 RT "A truncated bone morphogenetic protein receptor affects dorsal-
 RT ventral patterning in the early *Xenopus* embryo";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:10255-10259(1994).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=94344106; PubMed=8065329;
 RA Koenig B.B., Cook J.S., Wolsing D.H., Ting J., Tiesman J.P.,
 RA Correa P.E., Olson C.A., Pecquet A.L., Ventura F., Grant R.A.,
 RA Chen C., Wrana J.L., Massague J., Rosenbaum J.S.;
 RT "Characterization and cloning of a receptor for BMP-2 and BMP-4 from
 RT NIH 3T3 cells";
 RL Mol. Cell. Biol. 14:5961-5974(1994).
 RN [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Retina;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Heiton E., Kretzeman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Guichard J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- FUNCTION: Receptor for BMP-2 and BMP-4.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SUBUNIT: Heterodimer with a type-II receptor.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Widely expressed.
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. TGPB
 CC receptor subfamily.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; Z23154; CAA80678.1; -; mRNA.
 CC EMBL; D16250; BAA03769.1; -; mRNA.
 CC EMBL; U04672; AAA2154.1; -; mRNA.
 CC EMBL; BC042611; AAH42611.1; -; mRNA.
 CC FIR; A56238; A56238.
 CC HSSP; P36894; 1ES7.
 CC SMR; P36895; 55-143.
 CC Ensembl; ENSMUSG0000021796; Mus musculus.
 CC MGI; MGI:1338938; Bmr1a.
 CC GO; GO:0003615; C:extracellular space; TAS.
 CC GO; GO:0016021; C:integral to membrane; TAS.
 CC GO; GO:0009952; P:anterior/posterior pattern formation; IMP.
 CC GO; GO:0051216; P:cartilage development; IMP.
 CC GO; GO:0030154; P:cell differentiation; IGI.
 CC GO; GO:0009950; P:dorsal/ventral axis specification; IMP.
 CC GO; GO:0007398; P:ectoderm development; IMP.
 CC GO; GO:0048382; P:mesoderm development; IMP.
 CC GO; GO:0001880; P:Mullerian duct regression; IMP.
 CC InterPro; IPR000472; Activin receptor.
 CC InterPro; IPR000333; Actn_receptorII.
 CC InterPro; IPR000719; Prot_kinase.
 CC InterPro; IPR008271; Ser_thr_kin_AS.
 CC Pfam; PF01064; Activin_recip; 1.
 CC Pfam; PF00069; Pkinase; 1.
 CC PRINTS; PR00653; ACTIVIN2R.
 CC PRODOM; PD000001; Prot_kinase; 1.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
 CC PROSITE; PS00109; PROTEIN_KINASE_ST; 1.
 CC ATP-binding; Glycoprotein; Kinase; Nucleotide-binding; Receptor;
 CC Serine/threonine-protein kinase; Signal; Transmembrane.
 CC SIGNAL 1 23 Potential.
 CC CHAIN 24 532 Bone morphogenetic protein receptor type
 CC IA.
 CC TOPO_DOM 24 152 Extracellular (Potential).
 CC TRANSMEM 153 176 Potential.
 CC TOPO_DOM 177 532 Cytoplasmic (Potential).
 CC DOMAIN 234 525 Protein kinase.
 CC NP_BIND 240 248 ATP (By similarity).
 CC ACT_SITE 362 362 Proton acceptor (By similarity).
 CC BINDING 261 261 ATP (By similarity).
 CC CARBOHYD 73 73 N-linked (GLNac...) (Potential).
 CC DISULFID 61 82 By similarity.
 CC DISULFID 63 67 By similarity.
 CC DISULFID 76 100 By similarity.
 CC DISULFID 110 124 By similarity.
 CC DISULFID 125 130 By similarity.
 CC SEQUENCE 532 AA; 60063 MW; 70CC83CFB07CE9D5 CRC64;
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 Query Match 99.5%; Score 2823; DB 1; Length 532;
 Best Local Similarity 98.9%; Pred. No. 1e-186; 1; Indels 0; Gaps 0;
 Matches 526; Conservative
 QY 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTMKSDVDQKPKENGVTLPFLK 60
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 DB 1 MTQLYTYIRLLGACLFIIISHVQGNLDSMLHGTMKSDLDQKPKENGVTLPFLK 60
 |||||||
 QY 61 CYCSGHCPDDAINTTCITNGHCFPAITBEDDQGTTLTSGCMKYEGSDFOCKSPKQLRR 120
 |||||||

RC TISSUE=Placenta;
 RX MEDLINE=9330967; PubMed=8397373;
 RA ten Dijke P., Ichijo H., Franzen P., Schulz P., Sarraf J.,
 RA Toyoshima H., Heldin C.-H., Miyazono K.;
 RT "Activin receptor-like kinases: a novel subclass of cell-surface
 RT receptors with predicted serine/threonine kinase activity.";
 RL Oncogene 8:2879-2887(1993).
 RN [2]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Testis;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Atschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RX X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 55-143 IN COMPLEX WITH BMP-2.
 RP PubMed=10881198; DOI=10.1038/75903;
 RA Kirsch T., Sebald W., Dreyer M.K.;
 RT "Crystal structure of the BMP-2-BRIA ectodomain complex.";
 RL Nat. Struct. Biol. 7:492-496(2000).
 RN [4]
 RN DISEASE.
 RX MEDLINE=21275975; PubMed=11381269; DOI=10.1038/98919;
 RA Howe J.R., Bair J.L., Sayed M.G., Anderson M.E., Mitros F.A.,
 RA Petersen G.M., Velculescu V.E., Traverso G., Vogelstein B.;
 RT "Germline mutations of the gene encoding bone morphogenetic protein
 RT receptor 1A in juvenile polyposis.";
 RL Nat. Genet. 28:184-187(2001).
 RN [5]
 RP VARIANTS JPS ARG-124 AND TYR-376, AND VARIANT CD ASP-338.
 RX MEDLINE=21426344; PubMed=11536076;
 RA Zhou X.-P., Woodford-Richens K., Lehtonen R., Kurose K., Aldred M.,
 RA Hampel H., Launonen V., Virta S., Pillarski R., Salovaara R.,
 RA Bodmer W.F., Conrad B.A., Dunlop M., Hodgson S.V., Iwama T.,
 RA Jaervinen H., Kellokumpu I., Kim J.C., Leggett B., Markie D.,
 RA Mecklin J.-P., Neale K., Phillips R., Piris J., Rozen P.,
 RA Houllaton R.S., Aaltonen L.A., Tomlinson I.P.M., Eng C.;
 RT "Germline mutations in BMPRIA/ALK3 cause a subset of cases of juvenile
 RT polyposis syndrome and of Cowden and Bannayan-Riley-Ruvalcaba
 RT syndromes.";
 RL Am. J. Hum. Genet. 69:704-711(2001).
 RN [6]
 RP VARIANTS JPS ASP-62; TYR-82 AND CYS-443.
 RX PubMed=12417513;
 RA Sayed M.G., Ahmed A.F., Ringold J.R., Anderson M.E., Bair J.L.,
 RA Mitros F.A., Lynch H.T., Tinley S.T., Petersen G.M., Giardiello F.M.,
 RA Vogelstein B., Howe J.R.;
 RT "Germline SMAD4 or BMPRIA mutations and phenotype of juvenile
 RT polyposis.";
 RL Ann. Surg. Oncol. 9:901-906(2002).
 RN [7]
 RP VARIANT JPS ARG-110.
 RX PubMed=12136244; DOI=10.1007/s00439-002-0748-9;
 RA Friedl W., Uhlhaas S., Schulmann K., Stolte M., Loff S., Back W.,
 RA Mangold E., Stern M., Knebel H.P., Sutter C., Weber R.G.,
 RA Fistorius S., Burger B., Propping P.;
 RT "Juvenile polyposis: massive gastric polyposis is more common in MADH4
 RT mutation carriers than in BMPRIA mutation carriers.";
 RL Hum. Genet. 111:108-111(2002).
 RN [8]
 RP VARIANT JPS THR-470.
 RX PubMed=12630959; DOI=10.1034/j.1399-0004.2003.00008.x;
 RA Kim I.J., Park J.H., Kang H.C., Kim K.H., Kim J.H., Ku J.L.,
 RA Kang S.B., Park S.Y., Lee J.S., Park J.G.;
 RT "Identification of a novel BMPRIA germline mutation in a Korean
 RT juvenile polyposis patient without SMAD4 mutation.";
 RL Clin. Genet. 63:126-130(2003).
 CC -!- FUNCTION: Receptor for BMP-2 and BMP-4.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SUBUNIT: Heterodimer with a type-II receptor.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Highly expressed in skeletal muscle.
 CC -!- DISEASE: Defects in BMPRIA are a cause of juvenile polyposis
 CC syndrome (JPS) [MIM:174900]; also known as juvenile intestinal
 CC polyposis (JIP). JPS is an autosomal dominant gastrointestinal
 CC hamartomatous polyposis syndrome in which patients are at risk for
 CC developing gastrointestinal cancers. The lesions are typified by a
 CC smooth histological appearance, predominant stroma, cystic spaces
 CC and lack of a smooth muscle core. Multiple juvenile polyps usually
 CC occur in a number of Mendelian disorders. Sometimes, these polyps
 CC occur without associated features as in JPS; here, polyps tend to
 CC occur in the large bowel and are associated with an increased risk
 CC of colon and other gastrointestinal cancers.
 CC -!- DISEASE: Defects in BMPRIA are a cause of Cowden disease (CD)
 CC [MIM:158350]. CD is an autosomal dominant cancer syndrome
 CC characterized by multiple hamartomas and by a high risk for
 CC breast, thyroid and endometrial cancers.
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. TGFB
 CC receptor subfamily.
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 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; 222535; CAA80257.1; -; mRNA.
 CC EMBL; BC028383; AAH28383.1; -; mRNA.
 CC PIR; I37163; I37163.
 CC PDB; 1ES7; X-ray; B/D=55-143.
 CC PDB; 18EW; X-ray; C/D=24-152.
 CC Ensembl; ENSG0000010779; Homo sapiens.
 CC HGNC; HGNC:1076; BMPRIA.
 CC MIM; 601299; -.
 CC MIM; 158350; -.
 CC MIM; 174900; -.
 CC GO; GO:0016021; C:integral to membrane; TAS.
 CC GO; GO:0007179; P:transforming growth factor beta receptor si. . . TAS.
 CC InterPro; IPR000472; Activin_receptor.
 CC InterPro; IPR000333; Actn_receptorII.
 CC InterPro; IPR000719; Prot_kinase.
 CC InterPro; IPR008271; Ser_thr_pkin_AS.
 CC InterPro; IPR002290; Ser_thr_pkinase.
 CC InterPro; IPR003605; TGFBeta_recept_GS.
 CC InterPro; IPR001245; Tyr_pkinase.
 CC Pfam; PF01064; Activin_recpt; 1.
 CC Pfam; PF00069; Pkinase; 1.
 CC PRINTS; PR00653; ACTIVIN2R.
 CC PRODOM; PD000001; Prot_kinase; 1.
 CC SMART; SM00467; GS; 1.
 CC SMART; SM00220; S_TKc; 1.
 CC SMART; SM00219; TyrKc; 1.
 CC PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
 CC PROSITE; PS50011; PROTEIN_KINASE_ST; 1.
 CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 CC 3D-structure; ATP-binding; Disease mutation; Glycoprotein; Kinase;
 KW Nucleotide-binding; Receptor; Serine/threonine-protein kinase; Signal;
 KW Transferrase; Transmembrane.
 FT SIGNAL 1 23 Potential.

FT CHAIN 24 532 Bone morphogenetic protein receptor type
FT IA.
FT TOPO_DOM 24 152 Extracellular (Potential).
FT TRANSMEM 153 176 Potential.
FT TOPO_DOM 177 532 Cytoplasmic (Potential).
FT DOMAIN 234 525 Protein kinase.
FT NP_BIND 240 248 ATP (By similarity).
FT ACT_SITE 362 362 Proton acceptor (By similarity).
FT BINDING 261 261 ATP (By similarity).
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
FT DISULFID 61 82
FT DISULFID 63 67
FT DISULFID 76 100
FT DISULFID 110 124
FT DISULFID 125 130
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FT VARIANT 82 82 /FTid=VAR 022828.
FT VARIANT 124 124 C -> Y (in JPS).
FT VARIANT 130 130 /FTid=VAR 022829.
FT VARIANT 338 338 C -> R (in JPS).
FT VARIANT 376 376 /FTid=VAR 015533.
FT VARIANT 443 443 . C -> R (in JPS).
FT VARIANT 470 470 /FTid=VAR 022830.
FT VARIANT 59 62 A -> D (in CD).
FT VARIANT 64 65 C -> Y (in JPS).
FT VARIANT 69 70 C -> Y (in JPS).
FT VARIANT 75 78 /FTid=VAR 015535.
FT VARIANT 81 87 R -> C (in JPS).
FT VARIANT 95 101 /FTid=VAR 022831.
FT VARIANT 97 98 M -> T (in JPS).
FT VARIANT 99 100 /FTid=VAR 022832.
FT VARIANT 101 101 P -> T (in Ref. 1).

Query Match 97.4%; Score 2763; DB 1; Length 532;
Best Local Similarity 97.0%; Pred. No. 1.4e-182;
Matches 516; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTQLYTYIRLLGACFLIISHVQGNLDSMLHGTGKMSDVDDQKPKNGVTLAPEDTLPLFK 60
DB 1 MPQLYTYIRLLGAYLFIISHVQGNLDSMLHGTGKMSDSDDQKPKNGVTLAPEDTLPLFK 60
QY 61 CYCSGHCPCDDAINNTCTITNGHCFATIEEDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRR 120
DB 61 CYCSGHCPCDDAINNTCTITNGHCFATIEEDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRR 120
QY 121 TIECCTNLCNQYLQPTLPVVPVPPFDGSGVRLAVLISMAVCIVAMIVFSSCFYKHYC 180
DB 121 TIECCTNLCNQYLQPTLPVVPVPPFDGSGVRLAVLISMAVCIVAMIVFSSCFYKHYC 180
QY 181 KSISSRRGRNRDLEDEAFIPGESLKDLIDQSSGSGGLPLLVORTIAKQIOMVRQV 240
DB 181 KSISSRRGRNRDLEDEAFIPGESLKDLIDQSSGSGGLPLLVORTIAKQIOMVRQV 240
QY 241 GKGRYGEVVMGKRWGEKAVKVFVFTTEASWFRTEIYQTVLMRHNILGFLAADIKGTG 300
DB 241 GKGRYGEVVMGKRWGEKAVKVFVFTTEASWFRTEIYQTVLMRHNILGFLAADIKGTG 300
QY 301 SWTQLYLITYDHENGLYDFLKCATLDTRALLKLAYSACGLCHLHTEIYGTQGPATIAH 360
DB 301 SWTQLYLITYDHENGLYDFLKCATLDTRALLKLAYSACGLCHLHTEIYGTQGPATIAH 360
QY 361 RDLKSNLLIKKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGYTRYMAPEVLDLSLNK 420
DB 361 RDLKSNLLIKKNGSCCIIADLGLAVKFNSTNEVDIPLNTRVGYTRYMAPEVLDLSLNK 420
QY 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEYQLPYYNMVPSDPSYEDMREWVCVKRLR 480

DB 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEYQLPYYNMVPSDPSYEDMREWVCVKRLR 480
QY 481 PIVSNRWNSSDECLRAVLKLMSECAHNPAISRLTALRIKKTAKMVESQDVKI 532
DB 481 PIVSNRWNSSDECLRAVLKLMSECAHNPAISRLTALRIKKTAKMVESQDVKI 532
RESULT 6
Q06007 MOUSE
ID Q06007 MOUSE PRELIMINARY; PRT; 500 AA.
AC Q06007;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE BRK-IT.
GN Name=Bmpria;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=94344106; PubMed=8065329;
RX Koenig B.B., Cook J.S., Wolsing D.H., Ting J., Tiesman J.P.,
RA Correa P.E., Olson C.A., Pecquet A.L., Ventura F., Grant R.A.,
RA Chen G., Wrana J.B., Massague J., Rosenbaum J.S.;
RT "Characterization and cloning of a receptor for BMP-2 and BMP-4 from
RT NIH 3T3 cells.";
RT Mol. Cell. Biol. 14:5961-5974(1994).
CC -!- SUBUNIT: Interacts with AIP1. Part of a complex consisting of
CC AIP1, ACVR2, ACVR1B and MADH3 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; U04673; AAA21515.1; -; mRNA.
DR HSSP; P36894; 1ES7.
DR SMR; Q06007; 55-143.
DR MGI; MGI:1338938; Bmpria.
DR GO; GO:0005625; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0009952; P:anterior/posterior pattern formation; IMP.
DR GO; GO:0051216; P:cartilage development; IMP.
DR GO; GO:0030154; P:cell differentiation; IGI.
DR GO; GO:0009950; P:dorsal/ventral axis specification; IMP.
DR GO; GO:0007398; P:ectoderm development; IMP.
DR GO; GO:0048382; P:mesoderm development; IMP.
DR GO; GO:0001880; P:Mullerian duct regression; IMP.
DR InterPro; IPR000472; Activin receptor.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser Thr_kin_AS.
DR InterPro; IPR003605; TGFbeta_recept_GS.
DR Pfam; PF01064; Activin_recp; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00467; GS; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase; Transmembrane.
SQ SEQUENCE 500 AA; 56439 MW; 0E7A59A526888DD CRC64;

Query Match 92.2%; Score 2616; DB 2; Length 500;
Best Local Similarity 98.8%; Pred. No. 1.9e-172;
Matches 485; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTQLYTYIRLLGACFLIISHVQGNLDSMLHGTGKMSDVDDQKPKNGVTLAPEDTLPLFK 60
DB 1 MTQLYTYIRLLGACFLIISHVQGNLDSMLHGTGKMSDSDDQKPKNGVTLAPEDTLPLFK 60
QY 61 CYCSGHCPCDDAINNTCTITNGHCFATIEEDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRR 120
DB 61 CYCSGHCPCDDAINNTCTITNGHCFATIEEDDQGETTLTSGCMKYEGSDFQCKDSPKAQLRR 120

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DB 181 KSISRRGRYNRDLQDEAFIPVGSLSKDLIDQSQSSGSGSLPQLVQRTIAKIQMVROV 240
QY 241 GKGRYGEVWVGKRGKVAVKVFTTTEASWFRTEIYQTVLMRHNILGFIAADIKGTG 300
DB 241 GKGRYGEVWVGKRGKVAVKVFTTTEASWFRTEIYQTVLMRHNILGFIAADIKGTG 300
QY 301 SWTQLYLTIDYHENGSLYDFLKCATLDTALLKLAISAACGLCHLHTEIYGTGKPAIAH 360
DB 301 SWTQLYLTIDYHENGSLYDFLKCATLDTALLKLAISAACGLCHLHTEIYGTGKPAIAH 360
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DB 361 RDLKSKNLIKKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSKN 420
QY 421 HFQPYIMADYISFGLIIEWEMARRCITGGIVEEYQLPYNNMVPSPSYEDMREVVVCVKRL 480
DB 421 HFQPYIMADYISFGLIIEWEMARRCITGGIVEEYQLPYNNMVPSPSYEDMREVVVCVKRL 480
QY 481 PIVSNRWNDSDE 491
DB 481 PIVSNRWNDSDE 491

RESULT 7
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ID Q90754_CHICK PRELIMINARY; PRT; 533 AA.
AC Q90754;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Protein kinase.
GN Name=BRK-1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Shimabara M., Kawakami Y., Nakata Y., Yamamoto S., Nohno T.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; L49204; AAA97421.1; -; mRNA.
DR HSSP; P36894; 1ES7.
DR SMR; Q90754; 55-141.
DR Ensembl; ENSGALG0000002003; Gallus gallus.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005524; F:transforming growth factor beta receptor ac. .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007178; P:transmembrane receptor protein serine/threo. .; IEA.
DR InterPro; IPR000472; Actin receptor.
DR InterPro; IPR000333; Actin receptorII.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR003605; Tgfbeta_recept_AS.
DR Pfam; PF01064; Activin_recp; 1.
DR PRINTS; PR00653; ACTIVIN2R.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00467; GS; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR ATP-Binding; Kinase; Nucleotide-Binding;
KW Serine/Chreonine-protein kinase; Transferase; Transmembrane.
SQ SEQUENCE 533 AA; 60283 MW; C39C8267DB494DBE CRC64;
Query Match 91.0%; Score 2582.5; DB 2; Length 533;
Best Local Similarity 90.2%; Pred. No. 4.3e-170;
Matches 481; Conservative 22; Mismatches 29; Indels 1; Gaps 1;
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DB 1 MTRLRVCERLLGAYLLIILHVQGNLDSMLHGTGKMTNPDOKKQGNVTILAPEDTLPFLK 60
QY 61 CYCSGHCPCPDANNTCTITNGHCFALIEEDDOQGETTLTSGCMKYEGSDFOCKSPKQLRR 120
DB 61 CYCSGHCPCPDANNTCTITNGHCFALIEEDDEHGEPTLASGCMKYEGSDFOCKSPKQLRR 120
QY 121 TIECCRTNLCNOYLQPTLPVVIQPPFDGSRVRLAVLISMAVCIVAMIVFSSCFCKYKVC 179
DB 121 TIECCRTNLCNOYLQPTLPVVIQPPFDGSRVRLAVLISMAVCIVAMIVFSSCFCKYKVC 180
QY 180 KSISSRRGRYNRDLQDEAFIPVGSLSKDLIDQSQSSGSGSLPQLVQRTIAKIQMVROV 239
DB 181 KSISSRRGRYNRDLQDEAFIPVGSLSKDLIDQSQSSGSGSLPQLVQRTIAKIQMVROV 240
QY 240 VGGKRYGEVWVGKRGKVAVKVFTTTEASWFRTEIYQTVLMRHNILGFIAADIKGT 299
DB 241 VGGKRYGEVWVGKRGKVAVKVFTTTEASWFRTEIYQTVLMRHNILGFIAADIKGT 300
QY 300 GSWTQLYLTIDYHENGSLYDFLKCATLDTALLKLAISAACGLCHLHTEIYGTGKPAIA 359
DB 301 GSWTQLYLTIDYHENGSLYDFLKCATLDTALLKLAISAACGLCHLHTEIYGTGKPAIA 360
QY 360 HRDLKSKNLIKKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSK 419
DB 361 HRDLKSKNLIKKNGSCCIIADGLAVKFNSTNEVDIPLNTRVGTTRRYMAPEVLDLSK 420
QY 420 NHFQPYIMADYISFGLIIEWEMARRCITGGIVEEYQLPYNNMVPSPSYEDMREVVVCVKRL 479
DB 421 NHFQPYIMADYISFGLIIEWEMARRCITGGIVEEYQLPYNNMVPSPSYEDMREVVVCVKRL 480
QY 480 RIVSNRWNDSDECLRAVLKLMSECAHNPASRLTALRIKTKLAKMVESQDVKI 532
DB 481 RIVSNRWNDSDECLRAVLKLMSECAHNPASRLTALRIKTKLAKMVESQDVKI 533

RESULT 8
Q9PUP5.COTCO
ID Q9PUP5_COTCO PRELIMINARY; PRT; 533 AA.
AC Q9PUP5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Bone morphogenetic protein receptor 1A.
GN Name=BMPR-1A;
OS Coturnix coturnix (Common quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=9091;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20237589; PubMed=10772803; DOI=10.1006/dbio.2000.9684;
RA McPherson C.E., Varley J.E., Maxwell G.D.;
RT "Expression and regulation of type I BMP receptors during early avian
sympathetic ganglion development.";
RL Dev. Biol. 221:220-232(2000).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AF189777; AAF04582.1; -; mRNA.
DR HSSP; P36894; 1ES7.
DR SMR; Q9PUP5; 55-139.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
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DR GO:0005024; F:transforming growth factor beta receptor ac. . . ; IEA.
DR GO:000468; P:protein amino acid phosphorylation; IEA.
DR GO:0007178; P:transmembrane receptor protein serine/threo. . . ; IEA.
DR InterPro: IPR000472; Actin receptor.
DR InterPro: IPR000333; Actn receptorII.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser Thr_pkin_AS.
DR InterPro: IPR003605; TGFbeta_recept_GS.
DR Pfam: PF01064; Activin_recpt_1.
DR Pfam: PF00069; Pkinase; 1.
DR PRINTS: PR00653; ACTIVIN2R.
DR SMART: SM00467; GS; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding; Receptor;
KW Serine/threonine-protein kinase; Transferase; Transmembrane.
SQ SEQUENCE 533 AA; 60243 MW; 40519BB4034C0CCF CRC64;

Query Match 90.6%; Score 2570.5; DB 2; Length 533;
Best Local Similarity 89.7%; Pred. No. 2.9e-169;
Matches 478; Conservative 23; Mismatches 31; Indels 1; Gaps 1;

QY 1 MTQLYTYIRLLGACFLIIISHVQGNLDSMLHGTGKMSVDVQKPKENGVTLPAPEDTLPLK 60
DB 1 MTRLRVCELRLLGAYLLLIHVGQNLDSMLHGTGKMTNPDKQKQANGVTLPAPEDTLPLK 60

QY 61 CYCSGHCPCPDANNTCTINGHCFATIEEDDOGETTLTSGCMKYGSDFOCKDSPAQLRR 120
DB 61 CYCSGHCPCPDANNCTINGHCFATIEEDEHEGPTLASGCMKYGSDFOCKDSPAQLRR 120

QY 121 TIECCTNLCNQYLOPTLPV-VIGFFPDGSRVWLAVLISMAVCIVAMIVFSCFCYKH 179
DB 121 TIECCTDFCNDLOPTLPDSTDLGDFGSRVWLAVLISMAVCIVAMIVFSCFCYKH 180

QY 180 CKSISRGYNDRLQDEAFIPVGSLSKLDLDQSSGSGSLPLLQVQRTIAKQIQMVRQ 239
DB 181 CKSMARHCYNDRLQDEAFIPAGESLSKLDLDQSSGSGSLPLLQVQRTIAKQIQMVRQ 240

QY 240 VGGGRYGEVWVGKRGKAVKVFVFTTEASWFRTEIYQTVLMRHNILGFIAADIKGT 299
DB 241 VGGGRYGEVWVGKRGKAVKVFVFTTEASWFRTEIYQTVLMRHNILGFIAADIKGT 300

QY 300 GSWTQLYLTIDYHENGSLYDFLKCATLDRALLKLAYSAAACGLCHLHTEIYGTQKPA 359
DB 301 GSWTQLYLTIDYHENGSLYDFLKTLDNRALLKLAYSAAACGLCHLHTEIYGTQKPA 360

QY 360 HRDLKSKNLIKNGSCCCTADIGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDESLSK 419
DB 361 HRDLKSKNLIKNGSCCCTADIGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDESLSK 420

QY 420 NHFPQYIMADISFGLIIWEMARRCTIGIVVEEYQLPYYNMVPSDPSYEDMREVVCVKRL 479
DB 421 NHFPQYIMADISFGLIIWEMARRCVAGIVVEEYQLPYYDMVNDPSYEDMREVVCVKRL 480

QY 480 RPIVSNRNWNSDECLRAVLKMLSECWAHNPASRLTALRIKTKLAKWVESQDVKI 532
DB 481 RPIVSNRNWNSDECLRAVLKMLSECWAHNPASRLTALRIKTKLAKWVESQDVKI 533

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RESULT 9

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Q91578 XENLA
ID Q91578 XENLA PRELIMINARY; PRT; 527 AA.
AC Q91578;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE BMP receptor.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.

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OX NCBI_TaxID=8355;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=9500777; PubMed=7522972; DOI=10.1016/0092-8674(94)90409-X;
RA "Graf J., Melton D.;
RT "Studies with a Xenopus BMP receptor suggest that ventral mesoderm-
RT inducing signals override signals in vivo.";
RL Cell 79:169-179(1994).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; U16654; AAA58707.1; -; mRNA.
DR PIR; A54985; A54985.
DR HSP; P36894; IES7.
DR SMR; Q91578; 53-140.
DR GO:0016020; C:membrane; IEA.
DR GO:0005524; F:ATP binding; IEA.
DR GO:0004872; F:receptor activity; IEA.
DR GO:0005024; F:transforming growth factor beta receptor ac. . . ; IEA.
DR GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO:0007178; P:transmembrane receptor protein serine/threo. . . ; IEA.
DR InterPro: IPR000472; Activin_receptor.
DR InterPro: IPR000333; Actn_receptorII.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser Thr_pkin_AS.
DR InterPro: IPR003605; TGFbeta_recept_GS.
DR Pfam: PF01064; Activin_recpt_1.
DR Pfam: PF00069; Pkinase; 1.
DR PRINTS: PR00653; ACTIVIN2R.
DR SMART: SM00467; GS; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding; Receptor;
KW Serine/threonine-protein kinase; Transferase; Transmembrane.
SQ SEQUENCE 527 AA; 59800 MW; 53APB5BE8046512B CRC64;

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Query Match 78.3%; Score 2223; DB 2; Length 527;
Best Local Similarity 80.0%; Pred. No. 2.9e-145;
Matches 423; Conservative 44; Mismatches 52; Indels 10; Gaps 5;

QY 7 YIRLGGACFLIIISHVQGNLDSMLHGTGKMSVDVQKPKENGVTLPAPEDTLPLKCYCSGH 66
DB 6 FIACFGALLVI-HTQGQDFNLPHRTGKMSNDPKQENGVTLPAPEDTLPLKCYCSGY 64

QY 67 CPDDAINNTCTINGHCFATIEEDDOGETTLTSGCMKYGSDFOCKDSPAQLRRTECCR 126
DB 65 CPQNAVNTCTINGQCFAMIEEDDHGDIILTSGCMKYGSDFOCKDSPAQLRRTECCR 124

QY 127 TNLNQYLOPTLPVPIGPPFDG--SVRWLAVLISMAVCIVAMIVF--SSCFYKHYCKSI 183
DB 125 TDFCNRLDLETPSKI----SDGEYALRFALIIISLVVCLILVGFIIIIWIYKH--KLH 178

QY 184 SSRGRYNDRLQDEAFIPVGSLSKLDLDQSSGSGSLPLLQVQRTIAKQIQMVRQVKG 243
DB 179 SORMLYNNLPPDPAFIPAGESLSKLDLDQSSGSGSLPLLQVQRTIAKQIQMVRQVKG 238

QY 244 RYGEVWVGKRGKAVKVFVFTTEASWFRTEIYQTVLMRHNILGFIAADIKGTGWT 303
DB 239 RYGEVWVGKRGKAVKVFVFTTEASWFRTEIYQTVLMRHNILGFIAADIKGTGWT 298

QY 304 QLYLITDYHENGSLYDFLKCATLDRALLKLAYSAAACGLCHLHTEIYGTQKPAIAHRDL 363
DB 299 QWYLITDYHENGSLYDFLKTLDTRSLKLAYSAAACGLCHLHTEIYGTQKPAIAHRDL 358

QY 364 KSKNLIKNGSCCCTADIGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDESLSKNHQ 423
DB 359 KSKNLIKENWTCTCIADIGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDESLSKNHQ 418

QY 424 PYIMADISFGLIIWEMARRCTIGIVVEEYQLPYYNMVPSDPSYEDMREVVCVKRLRPIV 483
DB 419 AYIMADISFSLIIWEMTRRCTIGIVVEEYQLPYYDMVNDPSYEDMREVVCVKRLRPIV 478

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Qy 484 SNRWSDECLRAVLKLMSECHWAHPASRLTALRIKTKLAKWVESQDVKI 532
Db 479 SNRWSDECLRAVLKLMSECHWAHPASRLTALRIKTKLAKWVESQDVKI 527

RESULT 10
ID 042338_XENLA PRELIMINARY; PRT; 527 AA.
AC 042338;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE BMP receptor (LOC397711 protein).
GN Name=LOC397711;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Suzuki A., Shioda N., Ueno N.;
RT "Bone morphogenetic protein acts as a ventral mesoderm modifier in
RL early Xenopus embryos.";
RL Dev. Growth Differ. 37:581-588(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie H.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gichwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -|- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
CC -|- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; D32066; BAA22437.1; -; mRNA.
DR EMBL; BC070551; AAH70551.1; -; mRNA.
DR HSSP; P36894; 1ES7.
DR SMR; 042338; 53-140.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005024; F:transforming growth factor beta receptor ac. .; IEA.

Query Match 78.3%; Score 2222; DB 2; Length 527;
Best Local Similarity 80.0%; Pred. No. 3.5e-145;
Matches 423; Conservative 43; Mismatches 53; Indels 10; Gaps 5;
Qy 7 YIRLLGACLFIIISHVQGNLDSMLHGTGMKSDVDQKKPENGVTLAPEDTLPLFLKCYCSGH 66
Db 6 FIACFGALLVI-HTQGQDFNLPHTGTGKNSDPPKQENGVTLAPEDTLPLFLNLCYCSGY 64
Qy 67 CPDDAINNTCTNGHCFATIEEDDQGETTLTSCMKYEGSDFOCKDSPKQALRTIECCR 126
Db 65 CPQNAVNTCTNGQCFAMIEEDHGDIIITSGCMKEGSDFOCKDSPKALSRTIECCR 124
Qy 127 TNLCHQYLOPTLPVVGIFGFFG--SVRWLAVLISNAVCIVAMIVF--SSCFCKHYCKSI 183
Db 125 TDFCNRLDLEPTSPKTI-----SDGEYGLRFALISLVCLILVIGFILLIWIYKH--KLH 178
Qy 184 SSRGRYNRLDEQDEAFIPVGESLKDIDQSQSGSGGLPLLQVORTIAKQIOMVROVGKG 243
Db 179 SQRMLYNRLNDPDAFIPAGESLKDIDISQSGSGGLPLLQVORTIAKQIOMVROVGKG 238
Qy 244 RYGEVVMGKRGKAVKAVKVFVTEASWPRETEIYQTVLMRHNILGFIADIKGTGWSW 303
Db 239 RYGEVVMGKRGKAVKAVKVFVTEASWPRETEIYQTVLMRHNILGFIADIKGTGWSW 298
Qy 304 QLYLTDVHENGSLVDFLKCATLDTRALLKLAISAACGLCHLHTEIYGTGPKPAIHRDL 363
Db 299 QMYLITEYHENGSLVDFLKCTTLDTRSLKLAISAACGLCHLHTEIYGTGPKPAIHRDL 358
Qy 364 KSKNLIKNGSCCADIADGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDESLSKNHQ 423
Db 359 KSKNLIKNTCCADIADGLAVKFNSTNEVDIPLNTRVGTTRYMAPEVLDESLSKNHQ 418
Qy 424 PYIMADIVSFGIIWEMARRCITGIVEYQIPYNNMPSDPSYEDMRVWCVRLRPTV 483
Db 419 AYIMADIVSFLIIEWMTRRCITGIVEYQIPYNNMPSDPSYEDMRVWCVRLRPTV 478
Qy 484 SNRWSDECLRAVLKLMSECHWAHPASRLTALRIKTKLAKWVESQDVKI 532
Db 479 SNRWSDECLRAVLKLMSECHWAHPASRLTALRIKTKLAKWVESQDVKI 527

RESULT 11
042338_XENLA
ID 042338_XENLA PRELIMINARY; PRT; 527 AA.
AC 042338;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE 'BMP receptor' (LOC397712 protein).
GN Name=LOC397712;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
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OX NCBI_TaxID=8355;
RN [1] NUCLEOTIDE SEQUENCE.
RA Nucleotide sequence.
RP Suzuki A., Shoda N., Ueno N.;
RT "Bone morphogenetic protein acts as a ventral mesoderm modifier in
early Xenopus embryos."
RL Dev. Growth Differ. 37:581-588 (1995).
RN [2] NUCLEOTIDE SEQUENCE.
RP TISSUE=Ovary;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Richards S., Worley K.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3] NUCLEOTIDE SEQUENCE.
RP TISSUE=Ovary;
RC MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RX Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative."
RL Dev. Dyn. 225:384-391 (2002).
RN [4] NUCLEOTIDE SEQUENCE.
RP TISSUE=Ovary;
RC Klein S., Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; D32067; BAA22438.1; -; mRNA.
DR EMBL; BC071081; AAH71081.1; -; mRNA.
DR HSSP; P36894; 1ES7.
DR SMR; O42339; 53-140.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005024; F:transforming growth factor beta receptor ac. . .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007178; P:transmembrane receptor phosphorylation; IEA.
DR InterPro; IPR000472; Activin receptor.
DR InterPro; IPR000333; Actin receptor.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_kinase.
DR InterPro; IPR003605; TGFbeta_recept_GS.
DR Pfam; PF01064; Activin_recpt; 1.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00653; ACTIVIN2R.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00467; GS; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding; Receptor;
KW Serine/threonine-protein kinase; Transferase; Transmembrane.
SQ SEQUENCE 527 AA; 59807 MW; D24E46D8A1291074 CRC64;

Query Match 77.9%; Score 2211; DB 2; Length 527;
Best Local Similarity 79.4%; Pred. No. 2e-144;
Matches 421; Conservative 42; Mismatches 55; Indels 12; Gaps 5;
QY 9 RLLGAC---LFIISHVQGNLDSMLHGTGMSKSDVDOKKPENGVTLAPEDTLPLKCYCSG 65
DB 4 RLFIACFGVLLAIIHAQGGDFNILPHRTGMSKNSDPKPKQENGVTUAPEDTLPLKCYCSG 63
QY 66 HCPDDAINNTCITNGHCFATIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRRTIECC 125
DB 64 YCPQNAVNTCITNGQCFAMIEEDDHGDI IWTSGCMKEGSDFOCKDSPKALSRTIECC 123
QY 126 RTNLCNQYLQPTLPVPIVGPFDG--SVRWLAVLISMVAVCIAMIVF--SSCFYKHYCKS 182
DB 124 RTDFCNRLQPTLSPKIA---DGEYGLRFALIIISMVVCVFIAGFILLIWIYKH--KL 177
QY 103 ISSGRVNRDLQDEAFIPVGESLKLIDQSOSGSGGLPLLQVORTAKQIQMVROVCK 242
DB 178 HSQRMVLRNLDPPDAFIPAGESLKLIDISQSSGSGGLPLLQVORTAKQIQMVROVCK 237
QY 243 GRYEVMGKVRGEKVAVKVFTTTEASWFRTEIYQTVLMRHENILGFIAADIKGTGSM 302
DB 238 GRYEVMGKVRGEKVAVKVFTTTEASWFRTEIYQTVLMRHENILGFVAADIKGTGSM 297
QY 303 TOLYLITYHENGSLYDFLKCATLDTRALLKLAYSACGLCHLHTEIYGTQCKPAIAHRD 362
DB 298 TQWLYITEYHENGSLYDFLKCCTLDTRSLLLKLAYSACGLCHLHTEIYGTQCKPAIAHRD 357
QY 363 LKSNKILIKKNGSCCIIADGLAVKPNSTNEVDIPLNTRVGTTRRYMAPEVLDES LKKNHF 422
DB 358 LKSNKILIKENWTCIIADGLAVKPNSTNEVDIPLNTRVGTTRRYMAPEVLDES LKKNHF 417
QY 423 QPYIMADIYSFGLIIEWEMARCCITGGIVEEYQLPYNNVPSDPSYEDREVVVCVKLRPI 482
DB 418 QAYIMADIYSFSLIVWENTRRCITGGIVEEYQLPYNDVNPDPSPEDREVVVCVKLRPT 477
QY 483 VSNRWNDECLRAVLKLMSECAHNPASRLTALRIKKTAKWVESQDVKI 532
DB 478 VSNRWNDECLRAVLKLMSECAHNPASRLTALRIKKTAKWVESQDVKI 527

RESULT 12
O93243_BRAE PRELIMINARY; PRT; 527 AA.
ID O93243_BRAE PRELIMINARY; PRT; 527 AA.
AC O93243;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Type I serin/threonine kinase receptor.
GN Name=bmpria; Synonyms=BMPR-IA;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1] NUCLEOTIDE SEQUENCE.
RP STRAIN=AB line;
RA Nikaide M., Tada M., Takeda H., Kuroiwa A., Ueno N.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AB011826; BAA32748.1; -; mRNA.
DR HSSP; P36894; 1ES7.
DR SMR; O93243; 58-140.
DR ZFIN; ZDB-GENE-000502-1; bmpria.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005024; F:transforming growth factor beta receptor ac. . .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007178; P:transmembrane receptor phosphorylation; IEA.
DR GO; GO:0007178; P:transmembrane receptor phosphorylation; IEA.

```
DR InterPro; IPR000472; Activin_receptor.
DR InterPro; IPR000333; Actn_receptorII.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR InterPro; IPR003605; TGFbeta_recept_GS.
DR Pfam; PF01064; Activin_rec; 1.
DR PRINTS; PF00069; Pkinase; 1.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00467; GS; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding; Receptor;
KW Serine/threonine-protein kinase; Transferrase; Transmembrane.
SQ SEQUENCE 527 AA; 59657 MW; 6607C24551D3B9E9 CRC64;

Query Match 74.3%; Score 2109; DB 2; Length 527;
Best Local Similarity 75.8%; Pred. No. 2.2e-137;
Matches 402; Conservative 46; Mismatches 74; Indels 8; Gaps 5;

Qy 4 LYTIVRLGLACLF-ISHVQGNLDSMLGTGKMSDVKQKPENGVTLAPEDTLPLKCY 62
Db 5 LFTIVLTGVCLLTLCGAGQNDPHVLQGTGVR--LDSRRPGDDSTIAPEDAARFLSCH 62
Qy 63 CSGHCPDDAINNCTITNGHCPAIIEDDQGETTLTSGCMKYEGSDFOCKSPKRAQLRTI 122
Db 63 CSGHCPDDAKNCTETNGQCFAINEDBNDVILSSGCMKYEGSHFCKDSQFAQRTI 122
Qy 123 ECRTNLCNQYLQPTLPVVGIPFDDGSVRWLAVLISMAVICIVAMIVFSCFCYKHYCKS 182
Db 123 ECCQDFCNQDLKPELPRDSEP---PDPHWLAFLLISVTVCFCALICV-TVICVYRY-KW 177
Qy 183 ISSRGRVNRDLEODEAIPVGESIKULIDQSSGSGSGLPLLVQRTIAKIQIOMVROVGK 242
Db 178 QTERQVRHRLDLEODEAIPAGESLKLINQSQTSGSGSGLPLLVQRTIRKIQIOTVRMIGK 237
Qy 243 GRVGEVNMKGWKGKVAKVVFTEEASWPRETEIYQTVLMRHNILGFTAAADIKGTGSW 302
Db 238 GRVGEVWLGRWKGKVAKVVFTEEASWPRETEIYQTVLMRHNILGFTAAADIKGTGS 297
Qy 303 TQLYLITDYHENGSLYDFLKCATLDTALLKLAYSAAACGLCHLHTEIYGTQGPATAHRD 362
Db 298 TQLYLITDYHENGSLYDFLTTLDTQALLRLAFSAACGLCHLHTEIYGTQGPATAHRD 357
Qy 363 LKSNLILIKNGSCIIADGLAVKFNSTNEVDIPLNTRVGTTRYNAPEVLDESLSKNHF 422
Db 358 LKSNLILIKNGTCTCIADGLAVKFNSTNEVDIPLNTRVGTTRYNAPEVLDELTKNHF 417
Qy 423 QPYIMADIYSGLLIWMARRCITGGIVEYQVLPYNNMVPDPSYEDMRVVCVKRLRPI 482
Db 418 QAYIMADIYSGLLIWMARRCVTGGIIEYHYVPYEMVSDPSYEDMLSEVVCVKGLRPT 477
Qy 483 VSNRNSDECLRAVLKMLSCWAHPNPSRLTALRIKTKLARKVESQDVKI 532
Db 478 VSNRNSDECLRAVLKMLSCWAHPNPSRLTILRVKTKLAKWVESQDIKI 527
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RESULT 13

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Q4RGZ0_TETNG
ID Q4RGZ0_TETNG PRELIMINARY; PRT; 499 AA.
AC Q4RGZ0;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF15083, whole genome shotgun sequence.
DE (Fragment).
DE ORFNames=GSTENG0034592001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
```

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OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli B., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Cattolico L., Boulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RN Nature 431:946-957 (2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- FUNCTION: Plays a key role in the control of the eukaryotic cell
CC cycle. It is required in higher cells for entry into S-phase and
CC mitosis. Component of the kinase complex that phosphorylates the
CC repetitive C-terminus of RNA polymerase II. Catalytic component of
CC MPF (By similarity).
CC -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC mature oocytes (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; CAEE01015083; CAG12342.1; -; Genomic_DNA.
DR InterPro; IPR000472; Activin_receptor.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR InterPro; IPR002290; Ser_Thr_pkinase.
DR InterPro; IPR003605; TGFbeta_recept_GS.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF01064; Activin_rec; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00467; GS; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding; Receptor;
KW Serine/threonine-protein kinase; Transferrase; Transmembrane.
FT NON_TER
FT 1
SQ SEQUENCE 499 AA; 56419 MW; CDBAC3433C9B5429 CRC64;

Query Match 74.3%; Score 2107.5; DB 2; Length 499;
Best Local Similarity 78.4%; Pred. No. 2.7e-137;
Matches 403; Conservative 40; Mismatches 52; Indels 19; Gaps 7;

Qy 23 GQNLDLSMLHGTGMKSDVDQKPENGVTLAPEDTLPLKCYCSGCHCPDDAINTITNGHC 82
Db 1 GQNPDVVLQGTGKAE-----DSTIAPEDAARFLSCYSGCHCPDATNNTCQTNGQC 52
Qy 83 FAIIEEDDQGETTLTSGCMKYEGSDFOCKSPKRAQLRTIECRTNLCNQYLQPTLPVV 142
Db 53 FAIIEDEHGEPLLTSGCMKYEGSHFCKDSQFAQRTIECRTNLCNQYLQPTLPVLA 112
Qy 143 -IGPFPDGSVRWLAVLISMAVICIVAMIVFSCFCYKHYCKSSRRGY---NRDLEODEA 198
Db 113 PIG----GSPNWLAFLLISMTVC--CMLICVAVVYTRY--KWSEQRVYHKHRLDEQ-EV 165
Qy 199 FIPVGESLKDLDQSSGSGSGLPLLVQRTIAKIQIOMVROVGKRGYGVNMKGWKEVK 258
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Db 166 FIPAGESLRLDIHQSSGSGSLPLLVTQRTIAKQIQMVRQIKGKRGYGEVWLGWRGK 225
Qy 259 AVKVFTTTEASWFRTEIYQTVLMRHNILGFIAADIKGTGSWTQLYLITYDHENGLY 318
Db 226 AVKVFTTTEASWFRTEIYQTVLMRHNILGFIAADIKGTGAFTQFLITDYHENGSLY 285
Qy 319 DFLKCATLDTALLKLAYSAAAGLCHLHTEIYGTQKPAIAHRDLKSNILIKKNGSCCI 378
Db 286 DYLKUSTLTHMLLRLAYSAAGLCHLHTEIYGTQKPAIAHRDLKSNILIKKNGSCCI 345
Qy 379 ADLGLAVKNSDNEVDIPLNTRVGRTRYMAPEVLDSELSKNHFOPIYIMADIYSFGLI 438
Db 346 ADLGLAVKNSDNEVDVPLSTRVGRTRYMAPEVLDSELSKNHFOPIYIMADIYSFGL 405
Qy 439 EMARRCITGGIVEEYQLPYNNVPSDPSYEDMREVVCVKRLRPIVSNRNWNSDECLRAVLK 498
Db 406 EMARRCITGGIVEDYQLPYNNVPSDPSYEDMREVVCVKRLRPIVSNRNWNSDECLRAVLK 465
Qy 499 LMSECAWNPASRLTALRKTTLAKMVESQDKI 532
Db 466 LMSECAWNPASRLTILRVKTKLAKMVESQDKI 499

RESULT 14
O66HY1 BRARE
ID Q66HY1_BRARE PRELIMINARY; PRT; 534 AA.
AC Q66HY1;
DT 25-OCT-2004 (TremBLrel. 28, Created)
DT 25-OCT-2004 (TremBLrel. 28, Last sequence update)
DE zgc:92227.
GN ORFNames=zgc:92227;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]_TaxID=7955;
RP TISSUE=TISSUE SEQUENCE.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Matusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RA Director MGC Project;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC081626; AAH81626.1; -; mRNA.
DR SMR; Q66HY1; 63-147.
DR ZFIN; ZDB-GENE-040912-150; zgc:92227.
DR GO; GO:0016020; C.membrane; IEA.
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DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; P:protein-tyrosine kinase activity; IEA.
DR GO; GO:0005024; P:transforming growth factor beta receptor ac. . .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000472; Activin receptor.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR003605; TGFbetarecept_Gs.
DR InterPro; IPR001245; Tvr_kinase.
DR Pfam; PF01064; Activin_recp; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00467; GS; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding; Receptor;
DR Serine/threonine-protein kinase; Transferase; Transmembrane.
DR SEQUENCE 534 AA; 59781 MW; FF0B38D40DA3C212 CRC64;

Query Match 74.2%; Score 2104.5; DB 2; Length 534;
Best Local Similarity 77.2%; Pred. No. 4.6e-137;
Matches 397; Conservative 49; Mismatches 59; Indels 9; Gaps 6;

Qy 23 QNILDSDLHGTGKMSDVPKKPE--NGVTLAPEDTLPLFKVCYSGCHCPDDAINNCTING 80
Db 26 QGNPDYMLHGTGVKPGSDPRAQAGDGTVAPEDAARFLSCYSGCHCEDATNNTCEING 85
Qy 81 HCFAIIEEDDQGETTLTSGCMKYEGSDFOCKDSPKAQLRRTIECRTLNCQYLOFTLPP 140
Db 86 HCFAIIEDEHGEAMLTSKCMKYEGSHFOCKDSPNAQTRRTIECSTDFCNRLDQTLPP 145
Qy 141 VVIG--PFEDGSRVRLAVLISMVACIVAMIVFSSCFYKHYCKSISSRGYNRDLEQDEA 198
Db 146 PIPGKPPFPWNAHL--LAFLLSVTVCCFTLVAI--TIVCYRFP--KLQTRRRHYORDLGPIEA 201
Qy 199 FIPVGESLKLIDQSQSGSGSLPLLVTQRTIAKQIQMVRQIKGKRGYGEVWLGWRGK 258
Db 202 FIPAGESLKLIDLSQS--STGSGSGSLPLLVTQRTIAKHQMVRLQIKGKRGYGEVWLG 260
Qy 259 AVKVFTTTEASWFRTEIYQTVLMRHNILGFIAADIKGTGSWTQLYLITYDHENGLY 318
Db 261 AVKVFTTTEASWFRTEIYQTVLMRHNILGFIAADIKGTGTFTQFLITDYHENGSLC 320
Qy 319 DFLKCATLDTALLKLAYSAAAGLCHLHTEIYGTQKPAIAHRDLKSNILIKKNGSCCI 378
Db 321 DYLYKTTLDLQALLRLAYSAAAGLCHLHTEIYGTQKPAIAHRDLKSNILIKKNGTCCI 380
Qy 379 ADLGLAVKNSDNEVDIPLNTRVGRTRYMAPEVLDSELSKNHFOPIYIMADIYSFGLI 438
Db 381 ADLGLAVKNSDNEVDVPLSTRVGRTRYMAPEVLDSELSKNHFOPIYIMADIYSFGLI 440
Qy 439 EMARRCITGGIVEEYQLPYNNVPSDPSYEDMREVVCVKRLRPIVSNRNWNSDECLRAVLK 498
Db 441 EMARRCITGGIVEEYQLPYNNVPSDPSYEDMREVVCVKMRPVVSNRNWNSDECLRAVLK 500
Qy 499 LMSECAWNPASRLTALRKTTLAKMVESQDKI 532
Db 501 LMSECAWNPASRLTALRVKTKLAKMVESQDKI 534

RESULT 15
Q9BDI4 SHEEP
ID Q9BDI4_SHEEP PRELIMINARY; PRT; 502 AA.
AC Q9BDI4;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-FEB-2005 (TremBLrel. 29, Last annotation update)
DE Bone morphogenetic protein receptor type IB (Bone morphogenetic
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 9, 2005, 19:16:45 ; Search time 5253 Seconds
(without alignments)
5756.847 Million cell updates/sec

Title: US-10-600-645-2

Perfect score: 2838

Sequence: 1 MTQLVYIRLLGACLFIIISH.....TALRIKTKLAKWVESQDVKI 532

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 2842172553 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+pn.model -DEV=xlh
-Q/cgn2.1/USPTO.spool/US10600645/runat_02122005_103604_23280/app_query.fasta_1.711
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -NORM=ext -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10600645@CN 1_1_3367@runat_02122005_103604_23280 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOP=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

1: gb_ba.*

2: gb_in.*

3: gb_env.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pr.*

9: gb_ro.*

10: gb_ste.*

11: gb_sv.*

12: gb_un.*

13: gb_vi.*

14: gb_hcg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	ID	Description
1	2838	100.0	1599	9	RATRB4R1	D17667 Rat mRNA fo
2	2838	100.0	1813	6	AR169902	Sequence
3	2838	100.0	1813	6	AR382508	Sequence

4	2838	100.0	3003	6	CQ986812	Sequence
5	2838	100.0	3003	6	CS027157	Sequence
6	2838	100.0	3003	9	RATFALK3	D38082 Rat mRNA fo
7	2838	100.0	3167	6	CQ986810	Sequence
8	2838	100.0	3167	6	CQ986811	Sequence
9	2838	100.0	3167	6	CS027155	Sequence
10	2838	100.0	3167	6	CS027156	Sequence
11	2838	100.0	3167	9	S75359	S75359 bone morpho
12	2838	99.5	1599	9	AY365062	Mus muscu
13	2838	99.5	1599	9	MMALK3A	Z23154 M.musculus
14	2838	99.5	2070	6	A38817	A38817 Sequence 13
15	2838	99.5	2070	6	AR140650	Sequence
16	2838	99.5	2070	6	AR164274	Sequence
17	2838	99.5	2070	6	AR264352	Sequence
18	2838	99.5	2070	6	AR475173	Sequence
19	2838	99.5	2292	9	MUSEMPRC	D16250 Mus musculu
20	2838	99.5	2402	6	AR144415	Sequence
21	2838	99.5	2402	6	AR174013	Sequence
22	2838	99.5	2402	6	BD191976	BD191976 The use o
23	2838	99.5	2402	9	MMU04672	U04672 Mus musculu
24	2838	99.5	5288	9	BC042611	BC042611 Mus muscu
25	2838	98.6	2056	9	MMU04673	U04673 Mus musculu
26	2769	97.6	1599	6	CQ848002	Sequence
27	2769	97.6	2932	6	A38809	A38809 Sequence 5
28	2769	97.6	2932	6	AR140646	Sequence
29	2769	97.6	2932	6	AR164270	Sequence
30	2769	97.6	2932	6	CQ986807	Sequence
31	2769	97.6	2932	6	CS027152	Sequence
32	2769	97.6	2932	6	AR264348	Sequence
33	2769	97.6	2932	6	AR408534	Sequence
34	2769	97.6	2932	6	AR475169	Sequence
35	2769	97.6	2932	8	HSALK3A	Z22535 H.sapiens A
36	2763	97.4	3625	8	BC028383	BC028383 Homo sapi
37	2741	96.6	2892	6	CQ720881	Sequence
38	2680	94.4	2861	6	CQ718018	Sequence
39	2680	94.4	93893	8	AL669984	AL669984 Human DNA
40	2582.5	91.0	1969	5	CHKBR1R	L49204 Gallus gall
41	2570.5	90.6	1602	5	AF189777	AF189777 Coturnix
42	2523.5	88.9	239655	14	AC096969	AC096969 Rattus no
43	2223	78.3	2315	5	XLU16854	UI16854 Xenopus lae
44	2222	78.3	2333	5	BC070551	BC070551 Xenopus l
45	2222	78.3	2395	5	D32066	D32066 Xenopus lae

ALIGNMENTS

RESULT 1	RATRB4R1	Rat mRNA for bone morphogenetic protein 4 receptor, complete cds.	1599 bp	mRNA	linear	ROD 04-FEB-1999
LOCUS	D17667	GI:684975				
DEFINITION	bone morphogenetic protein 4 receptor.					
ACCESSION	Rattus norvegicus (Norway rat)					
VERSION	D17667.1					
KEYWORDS	Rattus norvegicus					
SOURCE	Rattus norvegicus					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.					
REFERENCE	1 (bases 1 to 1599)					
AUTHORS	Ikedo, T. and Takahashi, H.					
TITLE	Expression pattern of bone morphogenetic protein 4 receptor in embryo and adult rat					
JOURNAL	Unpublished					
REFERENCE	2 (bases 1 to 1599)					
AUTHORS	Takahashi, H.					
TITLE	Direct Submission					
JOURNAL	Submitted (16-SEP-1993) Hiroshi Takahashi, Tokyo Metropolitan Institute of Gerontology, Department of Pathology; 35-2 Sakaecho, Itabashi-ku, Tokyo 173, Japan (Tel:03-3964-3241(ex.3034), Fax:03-3579-4776)					
FEATURES	Location/Qualifiers					
source	1. .1599					
	/organism="Rattus norvegicus"					

ACCESSION AR169902
VERSION AR169902.1 GI:17907859
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1813)
AUTHORS Wozney,J.M., Celeste,A.J., Thies,R.Scott. and Yamaji,N.
TITLE BMP receptor proteins
JOURNAL Patent: US 6291206-A 1 18-SEP-2001;
FEATURES Location/Qualifiers
source 1..1813
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 4.54e-271 Length: 1813
Score: 2838.00 Matches: 532
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-600-645-2 (1-532) x AR169902 (1-1813)

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Qy      61 CysTyrCysSerGlyHisCysProAaspAlaIleAenAenThrCysIleThrAenGly 80
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Qy      121 ThrIleGluCysCysArgThrAenLeuCysAenGlnTyrIleuGlnProThrLeuPro 140
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Qy      141 ValValIleGlyProPhePheAaspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
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Qy      161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
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Qy      181 LysSerIleSerSerArgGlyArgTyrAsnArgAaspLeuGlnAaspGluAlaPheIle 200
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Qy      221 GlyLeuProLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
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Qy      261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
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Qy      281 ValLeuMetArgHisGluAenIleLeuGlyPheIleAlaAaspIleLysGlyThrGly 300
Db      901 GTGTTAATGGCTCATGAAATATATCTGGTTTATAGCTCGACACATTAAGGCGACCGGT 960

Qy      301 SerTrpThrGlnLeuTyrIleuThrAspTyrHisGluAenGlySerLeuTyrAaspPhe 320
Db      961 TCCTGGACTCAGCTGATTGATTACTGATTACATGAGAAATGGGCTCTCTATGACTTC 1020

Qy      321 LeuLysCysAlaThrLeuAaspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAaCys 340
Db      1021 CTGAAATGTGCCACCTGGACACACAGAGCCTACTCAAGTTAGCTTATTCTGCTGCCCTG 1080

Qy      341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db      1081 GGTCTGTGCCACCTCCACACAGAAATTTATGGCACGCAAGGCAAGCCTGCAATTTGCTCAT 1140

Qy      361 ArgAaspLeuLysSerLysAenIleLeuIleLysAenGlySerCysCysIleAlaAasp 380
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Qy      381 LeuGlyLeuAlaValLysPheAenSerAaspThrAenGluValAaspIleProLeuAenThr 400
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Db      1261 AGGGTGGGCAACAGGCGGTACATGGCTCCAGAAAGTGTGGACGAGAGCCTGAGTAAAAAC 1320

Qy      421 HisPheGlnProTyrIleMetAlaAaspIleTyrSerPheGlyLeuIleIleTyrGluMet 440
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Qy      461 ValProSerAaspProSerTyrGluAaspMetArgGluValValCysValLysArgLeuArg 480
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Qy      481 ProIleValSerAenArgTrpAenSerAaspGluCysLeuArgAlaValLeuLysLeuMet 500
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Qy      501 SerGluCysTrpAlaHisAenProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
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RESULT 3

AR382508 1813 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 1 from patent US 6610513.
DEFINITION AR382508
ACCESSION AR382508
VERSION AR382508.1 GI:40091231
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1813)
AUTHORS Wozney,J.M., Celeste,A.J., Thies,R.S. and Yamaji,N.

TITLE Receptor proteins
JOURNAL Patent: US 6610513-A 1 26-AUG-2003;
Genetics Institute, LLC; Cambridge, MA
FEATURES Location/Qualifiers
source 1..1813
/organism="unknown"
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ORIGIN

Alignment Scores:
Pred. No.: 4 54e-271 Length: 1813
Score: 2838.00 Matches: 532
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-600-645-2 (1-532) x AR382508 (1-1813)

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DB 61 ATGACTCAGCTATACACTTACATCAGATTACTGGGAGCCTGCTGTTCATCATTTCTCAT 120

QY 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetIysSerAspValAsp 40
DB 121 GTTCAAGGCGAGAACTAGATAGTATGCTCCATGGTACTGGTATGAATCAGACGTTGGAC 180

QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
DB 181 CAGAAGAAGCCCGAAATGGAGTGGAGCTTAGCACCAGAGGACACCTTACCTTTCTTAAAA 240

QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
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QY 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
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QY 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
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RESULT 4
CQ986812 3003 bp DNA linear PAT 25-JAN-2005
LOCUS Sequence 121 from Patent WO2005003158.
DEFINITION CQ986812
ACCESSION CQ986812
VERSION CQ986812.1 GI:58194651
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
1
REFERENCE Brunkov,M.E., Galas,D.J., Kovacevich,B., Mulligan,J.T.,
AUTHORS Paepke,B.W., van Ness,J. and Winkler,D.G.
TITLE Compositions and methods for increasing bone mineralization
JOURNAL Patent: WO 2005003158-A 121 13-JAN-2005;
Celltech R & D, Inc. (US)
FEATURES Location/Qualifiers

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ORIGIN
Alignment Scores:
Pred. No.: 8,56e-271 Length: 3003
Score: 2838.00 Matches: 532
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6

US-10-600-645-2 (1-532) x CQ986812 (1-3003)

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QY 481 ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
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QY 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
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RESULT 5
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LOCUS Sequence 90 from Patent WO2005014650.
DEFINITION CS027157
ACCESSION CS027157.1 GI:60496971
VERSION CS027157.1
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
1
REFERENCE Winkler,D.G., Shi,J. and Latham,J.
AUTHORS Antibodies specific for sclerostin and methods for increasing bone
.TITLE mineralization
JOURNAL Patent: WO 2005014650-A 90 17-FEB-2005;
CELLtech R & D, Inc. (US)
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
source
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/db_xref="taxon:10116"

ORIGIN

Alignment Scores:

Pred. No.: 8-56e-271 Length: 3003
Score: 2838.00 Matches: 532
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-600-645-2 (1-532) x CS027157 (1-3003)

Qy 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
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Db 143 GTTCAAGGCGAGATCTAGATAGTATGCTCCATGGTACTGGTATGAAATCAGACGTGGAC 202
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Qy 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
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Db 503 GTCGTTATAGGCCATCTTTTATGATGCGACGCTCCGATGGCTGGCTGTGCTCATCTATG 562
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LOCUS Rat mRNA for bone morphogenetic protein type IA receptor, complete cds.
DEFINITION Rat mRNA for bone morphogenetic protein type IA receptor, complete cds.

ACCESSION D38082
VERSION D38082.1 GI:1398909
KEYWORDS RAUK-3; bone morphogenetic protein type IA receptor; bone morphogenetic protein receptor; BMP receptor; serine/threonine kinase; transmembrane protein.
SOURCE Rattus norvegicus (Norway rat)

ORGANISM

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REFERENCE

1 (bases 1 to 3003)
Takeda,K., Oida,S., Ichijo,H., Iimura,T., Maruoka,Y., Amagasa,T.

AUTHORS

and Sasaki,S.
Molecular cloning of rat bone morphogenetic protein (BMP) type IA receptor and its expression during ectopic bone formation induced by BMP

JOURNAL

Biochem. Biophys. Res. Commun. 204 (1), 203-209 (1994)

PUBMED

7945360

REFERENCE

2 (bases 1 to 3003)

AUTHORS

Oida,S.

TITLE Direct Submission
JOURNAL Submitted (26-AUG-1994) Shinichiro Oida, Faculty of Dent., Tokyo Medical and Dental University, Department of Biochemistry, 1-5-45 Yushima, Bunkyo-ku, Tokyo 113, Japan (Tel:03-3813-6111(ex.5126), Fax:03-5684-8047)
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DEFINITION Sequence 119 from Patent WO2005003158.
ACCESSION CQ986810
VERSION CQ986810.1 GI:58194649
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
1
REFERENCE
AUTHORS Brunkow,M.E., Galas,D.J., Kovacevich,B., Mulligan,J.T.,
Paepker,B.W., van Ness,J. and Winkler,D.G.
TITLE Compositions and methods for increasing bone mineralization
JOURNAL Patent: WO 2005003158-A 119 13-JAN-2005;
Celltech R & D, Inc. (US)
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VERSION CS027155.1 GI:60496969
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REFERENCE
AUTHORS Winkler,D.G., Shi,J. and Latham,J.
TITLE Antibodies specific for sclerostin and methods for increasing bone
mineralization
JOURNAL Patent: WO 2005014650-A 88 17-FEB-2005;
Celltech R & D, Inc. (US)
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QY 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db 1606 GTGCTAGTGACCCATCTTATGAAGACATGCGTGAGGTCTGTGTGTGTAAGCCCTTGCGG 1665
QY 481 ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1666 CCAATCGTCTCTAAACCGCTGGAACAGTGAATGATGATGATGCTTCGAGCCGTTTTGAAGCTGATG 1725
QY 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520

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RESULT 10
CS027156
LOCUS   CS027156               3167 bp    DNA          linear    PAT 03-MAR-2005
DEFINITION   Sequence 89 from Patent WO2005014650.
ACCESSION   CS027156
VERSION     CS027156.1   GI:60496970
KEYWORDS
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
           Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE   1
AUTHORS    Winkler,D.G., Shi,J. and Latham,J.
TITLE      Antibodies specific for sclerostin and methods for increasing bone
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JOURNAL    Patent: WO 2005014650-A 89 17-FEB-2005;
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Score:          2838.00      Matches:      532
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US-10-600-645-2 (1-532) x CS027156 (1-3167)

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Qy      121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
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 DEFINITION mRNA, complete cds.
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 VERSION AY365062.1 GI:34334005
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
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 1 (bases 1 to 1599)
 Shalamanov, P.D., Morty, R.E. and Eickelberg, O.
 Expression of bone morphogenic protein receptor 1a in the mouse
 Unpublished
 2 (bases 1 to 1599)
 Shalamanov, P.D., Morty, R.E. and Eickelberg, O.
 Direct Submission
 Submitted (11-AUG-2003) Internal Medicine, University of Giessen
 Medical Centre, Aulweg 123 (Rooms 6-11), Giessen, Hessen 35392,
 Germany

FEATURES

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Location/Qualifiers
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ACCESSION Z23154
VERSION Z23154.1 GI:437868
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SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
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REFERENCE 1 (bases 1 to 1599)
AUTHORS Dewulf,N., Verschueren,K., Lonnoy,O., Moren,A., Grimsby,S., Vande
          Spieghe,K., Miyazono,K., Huylebroeck,D. and Ten Dijke,P.
TITLE Distinct spatial and temporal expression patterns of two type I
        receptors for bone morphogenetic proteins during mouse
        embryogenesis
JOURNAL Endocrinology 136 (6), 2652-2663 (1995)
PUBMED 7750489
REFERENCE 2 (bases 1 to 1599)
AUTHORS Miyazono,K.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-1993) Kohei Miyazono, Ludwig Institute for Cancer
        Research, Biomedical, Center, Uppsala, S-751 24, Sweden
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Pred. No.: 1,196-269 Length: 1599
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Best Local Similarity: 98.87% Mismatches: 1
Query Match: 99.47% Indels: 0
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Qy 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
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LOCUS A38817 2070 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 13 from Patent WO9411502.
ACCESSION A38817
VERSION A38817.1 GI:2295247
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 2070)
AUTHORS Miyazono,K., Djike,P.T., Franzen,P., Yamashita,H. and Heldin,C.
TITLE ACTIVIN RECEPTOR-LIKE KINASES, PROTEINS HAVING SERINE THREONINE
KINASE DOMAINS AND THEIR USE
JOURNAL Patent: WO 9411502-A 13 26-MAY-1994;
COMMENT LUDWIG INST CANCER RES (GB)
Other publication CA 2149441 940526
Other publication AU 5432094 940608
Other publication NZ 257631 960326
Other publication JP 8505049T 960604.

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Query Match: 99.47% Indels: 0
DB: 6 Gaps: 0
US-10-600-645-2 (1-532) x A38817 (1-2070)
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QY 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
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QY 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
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LOCUS AR140650 Sequence 13 from patent US 6207814.
DEFINITION AR140650
ACCESSION AR140650
VERSION AR140650.1 GI:14483146
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 2070)
AUTHORS Miyazono,K., ten Dijke,P., Franzen,P., Yamashita,H. and
Heidin,C.-H.
TITLE Activin receptor-like kinases, ALK-3 and ALK-6, and nucleic acids
encoding them
JOURNAL Patent: US 6207814-A 13 27-MAR-2001;
FEATURES Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.: 1.65e-269 Length: 2070
Score: 2823.00 Matches: 526
Percent Similarity: 99.81% Conservative: 5
Best Local Similarity: 98.87% Mismatches: 1
Query Match: 99.47% Indels: 0
DB: 6
Gaps: 0

US-10-600-645-2 (1-532) x AR140650 (1-2070)

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Job time : 5300 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 9, 2005, 17:20:39 ; Search time 614 Seconds
(without alignments)

5774.620 Million cell updates/sec

Title: US-10-600-645-2

Perfect score: 2838

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Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2838	100.0	3167	14	Adw28816 Rat bone

5	2838	100.0	3167	14	Adw28815 Rat bone
6	2838	100.0	3167	14	Adx97428 Rat bone
7	2838	100.0	3167	14	Adx97429 Rat bone
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9	2823	99.5	2070	2	Aaz09847 Human MAL
10	2823	99.5	2070	14	Ady51875 Murine AL
11	2823	99.5	2402	2	AAQ90184 BRK-1 DNA
12	2823	99.5	2402	2	Aat27228 Bone morph
13	2823	99.5	2402	2	Aat28021 Mouse BMP
14	2823	99.5	2402	2	Aav71972 Mouse BMP
15	2798	98.6	2056	2	AAQ90183 Truncated
16	2769	97.6	1599	13	Adq98877 Antagonis
17	2769	97.6	1599	13	Adr73164 Human bon
18	2769	97.6	2623	8	Adw53821 DNA used
19	2769	97.6	2932	2	AAQ66636 Human Act
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21	2769	97.6	2932	2	Aaz09843 Human HAL
22	2769	97.6	2932	5	Aas87057 DNA encod
23	2769	97.6	2932	10	ACF05952 Human bon
24	2769	97.6	2932	14	Adw28812 Human bon
25	2769	97.6	2932	14	Adx07490 Cyclin-de
26	2769	97.6	2932	14	Adx97425 Human bon
27	2769	97.6	2932	14	Ady51867 Human ALK
28	2769	97.6	2932	14	Aec02077 Nuclcotid
29	2763	97.4	3631	14	Ady81406 Human act
30	2635.5	92.9	1743	10	Ado7106 Novel cod
31	2635.5	92.9	1743	14	Adu40263 Novel hum
32	2604.5	91.8	1929	10	Ado7107 Novel cod
33	2604.5	91.8	1929	14	Adu40264 Novel hum
34	2601	91.6	2730	5	AAS87064 DNA encod
35	2129.5	75.0	1695	5	AAS87063 DNA encod
36	2011	70.9	1185	12	Ach87174 Human Gen
37	1972	69.5	1612	5	Aad11871 Wild-type
38	1968	69.3	1612	5	Aad11872 Booroola
39	1952	68.8	1575	8	ACD13394 Human DNA
40	1952	68.8	1575	14	Adw28813 Human bon
41	1952	68.8	1575	14	Adx97426 Human bon
42	1952	68.8	2032	6	Abk92206 Prostate
43	1952	68.8	2032	6	Abt07695 Breast ca
44	1952	68.8	2032	6	Abk90314 DNA encod
45	1952	68.8	2032	8	Abt17075 Androgen-

ALIGNMENTS

RESULT 1
AAQ83530
ID AAQ83530 standard; DNA; 1813 BP.
XX
AC AAQ83530;
XX
DT 25-MAR-2003 (revised)
DT 28-SEP-1995 (first entry)
XX
Sequence encoding bone morphogenic protein receptor CPK1-23a.
XX
Bone morphogenic protein; receptor; serine/threonine kinase; BMP; bone;
cartilage; injury; treatment; inhibition; ss.
XX
Rattus rattus.
XX
FH Key Location/Qualifiers
CDS 61..1659
FT /*tag= a
FT /product= "Bone morphogenic protein receptor."
XX
PN WO9507982-A1.
XX
PD 23-MAR-1995.
XX
PF 07-SEP-1994; 94WO-US010080.
XX
PR 17-SEP-1993; 93US-00123934.

XX ADW28817;
AC
XX
XX
DT 07-APR-2005 (first entry)
XX
DE Rat bone morphogenetic protein (BMP) receptor type 1 DNA Seq 121.
XX
XX receptor; bone morphogenetic protein; bone injury; antibody production;
KW TGF beta antagonist; BMP-antagonist; osteopathic; osteopenias;
KW osteoporosis; gene; ds.
XX
XX Rattus norvegicus.
OS
XX
XX Key Location/Qualifiers
FH 83..1681
FT /*tag= a
FT /product= "BMP receptor type 1 protein"
XX
XX WO2005003158-A2.
XX
XX 13-JAN-2005.
XX
XX 15-JUN-2004; 2004WO-US018910.
XX
XX 16-JUN-2003; 2003US-00463190.
XX
XX (CLLT) CELLTECH R & D INC.
XX
XX Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paepers BW;
PI Van Ness J, Winkler DG;
XX
XX WPI: 2005-081936/09.
XX P-PSDB; ADW28803.
XX
XX New antibody or antigen-binding fragment that binds specifically to
PT sclerostin polypeptide and which inhibits binding of sclerostin
PT polypeptide to a bone morphogenic protein, useful for increasing bone
PT mineral content or density.
XX
XX Disclosure; SEQ ID NO 121; 205pp; English.
XX
XX This invention relates to a novel antibody or antigen-binding fragment
CC that binds specifically to a sclerostin (SOST) polypeptide and impairs
CC formation of a sclerostin homodimer. Specifically, it refers to an
CC antibody that competitively inhibits binding of the sclerostin
CC polypeptide to a bone morphogenic protein (BMP) type I receptor binding
CC site or a BMP type II receptor binding site. The present invention
CC describes a hybridoma cell capable of producing the antibody and a host
CC cell for antibody expression. Furthermore, it provides a nucleic acid
CC molecule encoding a transforming growth factor-beta (TGF-beta) binding
CC protein known as SOST (and also BSR) and methods for detection thereof.
CC Accordingly, such antibodies and osteopathic compositions of the
CC invention can be used for treating osteopenia, osteoporosis, fractures
CC and other disorders related to low bone mineral content and density. As
CC such, these compositions improve bone mineralization and can be described
CC as TGF-beta antagonists and/ or BMP-antagonists. This polynucleotide is a
CC bone morphogenetic protein receptor type 1 DNA sequence given in an
CC exemplification of the invention.
XX
XX Sequence 3003 BP; 840 A; 626 C; 654 G; 883 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 9,236-294 Length: 3003
Score: 2838.00 Matches: 532
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-600-645-2 (1-532) x ADW28817 (1-3003)

QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyValaCysLeuPheIleSerHis 20
|||||
DB: |||||

83 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCCTGTCTGTTCATCTCTCAT 142
QY
21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
DB
143 GTTCAAGGGCAGAACTAGATAGTATGCTCCATGGTACTGGTATGAATCAGACGTGGAC 202
QY
41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
DB
203 CAGAGAAGCCGGAAATAGAGTGAGTACGTTAGCACAGAGGACACCTTACCTTTCTTAAAA 262
QY
61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
DB
263 TGTATTGTCTCAGGACACTGCCAGATGACGCTATTATAAACACATGCATAACTAATGGC 322
QY
81 HisCysPheAlaIleIleGluGluAspAspGlnGlyThrThrLeuThrSerGlyCys 100
DB
323 CATTTGCTTTGCCATTATAGAAGAAGATGATCAGGGAGAACCCAGTTAACTTCTGGGTGT 382
QY
101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
DB
383 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCAAAAGCCAGCTACGAGG 442
QY
121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrIleGlnProThrLeuProPro 140
DB
443 ACAATAGAATGTTGTCGGACCAATTTGTGCAACCAATATTTCAGAGCTACACATGCCCCCT 502
QY
141 ValValIleGlyProPhePheAspGlySerValArgTPrLeuAlaValLeuIleSerMet 160
DB
503 GTTCGTTATAGGCCCATTCCTTTGATGGCAGCGTCCGATGGCTGGCTGCTCTCTATG 562
QY
161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
DB
563 GCTGCTGTATTGTGCCCATGATCGTCTTCTCCAGCTGCTTCTGTACAAACATTAATTT 622
QY
181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
DB
623 AAGAGTATCTCAAGCAGAGAGTGGTTACAACCGTGACTTGGAAACAGGATGAAGCATTTAT 682
QY
201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
DB
683 CAGTAGAGGAGATCACTGAAGACCTGATTGACCACTGCTCAAGAGCTCTGGTAGTGATCT 742
QY
221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
DB
743 GGATTAACCTTTATTGTTTCAGCGAATATTGCCAAACAGATTGAGTGGTTCGGCAGTT 802
QY
241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
DB
803 GGTAAAGGCCGGGTATGGAGAAAGTATGGATGGGTAAATGGGTGTTGAAAAAGTGGCTGTC 862
QY
261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
DB
863 AAGATATTTTTCACCTGAAGAAGCTAGCTGGTTTAGAGAAACAGAAATCTACCCAGACG 922
QY
281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
DB
923 GTGTTAATGCGTCATGAATAATATCTTGGTTTTATAGCTGCAGACATTAAGAGCACCGGT 982
QY
301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
DB
983 TCCTGGACTCAGCTGTATTGATTGATTACTGATTACCATGAGAAATGGGTCTCTCTATGACTTC 1042
QY
321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
DB
1043 CTGAATAATGGCCACCCCTGGACACCCAGAGCCCTACTCAAGTTAGCTTATTCTGCTGCTGT 1102
QY
341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
DB
1103 GGTCTGTGCCACTCCACACAGAAATTTATGSCAGCAGCAGGCAAGGCTGCAATTTGCTCAT 1162
QY
361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysIleAlaAsp 380
DB
1163 CGAGACCTCAAGAGAGCAAAACATCCTTTATAAGAAAAATGGTAGTTGCTGTATTGCTGAC 1222

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QY 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
DB 1223 CTGGGCGCTAGCTGTTAAATTCACACAGTGACACAAATGAAGTTGACATACCCCTTGAACACC 1282
QY 401 ArGValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLysAsn 420
DB 1283 AGGTTGGGACACAGCGGTACATGGCTCCAGAAAGTGTGGACGACGAGCTGAGTAAAC 1342
QY 421 HisPheGlnProTyrIleMetAlaPheIleTyrSerPheGlyLeuIleIleTrpGluMet 440
DB 1343 CATTTCACGCGCTACATCATGCTGACATCTACAGCTTTGGTTTGATCATTTTGGGAGATG 1402
QY 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
DB 1403 GCCCGTGCCTGTATTACAGAGGAATCGTGGAGGAATATCAATATACCATATTTACAAATG 1462
QY 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
DB 1463 GTGCGTAGTGACCATCTTATGAGACATGCGTGAGGTCGTGTGTGTGTAACGCTTGGCG 1522
QY 481 ProfileValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
DB 1523 CCAATCGTCTCTAACCGCTGGAACAGTGATGAATGTCTTCGAGCGCTTTTGAAGCTGATG 1582
QY 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
DB 1583 TCAGAAATGCTGGGCGCCATAATCCAGCATCCAGACTCACAGCTTTTGAGAAATCAAGAAGACG 1642
QY 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
DB 1643 CTCGCAAGATGTTGAATCCAGGATGTAAGATT 1678
```

RESULT 3

```
ADX97430
ID ADX97430 standard; DNA; 3003 BP.
XX
AC ADX97430;
XX
DT 05-MAY-2005 (first entry)
XX
DE Rat bone morphogenic protein type I receptor encoding DNA, SEQ ID 90.
XX
KW antibody; sclerostin; SOST; bone morphogenic protein receptor;
KW Transforming Growth Factor; osteoporosis; gene therapy; bone repair;
KW osteopenia; osteoporosis; bone injury; gene; ds.
XX
OS Rattus norvegicus.
XX
FH Key Location/Qualifiers
CDS 83..1681
FT /*tag= a
FT /product= "Rat bone morphogenic protein type I receptor"
XX
XX WO2005014650-A2.
XX
XX 17-FEB-2005.
XX
XX 15-JUN-2004; 2004WO-US018912.
XX
XX 16-JUN-2003; 2003US-0478977P.
XX
XX (CLT ) CELLTECH R & D INC.
XX
XX Winkler DG, Shi J, Latham J;
XX
XX WPI: 2005-163219/17.
XX
XX P-PSDB; ADX97416.
XX
XX New isolated antibody specific for a sclerostin polypeptide, useful for
XX increasing bone mineralization or for treating or preventing conditions
XX associated with low bone mineral density, e.g. osteoporosis or
XX osteopenia.
```

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XX
PS Disclosure; SEQ ID NO 90; 157pp; English.
XX
CC The invention relates to a novel isolated antibody, or its antigen-
CC binding fragment, which binds specifically to a sclerostin (SOST)
CC polypeptide. The SOST polypeptide comprises any of 6 sequences having 190
CC or 213 amino acids, fully defined in the specification (ADX97341,
CC ADX97360, ADX97398, ADX97400, ADX97402 or ADX97408). The antibody
CC competitively inhibits binding of the SOST polypeptide to a bone
CC morphogenic protein (BMP) Type I Receptor binding site and a BMP Type II
CC capable of binding to a BMP Type I Receptor polypeptide. The invention
CC further comprises a hybridoma cell producing the new antibody; a host
CC cell that is capable of expressing the new antibody; a composition
CC comprising the new antibody, or its antigen-binding fragment, and a
CC physiological carrier; an immunogen comprising a peptide comprising 6, 7,
CC 8, 9, 10, 11, 12, or at least 21-50 or 20-75 consecutive amino acids of
CC the SOST polypeptide; methods for producing an antibody that specifically
CC binds to the SOST polypeptide; and methods for identifying an antibody
CC that modulates a Transforming Growth Factor (TGF)-beta signaling pathway,
CC that impairs binding of a BMP to the SOST polypeptide, that impairs SOST
CC homodimer formation, or that increases bone mineral content. The novel
CC antibody and compositions have osteopathic activity. The SOST nucleic
CC acids may be used in gene therapy. The composition and methods are useful
CC for increasing bone mineralization, which may treat or prevent diseases
CC or conditions associated with low bone mineral density, such as
CC osteopenia, osteoporosis or bone fractures. This polynucleotide sequence
CC represents a rat bone morphogenic protein type I receptor encoding DNA of
CC the invention.
XX
SQ Sequence 3003 BP; 840 A; 626 C; 654 G; 883 T; 0 U; 0 Other;
```

Alignment Scores:

```
Pred. No.: 9.23e-294 Length: 3003
Score: 2838.00 Matches: 532
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-600-645-2 (1-532) x ADX97430 (1-3003)

QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleSerHis 20
DB 83 ATGATCTAGCTATACACTTACATCAGATTACTGGAGCGCTGCTGTTTCATCATTTCTCAT 142
QY 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
DB 143 GTTCAAGGCGAAGATCTAGATAGTAGTATGCTCCATGCTGTTGTAATAATCAGACGTGAC 202
QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
DB 203 CAGAAGAAGCGGAAAAATGGAGTGACGTTAGCACCAGAGGACACCTTACCTTTCTTAAAA 262
QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
DB 263 TGCTATTGCTCAGGACACTGCCCCAGATGACCTATTATAACACATGATCAATTAATGCG 322
QY 81 HisCysPheAlaIleIleGluGluAspGlnGlyGluThrThrLeuThrSerGlyCys 100
DB 323 CATTGCTTTGCCATTATAGAAAGATGATCAGGAGAAACACGTTTAACTTCTGGGTGT 382
QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
DB 383 ATGAAGTATGAAGCTCTGATTTTCAATGCAAGGATTCAACCAAAAGCCAGCTACGACG 442
QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
DB 443 ACAATAGAAATGTTTCGAGCAACCAATTTGTGCAACCAATATTTTGCAGCTTACACTGC 502
QY 141 ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
DB 503 GTCGTTATAGGCCCATTCCTTTTGATGGCAGCGCTCCGATGGCTGGCTGCTCATCTCTATG 562
```

Qy 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrIleYsHisTyrCys 180
Db 563 GCTGCTGTATTGTGCGCATGATCGTCTCTCCAGCTGCTCTCTGTACAAACATTACTGT 622

Qy 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluInAspGluAlaPheIle 200
Db 623 AAGAGTATCTCAAGCAGAGGTGCTTACAAACCGTGACTTGGAAACAGGATGAAGCATTTATT 682

Qy 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
Db 683 CCAAGTAGAGATCACTGAAAGACCTGATTGACCAGTCACAAAGCTCTGGTAGTGATCT 742

Qy 221 GlyLeuProLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 743 GGATTACCTTTATTGGTTCAGCAACTATTGCCAAACAGATTACAGTGGTTCGCCAGGTT 802

Qy 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
Db 803 GGTAAAGGCCGATATGAGAAGTATGATGGTAAATGGCGTGGTGAAGTGGCTGTC 862

Qy 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
Db 863 AAAGTATTTTACCCTGGAAGAGCTAGCTGGTTTAGAGAAACAGAAATCTTACCAAGC 922

Qy 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db 923 GTGTTAATGCTCATGAAATATATCTTGGTTTTATAGCTGCAGACATTAAGACACCGGT 982

Qy 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db 983 TCCTGGACTCAGCTGATTTGATTACTGATTACCATGAGAATGGGTCTCTCTATGACTTC 1042

Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db 1043 CTGAAATGTGCCACCTCCACAGAAATTTATGGCAGCAAGCAAGCTGCAATGCTCAT 1102

Qy 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1103 GGTCTGTGCCACCTCCACAGAAATTTATGGCAGCAAGCAAGCTGCAATGCTCAT 1162

Qy 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
Db 1163 CGAGACTGAAGAGCAAAACATCCTATTAAAGAAAATGGTAGTTGCTGTATTGCTGAC 1222

Qy 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db 1223 CTGGGCTAGCTGTTAAATTCACAGTGACACAAATGAAGTTGACATACCCCTTGAACACC 1282

Qy 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
Db 1283 AGGTTGGACCAAGCGGTACATGGCTCCAGAAAGTCTGACAGAGCTTGAGTAAAAAC 1342

Qy 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
Db 1343 CATTTCCAGCCCTACATCATGCTGACATCTACAGCTTTGGTTTGATCATTTGGGAGATG 1402

Qy 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db 1403 GCCCGTGCCTGATTACAGAGGAATCGTGGAGAAATATCAATTACCATATTACAACATG 1462

Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db 1463 GTGCTTAGTACCCATCTTATGAAGACATCGGTGAGGTGCTGTGTGTGAACCTTGCCG 1522

Qy 481 ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1523 CCAATGCTCTTAACCGCTGGAACAGTGATGATGCTTCGAGCCGCTTTTGAAGCTGATG 1582

Qy 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
Db 1583 TCAGATGTGGGCCCAATATCCAGCATCCAGACTCACAGCTTTCAGATCAAGAAGACG 1642

Qy 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db 1643 CTCGCAAGATGGTTGAATCCAGGATGTAAAGATT 1678

RESULT 4
ADM28816
ID ADM28816 standard; DNA; 3167 BP.
XX
AC ADM28816;
XX
DT 07-APR-2005 (first entry)
XX
DE Rat bone morphogenetic protein (BMP) receptor type 1 DNA Seq 120.
XX
KW receptor; bone morphogenetic protein; bone injury; antibody production;
XX TGF beta antagonist; BMP-antagonist; osteopathic; osteopenias;
XX osteoporosis; gene; de.
XX
OS Rattus norvegicus.
XX
FH Key Location/Qualifiers
FT CDS 226..1824
FT /*tag= a
FT /product= "BMP receptor type 1 protein"
XX
XX WO2005003158-A2.
XX
XX 13-JAN-2005.
XX
XX 15-JUN-2004; 2004WO-US018910.
XX
XX 16-JUN-2003; 2003US-00463190.
XX
XX (CLLT) CELLTECH R & D INC.
XX
XX Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paepers BW;
PI Van Ness J, Winkler DG;
XX
XX WPI: 2005-081936/09.
XX P-PSDB; ADM28802.
XX
XX New antibody or antigen-binding fragment that binds specifically to
XX sclerostin polypeptide and which inhibits binding of sclerostin
XX polypeptide to a bone morphogenic protein, useful for increasing bone
XX mineral content or density.
XX
XX Disclosure; SEQ ID NO 120; 205pp; English.
XX
XX This invention relates to a novel antibody or antigen-binding fragment
XX that binds specifically to a sclerostin (SOST) polypeptide and impairs
XX formation of a sclerostin homodimer. Specifically, it refers to an
XX antibody that competitively inhibits binding of the sclerostin
XX polypeptide to a bone morphogenic protein (BMP) Type I receptor binding
XX site or a BMP Type II receptor binding site. The present invention
XX describes a hybridoma cell capable of producing the antibody and a host
XX cell for antibody expression. Furthermore, it provides a nucleic acid
XX molecule encoding a transforming growth factor-beta (TGF-beta) binding
XX protein known as SOST (and also BEER) and methods for detection thereof.
XX Accordingly, such antibodies and osteopathic compositions of the
XX invention can be used for treating osteopenia, osteoporosis, fractures
XX and other disorders related to low bone mineral content and density. As
XX such, these compositions improve bone mineralization and can be described
XX as TGF-beta antagonists and/or BMP-antagonists. This polynucleotide is a
XX bone morphogenetic protein receptor type 1 DNA sequence given in an
XX exemplification of the invention.
XX
XX Sequence 3167 BP; 908 A; 647 C; 688 G; 924 T; 0 U; 0 Other;

Alignment Scores:
Pred. NO.: 9,99e-294 Length: 3167
Score: 2838.00 Matches:
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0


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Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
US-10-600-645-2 (1-532) x ADW28816 (1-3167)

QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
DB 226 ATGACTCAGCTATACACTTACATCAGATTACTGGAGGCTGCTCTGTTTCATCTCAT 285
QY 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
DB 286 GTTCAAGGCGAGAACTAGATAGTATGCTCCATGCTACTGGTATCAAAATCAGACGTCGAC 345
QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
DB 346 CAGAAAGAGCCGGAATAATGGAGTACGTTAGCACAGAGGACACCTTACCTTTCTTAAAA 405
QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
DB 406 TGCTATTGCTCAGGACACTGCCACATGACGCTATTATACACATGATTAACCTAATGGC 465
QY 81 HisCysPheAlaIleIleGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
DB 466 CATTGCTTGCCATTATAGAAGATGATCAGGGAGAAACACCGTTAACTTCTGGGTGT 525
QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
DB 526 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCAAAAGCCAGCTACGCAGG 585
QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
DB 586 ACAATAGAAATGTTGTCGGACCAATTTGTGCAACCAATATTTGCAGCCTTACACTGCCCCCT 645
QY 141 ValValIleGlyProPhePheAspGlySerValArgTyrLeuAlaValIleSerMet 160
DB 646 GTCGTATATAGGCCCATCTCTTGATGCGAGCGTCCGATGGCTGGCTGCTCATCTCTATG 705
QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
DB 706 GCTGTCGTATGTCGCCATGATGCTCTTCTCCAGCTGCTTCTGTGTACAAAACATTACTGT 765
QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
DB 766 AAGAGTATCTCAAGCAGAGGTCGTTACAAACCGTGACTTGGAAACAGATGAAGCATTTAT 825
QY 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
DB 826 CCAGTAGGAGAAATCACTGAAAGACCTGATTGACCAAGTCACAAAGCTCTGGTAGTGATCT 885
QY 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
DB 886 GGATTTACCTTTATTGGTTTTCAGCGAACTATTGCCAAACAGATTTCAGATGGTTTCGGCAGGTT 945
QY 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTyrArgGlyGluLysValAlaVal 260
DB 946 GGTAAAGCCCGGTATGGAGAGTATGGATGGGTAATGGCGTGGTGAAGAAAGTGGCTGTC 1005
QY 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
DB 1006 AAAGTATTTTACCACCTGAAGAAGCTAGCTGGTTTATAGAGAAACAGAAATCTACCAGAGC 1065
QY 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
DB 1066 GTGTTAATGCGTCATGAAATAATATCTTGGTTTTTATAGCTGCAGACATTTAAAGGCCACCGGT 1125
QY 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
DB 1126 TCCTCGACTCAGCTGATTTGATTTACTGATTACCATGAGATGGGTCTCTCTATGACTTC 1185
QY 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
DB 1186 CTGAAATGTGCCACCTGGACACACAGAGCCCTACTCAAGTTAGCTTATTCTGCTGCTGT 1245
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QY 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
DB 1246 GGTCTGTGCCACCTCCACACAGAAATTTATGGCAGCAAGGCAAGCCTGCAATTTGCTCAT 1305
QY 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
DB 1306 CGAGACCTGAGAGCAAAACATCTTATTAAAGAAAATGGTAGTTGCTGATTGCTGAC 1365
QY 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAlaAspIleProLeuAsnThr 400
DB 1366 CTGGCCCTAGCTGTATAATTCAACAGTCACACAAATGAAGTTGACATACCTTGAACACC 1425
QY 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLysSerLysAsn 420
DB 1426 AGGTGGGCAACAGCGGTATATGGCTCCAGAAAGTCTGGACGAGCCTGAGTAAAAAC 1485
QY 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTyrGluMet 440
DB 1486 CATTTCCAGCCCTACATCATCTGCTGACATCTACAGCTTTGGTTGATCATTTGGGAGATG 1545
QY 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
DB 1546 CCCCCTGCTGTATTTACAGGAGGAATCGTGGAGGAATATCAATTACCATATTTACACATG 1605
QY 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
DB 1606 GTGCTAGTAGCCCATCTTATGAAGACATGCTGAGGTCGTGTGTGTAACGCTTGGCG 1665
QY 481 ProIleValSerAsnArgTyrAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
DB 1666 CCAATGCTCTTAACCGCTGGAAACAGTGATGAATGTCTTCGAGCCGTTTGAAGCTGATG 1725
QY 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
DB 1726 TCAGAAATGCTGGGCCATAATCCAGACTCCAGACTCAGAGCTTTGAGAATCAAGAAGACG 1785
QY 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
DB 1786 CTCGAAAGATGGTTGAATCCCGGATGTAAGATTT 1821

RESULT 5
ADW28815
ID ADW28815 standard; DNA; 3167 BP.
XX AC ADW28815;
XX DT 07-APR-2005 (first entry)
XX DE Rat bone morphogenetic protein (BMP) receptor type 1 DNA Seq 119.
XX KW receptor; bone morphogenetic protein; bone injury; antibody production;
XX KW TGF beta antagonist; BMP-antagonist; osteopathic; osteopenias;
XX KW osteoporosis; gene; ds.
XX OS Rattus sp.
XX FH Key Location/Qualifiers
XX FT 226..1824
XX FT /*tag= a
XX FT /product= "BMP receptor type 1 protein"
XX PN WO2005003158-A2.
XX PD 13-JAN-2005.
XX PF 15-JUN-2004; 2004WO-US018910.
XX PR 16-JUN-2003; 2003US-00463190.
XX PA (CLLT ) CELLTECH R & D INC.
XX PI Brunkow ME, Galas DJ, Kovacevich B, Mulligan JT, Paepfer BW;
XX PI Van Ness J, Winkler DG;
```

XX WPI; 2005-081936/09.
 DR P-PSDB; ADW28801.
 XX
 PT New antibody or antigen-binding fragment that binds specifically to
 PT sclerostin polypeptide and which inhibits binding of sclerostin
 PT polypeptide to a bone morphogenic protein, useful for increasing bone
 PT mineral content or density.
 XX
 XX Disclosure; SEQ ID NO 119; 205pp; English.
 XX
 CC This invention relates to a novel antibody or antigen-binding fragment
 CC that binds specifically to a sclerostin (SOST) polypeptide and impairs
 CC formation of a sclerostin homodimer. Specifically, it refers to an
 CC antibody that competitively inhibits binding of the sclerostin
 CC polypeptide to a bone morphogenic protein (BMP) Type I receptor binding
 CC site or a BMP Type II receptor binding site. The present invention
 CC describes a hybridoma cell capable of producing the antibody and a host
 CC cell for antibody expression. Furthermore, it provides a nucleic acid
 CC molecule encoding a transforming growth factor-beta (TGF-beta) binding
 CC protein known as SOST (and also BEER) and methods for detection thereof.
 CC Accordingly, such antibodies and osteopathic compositions of the
 CC invention can be used for treating osteopenia, osteoporosis, fractures
 CC and other disorders related to low bone mineral content and density. As
 CC such, these compositions improve bone mineralization and can be described
 CC as TGF-beta antagonists and/or BMP-antagonists. This polynucleotide is a
 CC bone morphogenetic protein receptor type 1 DNA sequence given in an
 CC exemplification of the invention.
 XX
 SQ Sequence 3167 BP; 908 A; 647 C; 688 G; 924 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 9,99e-294 Length: 3167
 Score: 2838.00 Matches: 532
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0

US-10-600-645-2 (1-532) x ADW28815 (1-3167)

QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleSerHis 20
 DB 226 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCCCTGCTGTTTCATCTCAT 285
 QY 21 valGlnGlyClnAsnLeuAspSerMetLeuHisGlyThrGlyMetIysSerAspValAsp 40
 DB 286 GTTCAAGGGCAGAACTCTAGATAGTATGCTCCATGGTACTGGTATGAAATCAGACGTGGAC 345
 QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
 DB 346 CAGAAAGCCGGAAATGGAGTGACGTGTAGCACCAGAGACACCTTACTCTTTCTTAAAA 405
 QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
 DB 406 TGCTATTGCTCAGACACATGCCAGATGACGCTATTATAACACATGCACTAATATGGC 465
 QY 81 HisCysPheAlaIleIleGluGluAspAspGlnGlyThrThrLeuThrSerGlyCys 100
 DB 466 CATTTGCTTTGCCATTATAGAAGAAGATGATCAGGGAGAAACCAACGTTAACTCTGGGTGT 525
 QY 101 MetLysTyrGluGlySerPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
 DB 526 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGATTCACAAAGCCAGCTACGACGG 585
 QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrIleGlnProThrLeuProPro 140
 DB 586 ACAATAGATGTTGTTCGGACCAATTTGTGCAACCATATTTGCAGCTACACTGCCCTCT 645
 QY 141 valValIleGlyProPhePheAspGlySerValArgTyrLeuAlaValLeuIleSerMet 160
 DB 646 GTCGTTATAGGCCCAATCTTTGTATGGCAGCGTCCGATGGCTGGCTGTGCTCTCTATG 705

QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrIysHisTyrCys 180
 DB 706 GCTGTCTGTATTGTCGCCCATGATCGTCTTCTCCAGCTGCTTCTGTTCACAAACATTACTGT 765
 QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
 DB 766 AAGAGTATCTCAAGCAGAGGTCGTTACAAACCGTGACTTGGAAACAGGATGAAGCATTTATT 825
 QY 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
 DB 826 CCAGTAGGAAGATCACTGAAAGACCTGATTGACCACTCACAAGCTCTGTGTAGTGATCT 885
 QY 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
 DB 886 GGATTACCTTTATTGTTTTCAGCGAACTATTGCCAAACAGATTCCAGATGGTTCCGCGAGTT 945
 QY 241 GlyLysGlyArgTyrGlyGluValTyrMetGlyLysTyrArgGlyGluLysValAlaVal 260
 DB 946 GGTAAAGGCCGCTATGGAGAAGTATGGATGGGTAAATGGCGTGGTGAAGGTTGGCTGTC 1005
 QY 261 LysValPhePheThrThrGluGluAlaSerTyrPheArgGluThrGluIleTyrGlnThr 280
 DB 1006 AAGATTATTTTACCCTGAAAGAGCTAGTGGTTTAGAGAAACAGAAATCTACCAAGC 1065
 QY 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
 DB 1066 GTGTTAATCGGTCATGAAATATATCTGGTTTATAGCTGCAGACATTAAGGCACCGGT 1125
 QY 301 SerTyrThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
 DB 1126 TCTCGACTCAGCTGTATTGTTACTGATTACCATGAGATGGGTCTCTATGACTTC 1185
 QY 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
 DB 1186 CTGAAATGTCACCCCTGCACACACAGAGCCCTACTCAAGTTAGCTTATTCTGCTGCTGT 1245
 QY 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
 DB 1246 GGTCTGTGCCACTCCACACAGAAATTTATGGCAGCAGGCAAGGCTGCATTTGCTCAT 1305
 QY 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
 DB 1306 CGAGACCTCAGAGCAAAACATCTCTATTAAGAAAAATGGTAGTTGCTGTATTGCTGAC 1365
 QY 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
 DB 1366 CTGGGCCCTAGCTGTGTTAAATTCAACAGTGCACAAATGAAGTTGACATACCCCTTGAACACC 1425
 QY 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
 DB 1426 AGGGTGGGCACCGCGGTACATGGCTCCAGAAAGTGTCTGGACGAGGCTGAGTAAAC 1485
 QY 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTyrGluMet 440
 DB 1486 CATTTCCAGCCCTACATCATGCTGCATCTCAGCTTTGGTTTGTATCATCTTTGGGAGATG 1545
 QY 441 AlaArgArgCysIleThrGlyIleValGluTyrGlnLeuProTyrTyrAsnMet 460
 DB 1546 GCCCGCTCGTGTTATACAGGAGAAATCGTGGAGGAATATCAATATACCATATTACCAATG 1605
 QY 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
 DB 1606 GTGCTAGTGACCCATCTTATGAAGACATGCGGTGAGTGTGTGTGTGAACGCTTGGCG 1665
 QY 481 ProfileValSerAsnArgTyrAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
 DB 1666 CCAATCGTCTCTAACCGCTGGAAACAGTGAATGCTTCGAGCCGCTTTTGAAGCTGATG 1725
 QY 501 SerGluCysTyrAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysThr 520
 DB 1726 TCAGAAATGTGGGCCCATTAATCCAGACTCCAGACTTCAGAGCTTTTGAGATCAAGAAGC 1785
 QY 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532

Db	1126	TCCTGGACTGACGTGTTATTTGATTACTGATTACCATGGAATGGGTCTCTCTATGACTTC	1185
Qy	321	LeuLysCysAlaIthrLeuAspThrArgAlaLeuLeuLysLeuAlaItyrSerAlaAlaCys	340
Db	1186	CTGAAATGTGCGACCCCTGGACACAGAGCCCTACTCAAGTTAGCTTATTCTGCTGCCTGT	1245
Qy	341	GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis	360
Db	1246	GGTCTGTGCCACCTCCACACAGAAATTTATGGCACGAAGCAAGCCTGCAATTTGCTCAT	1305
Qy	361	ArgAspLeuLysSerLysAsnIleLeuIleLysAsnGlySerCysCysIleAlaAsp	380
Db	1306	CGAGACCTGAAGACCAAAACATCCTTATTAGAAAAATGGTAGTTGCTGTATTCTGCTGAC	1365
Qy	381	LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr	400
Db	1366	CTGGCCCTAGCTGTTAAATTCAACAGTGACACAAATGAAGTTGACATACCCTTGAACACC	1425
Qy	401	ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn	420
Db	1426	AGGCTGGGCACACAGCGGTACATGGCTCCAGAAGTGTGGACGAGAGCCTGAGTAAAAAC	1485
Qy	421	HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTyrGluMet	440
Db	1486	CATTTCAGCGCCTACATCATGGCTGACATCTACAGCTTGTGGTTGATCATTTGGGAGATG	1545
Qy	441	AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet	460
Db	1546	GCCCGTCGCTGATTACAGGAGGAATCGTGGAGGAATATCAATTACCATTACAAACATG	1605
Qy	461	ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg	480
Db	1606	GTGCCTAGTCACCCATCTTATGAAAGACATGCGTGAGGTGCGTGTGTGTGAAACGCTTCGGG	1665
Qy	481	ProIleValSerAsnArgTyrAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet	500
Db	1666	CCAATCGCTCTTAACCCGCTGAAACAGTGATGAATGTCTTCGAGCCGTTTTGAAGCTGATG	1725
Qy	501	SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr	520
Db	1726	TCAGATGCTGGGCCCATATCCAGCATCCAGACTCACAGCTTGAGATCAAGAGACG	1785
Qy	521	LeuAlaLysMetValGluSerGlnAspValLysIle	532
Db	1786	CTGCGAAAGATGGTTGAATCCAGAGTGAAGATT	1821

RESULT	7
ADX97429	
ID	ADX97429 standard; DNA; 3167 BP.
AC	ADX97429;
XX	
XX	05-MAY-2005 (first entry)
DT	
XX	Rat bone morphogenic protein type I receptor encoding DNA, SEQ ID 89.
DE	
XX	antibody; sclerostin; SOST; bone morphogenic protein receptor;
KW	Transforming Growth Factor; osteopathic; gene therapy; bone repair;
KW	osteopenia; osteoporosis; bone injury; gene; ds.
XX	
OS	Rattus norvegicus.
XX	
Key	Location/Qualifiers
FH	226..1824
CDS	/tag= a
FT	/product= "Rat bone morphogenic protein type I receptor"
FT	
XX	
PN	WO2005014650-A2.
PX	
XX	
PD	17-FEB-2005.
XX	
PF	15-JUN-2004; 2004WO-US018912.
XX	

Db ||||| 466 CATTGCTTTGCCATTATAGAACAGATGATCAGGAGAAACACCGTTAACTTCIGGGTGT 525
Qy ||||| 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db ||||| 526 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGAGATTACCAAAAAGCCAGCTAGCCAGG 585
Qy ||||| 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
Db ||||| 586 ACAATAGAAATGTGTGCGACCAATTTGTGCAACCAATATTTGCGACCTACACTGCCCCCT 645
Qy ||||| 141 ValValIleGlyProPhePheAspGlySerValArgTTPLeuAlaValLeuIleSerMet 160
Db ||||| 646 GTCTGTATAGGCCCATCTCTTGATGGCAGCGTCCGATGGCTGGCTGTCTCATCTCTATG 705
Qy ||||| 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrIleHisTyrCys 180
Db ||||| 706 GCTGTCTGTATTGTGCCATGATCGTCTTCTCAGCTGCTTCTGTTTACAAACATTACTGT 765
Qy ||||| 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
Db ||||| 766 AAGAGTATCTCAAGCAGAGGTCGTTACAAACCGTGACTTGGAAACAGGATGAAGCATTTATT 825
Qy ||||| 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySer 220
Db ||||| 826 CCAGTAGGAGATCACTGAAGACCTGATTGACCAAGCTCACAAGGCTCTGGTAGTGATCT 885
Qy ||||| 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db ||||| 886 GGATTACCTTTATTGTTTCCAGCGAACTATTGCAACAGATTCAGATGGTTCCGCGAGTT 945
Qy ||||| 241 GlyLysGlyArgTyrGlyGlnValTrpMetGlyLysTyrTrpArgGlyGluLysValAlaVal 260
Db ||||| 946 GGTAAAGCCGCTATGGAGAGTATGGATGGGTAAATGGCGTGGTGAATAAGTGGCTGTC 1005
Qy ||||| 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
Db ||||| 1006 AAGTATTTTTCACCTGAAGAGCTAGCTGGTTTAGAGAAACAGAAATCTACAGAGC 1065
Qy ||||| 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db ||||| 1066 GTGTTAATGCGTCATGAAATATACTTGGTTTTATAGCTGCAGACATTAAGGCCACCGT 1125
Qy ||||| 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db ||||| 1126 TCTCGACTCAGCTGATTGATTGATTCTGATTACCATGAAATGGGTCTCTCTATGACTTC 1185
Qy ||||| 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db ||||| 1186 CTGAATGTGCCACCTGGACACCAAGCCCTACTCAAGTTAGCTTTATCTGCTGCTGT 1245
Qy ||||| 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db ||||| 1246 GTCTGTGCCACCTCCACACAGAAATTTATGCGCAAGGCAAGCCGCAATTCCTCAT 1305
Qy ||||| 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
Db ||||| 1306 CGAGACCTGAGAGCAAAACATCTTATTAGAAAAATGGTAGTTGCTGATTGCTGAC 1365
Qy ||||| 381 LeuGlyLeuAlaValIlePheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db ||||| 1366 CTGGGCTAGCTGTAAATTTCAACAGTGACACAAATGAAGTTGACATACCTTTGAACACC 1425
Qy ||||| 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
Db ||||| 1426 AGGTTGGGACCCAGGGGTACATGGCTCCAGAAGTGTGGACGAGGCTGAGTAAAC 1485
Qy ||||| 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
Db ||||| 1486 CATTTCAGCCCTACATCATGCTGACATCTACAGCTTGGTTTGTGATCATTTGGGAGATG 1545
Qy ||||| 441 AlaArgArgCysIleThrGlyIleValGluTyrGlnLeuProTyrTrpAsnMet 460

Db ||||| 1546 GCCCGTCTGCTGATTATACAGGAGGAATCGTGAGGAAATATCAATTACCATATTTACAACATG 1605
Qy ||||| 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db ||||| 1606 GTGCCTAGTAGCCCATCTTATGAAGACATGCGTGAGGTCTGTGTGTGTAACCGCTTGCGG 1665
Qy ||||| 481 ProIleValSerAsnArgTTPAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db ||||| 1666 CCAATCGTCTTACCCGCTGGACAGTGAATGTCTTCGAGCGCTTTTGAAGCTGATG 1725
Qy ||||| 501 SerGluCysTTPAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
Db ||||| 1726 TCAGAACTCTGGGCCATAATCCAGCATCCAGACTCACAGCTTTCAGAAATCAAGAAGACG 1785
Qy ||||| 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db ||||| 1786 CTCGCAAGATGTTGAATCCAGGATGTAAGATT 1821
RESULT 8
AAQ66640 standard; cDNA; 2070 BP.
ID AAQ66640
XX
AC AAQ66640;
XX
DT 25-MAR-2003 (revised)
DT 20-JAN-1995 (first entry)
XX
DE Mouse Activin receptor-like kinase 3 (mALK-3) cDNA.
KW serine threonine kinases; activin receptors; Act-R; superfamily;
KW transforming growth factor; TGF; diagnostics; detection; therapy;
KW rheumatoid arthritis; glomerular nephritis; fibrosis; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT 5'UTR 1..216
FT CDS /*tag= a
FT 217..1815
FT /*tag= b
FT /product= "activin receptor-like kinase 3"
FT 1816..2070
FT 3'UTR /*tag= c
XX
PN WO9411502-A2.
XX
PD 26-MAY-1994.
XX
PF 17-NOV-1993; 93WO-GB002367.
XX
PR 17-NOV-1992; 92GB-00024057.
PR 08-MAR-1993; 93GB-00004677.
PR 08-MAR-1993; 93GB-00004680.
PR 28-MAY-1993; 93GB-00011047.
PR 02-JUL-1993; 93GB-00013763.
PR 03-AUG-1993; 93GB-00016099.
PR 15-OCT-1993; 93GB-00021344.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Miyazono K, DiJke P, Franzen P, Yamashita H, Heldin C;
XX
DR WPI; 1994-183503/22.
XX
DR P-PSDB; AAR55372.
XX
PT Activin receptor-like kinase(s) with serine/threonine kinase domains -
PT have activin/TGF beta-type I receptor function and can be used in
PT diagnosis or therapy or rheumatoid arthritis, glomerular nephritis,
XX fibrosis, etc.
PS Claim 21; Page 65-67; 97pp; English.
XX
CC The inventors have identified a new family of receptor kinases called

CC activin receptor-like kinases (ALK). Their discovery was based on the
 CC realisation that receptor serine/threonine kinases form a new receptor
 CC family, which may include the type II receptors for other proteins in the
 CC transforming growth factor (TGF) beta superfamily. The activin receptor
 CC type II sequences from mouse and the daf1 gene product of C.elegans have
 CC high sequence similarity and were used to design degenerate primers to
 CC clone related cDNA's (see AA06643-49). Six distinct putative receptor
 CC serine/threonine kinases (ALK 1-6, of which human ALK 1-5 are AA06634-38
 CC respectively, and the mouse ALK-1,3,4, and 6 are AAQ6639-42 respectively)
 CC were identified. mALK-3 was obtained from a mouse lambdaEX 10x cDNA
 CC library using hALK-3 cDNA as a probe. Two overlapping clones were
 CC identified that together covered the complete sequence of mALK-3.
 CC Products of the invention can be used in therapy, eg. to modulate
 CC conditions associated with activin or TGF beta activity. These conditions
 CC include fibrosis, eg. liver cirrhosis and pulmonary fibrosis, cancer,
 CC rheumatoid arthritis and glomeronephritis. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX

SQ Sequence 2070 BP; 592 A; 415 C; 479 G; 583 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.: 2.17e-292 Length: 2070
 Score: 2823.00 Matches: 526
 Percent Similarity: 99.81% Conservatives: 5
 Best Local Similarity: 98.87% Mismatches: 1
 Query Match: 99.47% Indels: 0
 DB: 2 Gaps: 0

US-10-600-645-2 (1-532) x AAQ66640 (1-2070)

QY 1 MetThrGlnLeuTyrThrTrpIleArgLeuLeuGlyValaCysLeuPheIleSerHis 20
 DB |||||
 217 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCCTGCTGTTTCATCTTCAT 276
 QY 21 ValGlnGlyClnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
 DB |||||
 277 GTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGGCACCTGGTATGAATCAGACTTGGAC 336
 QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
 DB |||||
 337 CAGAGNAGCCAGAAATGAGTGACTTTAGCACCCAGAGGATACCTTGGCTTTCTTAAAG 396
 QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
 DB |||||
 397 TGTATTGCTCAGGACACTGCCCCAGATGATGCTATTATAAACAACATGCACTAATGCG 456
 QY 81 HisCysPheAlaIleIleGluGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
 DB |||||
 457 CATTTGCTTTGCCATTATAGAAAGATGATCAGGGAGAAACCAATTAACCTTCGGGTGT 516
 QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
 DB |||||
 517 ATGAGTATGAGGCTCTGATTTTCAATGCAAGGATTCACCGAAGAACCCAGCTACGCAGG 576
 QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
 DB |||||
 577 ACAATAGATGTTGTCGACCAATTTGTGCAACCAAGTATTGCGAGCTACACTGCCCTCT 636
 QY 141 ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuLeuSerMet 160
 DB |||||
 637 GTTGTATTAGTCCGTTCTTTGATGGCAGCATCCGATGGCTGGTGTGCTCATTTCCATG 696
 QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
 DB |||||
 697 GCTGTCTGTATAGTGTGATGATCATCTTCTCAGCTGCTTTGCTATAGCAATTATTGT 756
 QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
 DB |||||
 757 AAGAGTATCTCAGCAGGGGCTGTTACACCGTGATTTGGAACAGGATGAGCAATTATT 816
 QY 201 ProValGlyClnSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySer 220
 DB |||||
 817 CCAGTAGGAGAAATCATTTAAAGACCTGATTGACCACTGCCAAGCTCTGGGAGTGGATCT 876

QY 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
 DB |||||
 877 GGATTCCTCTTATTGGTTGAGCGAATATTGCCAAACAGATTACAGATGGTTCCGCGAGTT 936
 QY 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
 DB |||||
 937 GGTAAAGGGCGCTATCGAAGAAGTATGCATGGGTAAATGGCTGCTGAAAAAGTGGCTGTC 996
 QY 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
 DB |||||
 997 AAAGTGTGTTTTTACCCTGAAAGAAGCTAGCTGGTTTAGAGAAAAACAGAAATCTACCAAG 1056
 QY 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
 DB |||||
 1057 GTGTTAATGGCTCATGAAATAATATATCTGGTTTTATAGCTGCAGACATTAAGGCGACTGGT 1116
 QY 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
 DB |||||
 1117 TCTGGACTCAGCTGATTGTTGATTACTGATTACCATGAAATGGATCTCTCTATGACTTC 1176
 QY 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
 DB |||||
 1177 CTGAAATGTGCCACACTAGACACACAGAGCCCTACTCAAGTTAGCTTATTTCGGCTGCTGT 1236
 QY 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
 DB |||||
 1237 GGTGTGTGCACCTCCACACAGAAATTTATGTACCCAGGGAAGCTGCAATGTTCTCAT 1296
 QY 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
 DB |||||
 1297 CGAGACCTCAAGAGCAAAACATCCTTTAATAAGAAAAATGGAAGTTGCTGTATTGCTGAC 1356
 QY 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
 DB |||||
 1357 CTGGGCTAGCTGTTAAATTCACAGTGATACAAATGAAAGTTGACATACCCTTTGAATACC 1416
 QY 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
 DB |||||
 1417 AGGTTGGGACCAACAGCGGTACATGGCTCCAGAAAGTGCTGGATGAAAGCCTGAATAAANA 1476
 QY 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
 DB |||||
 1477 CATTTCCAGCCCTACATCATGCTGACATCTATAGCTTTGGTTTGATCATTTTGGGAAATG 1536
 QY 441 AlaArgArgCysIleThrGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
 DB |||||
 1537 GCTCGTGTGTGTTATACAGGAGGAATCGTGGAGGAATATCAATTACCATATTACAACATG 1596
 QY 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
 DB |||||
 1597 GTGCCAGTGACCCCTCTCTATGAGGACATGCGGTGAGGTGTGTGTGTGAAACCTTTCGCG 1656
 QY 481 ProfileValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
 DB |||||
 1657 CCAATCGTGTCTAACCGCTGGAACAGCGATGAATGTCTTCGAGCAGCTTTTGAAGCTAATG 1716
 QY 501 SerGluCysTrpAlaHisAsnProLysArgLeuThrAlaLeuArgIleLysLysThr 520
 DB |||||
 1717 TCAGAAATGTTGGGCCCATAAATCCAGCTCCAGACTCACAGCTTTTGAGATCAAGAAGACA 1776
 QY 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
 DB |||||
 1777 CTTGCAAAATGGTTGAATCCCGAGGATGTAAGAATT 1812

RESULT 9

AAZ09847
 ID AAZ09847 standard; cDNA; 2070 BP.
 XX
 AC AAZ09847;
 XX
 DT 26-NOV-1999 (first entry)
 XX

DE Human mALK-3 from clone ME-7 and ME-D CDNA.
 XX mALK-3; activin receptor-like kinase; therapy; activin; TGF-beta; cancer;
 KW fibrosis; liver cirrhosis; pulmonary fibrosis; glomerulonephritis; mouse;
 KW rheumatoid arthritis; detection; diagnosis; drug screening; ds.
 XX Mus sp.
 OS
 FH Key Location/Qualifiers
 FT CDS 217..1815
 TT /*tag= a
 XX /product= "mALK-3"
 XX
 PN W09946386-A1.
 XX
 XX 16-SEP-1999.
 PD
 XX 12-MAR-1999; 99WO-US005735.
 PF
 XX 13-MAR-1998; 98US-00039177.
 PR
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA
 XX Miyazono K, Imamura T, Ten Dijke P;
 PI
 XX WPI; 1999-551413/46.
 DR
 DR P-PSDB; AAY33305.
 XX
 PT New isolated activin receptor-like kinases, used to develop products for
 PT treating e.g. fibrosis, cancer, rheumatoid arthritis and
 PT glomerulonephritis.
 PT
 XX Disclosure; Page 88-91; 110pp; English.
 PS
 XX This invention describes novel human and murine activin receptor-like
 CC kinases (ALK's). The novel ALK products can be used in therapy, e.g. to
 CC modulate conditions associated with activin or TGF-beta activity, such as
 CC fibrosis, e.g. liver cirrhosis and pulmonary fibrosis, cancer, rheumatoid
 CC arthritis and glomerulonephritis. The products can also be used for
 CC detection, diagnosis and drug screening. This sequence encodes the murine
 CC mALK-3 protein isolated from clones ME-7 and ME-D
 XX
 SQ Sequence 2070 BP; 592 A; 414 C; 480 G; 584 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,17e-292 Length: 2070
 Score: 2823.00 Matches: 526
 Percent Similarity: 99.81% Conservative: 5
 Best Local Similarity: 98.87% Mismatches: 1
 Query Match: 99.47% Indels: 0
 DB: 2 Gaps: 0

US-10-600-645-2 (1-532) x AAZ09847 (1-2070)

QY 1 MetThrGlnLeuThrThrThrileArgLeuLeuGlyAlaCysLeuPheileSerHis 20
 DB 217 ATGACTCAGCTATACACTTACATCAGATTACTGGGAGCCTGCTGTTCATCATTTCTCAT 276
 QY 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetIysSerAspValaAsp 40
 DB 277 GTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGGCAGCTGGTATGAAATCAGACTTGGAC 336
 QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
 DB 337 CAGAGAAGCCAGAAATGGAGTACTTTAGCACCAGAGGATACCTTGCCTTCTCTAAAG 396
 QY 61 CysTyrCysSerGlyHisCysProAspAspAlaileAsnAsnThrCysileThrAnGly 80
 DB 397 TGTATTGTCTCAGGACACTGCCAGATGATGCTATTATAACACATGACATGATAACTAATGGC 456
 QY 81 HisCysPheAlaileileGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
 DB 457 CATTTGCTTGGCATTATAGAGAAGATGATCAGGGAGAAACACACATTAACTTCTGGGTCT 516

QY 101 MetIysTyrGluGlySerAspPheGlnCysIysAspSerProLysAlaGlnLeuArgArg 120
 DB 517 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCCACGAAAGCCAGCTAGCAGG 576
 QY 121 ThrileGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
 DB 577 ACATATAGAAATGTTGTCGGACCAATTTGTGCAACAGTATTTGCGACCTACACTGCCCT 636
 QY 141 ValValileGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
 DB 637 GTTGTATAGTCCGTTCTTTGATGGCAGCATCCGATGGCTGGTGTGCTCATTTCCATG 696
 QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrIysHisTyrCys 180
 DB 697 GCTGTCTGTATAGTTGCTATCATCTCTCCAGCTCTTTTGTCTTAAGCATTTATTGT 756
 QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGlnAspGluAlaPheile 200
 DB 757 AAGAGTATCTCAGCAGGGGTCGTTACAACTGATTTGGAAACAGGATGAGCATTTATT 816
 QY 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
 DB 817 CCAGTAGGAGAAATCATTTGAAAGACCTGATTGACCACTCCCAAGCTCTGGAGGTGATCT 876
 QY 221 GlyLeuProLeuLeuValGlnArgThrileAlaLysGlnIleGlnMetValArgGlnVal 240
 DB 877 GGATTTGCCCTTTATTGGTTTCAGCGAACTATTCCCAACAGATTCAGATGGTTCCGCGAGTT 936
 QY 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
 DB 937 GGTAAAGCCCTATGGAGAAAGTATGGATGGTAAATGGCGTGTGTAAGAGTGGCTGTC 996
 QY 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
 DB 997 AAAGTGTGTTTACCACCTGAAGAAGTAGCTGGTTTAGAGAAACAGAAATCTTACCAGACG 1056
 QY 281 ValLeuMetArgHisGluAsnIleLeuGlyPheileAlaAlaAspIleLysGlyThrGly 300
 DB 1057 GTGTAAATGCGTCATGAAATATATCTTGGTTTTATAGCTGCAGACATTAAGGGCACTGGT 1116
 QY 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
 DB 1117 TCCTGGACTCAGCTGTATTGATTACTGATTACCATGAAATGGATCTCTCTATGACTTC 1176
 QY 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
 DB 1177 CTGAAATGTGCCACACTAGACACAGAGCCCTACTCAAGTTAGCTTATTCTGCTGCTGTGT 1236
 QY 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
 DB 1237 GGTCTGTGCCACCTCCACACAGAAATTTATGGTACCCAGGGAAGCCCTGCAATTCCTCAT 1296
 QY 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
 DB 1297 CGAGACCTGAAGAGCAAAACATCCTTATTAGAAAAATAGAGTTGCTGTATTGCTGAC 1356
 QY 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
 DB 1357 CTGGCCTAGCTGTATAATTCAACAGTGATACAAATGAAGTTGACATACCTTGAATACC 1416
 QY 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerIysAsn 420
 DB 1417 AGGTGGGCACCAAGCGGTACATGGCTCCAGAAGTGTGGATGGAAGCTGAAATGAAAC 1476
 QY 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
 DB 1477 CATTTCCAGCCCTACATCATGCTGACATCTATAGCTTTGGTTTGGTTCATTTGGGAATG 1536
 QY 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTrpAsnMet 460
 DB 1537 GCTCGTCTGTATTACAGGAGGAATCGTGGAGGAATCAATTAACATATTTACAACATG 1596

Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
 Db 1597 GTGCCAGTGACCCATCCTATGAGGACATGCGTGGGTTGTGTGTGAAACGCTTGGG 1656
 Qy 481 ProIleValSerAsnArgTTPAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
 Db 1657 CCAATCGTGTCTAACCGCTGGAACAGCGATGAATGTCTTCGAGCAGTCTTTGAAGCTAATG 1716
 Qy 501 SerGluCysTTPAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
 Db 1717 TCAGATGTTGGGCCCAATATCCAGCTCCAGACTCAGCTTTGAGATCAGAAGACA 1776
 Qy 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
 Db 1777 CTTGCAAAAATGGTTGAATCCAGGATGTTAAAGATT 1812

RESULT 10

ADY51875

ID ADY51875 standard; cDNA; 2070 BP.

XX AC ADY51875;

XX DT 19-MAY-2005 (first entry)

XX DE Murine ALK-3 cDNA (clones ME-7 & ME-D) Seq 13.

XX KW gene; ss; antibody production; serine-threonine kinase receptor;
 KW activin like kinase; transforming growth factor beta; liver cirrhosis;
 KW pulmonary fibrosis; cancer; rheumatoid arthritis; glomerulonephritis;
 KW hepatocytic; antiinflammatory; respiratory-gen.; cytosstatic;
 KW antirheumatic; antiarthritic; nephrotropic.

XX OS Mus musculus.

XX FH Key Location/Qualifiers
 XX CDS 217..1815

XX FT /*tag= a

XX FT /product= "ALK-3 protein"

XX US2005048607-A1.

XX PD 03-MAR-2005.

XX PF 19-DEC-2003; 2003US-00739413.

XX PR 17-NOV-1992; 92GB-00024057.

XX PR 08-MAR-1993; 93GB-00004677.

XX PR 08-MAR-1993; 93GB-00004680.

XX PR 28-MAY-1993; 93GB-00011047.

XX PR 02-JUL-1993; 93GB-00013763.

XX PR 03-AUG-1993; 91GB-00036099.

XX PR 15-OCT-1993; 93GB-00021344.

XX PR 17-NOV-1993; 93WO-GB002367.

XX PR 30-OCT-1995; 95US-00436265.

XX PR 13-MAR-1998; 98US-00039177.

XX PR 12-MAR-1999; 99US-00267963.

XX PA (MIYA/) MIYAZONO K.

XX PA (IMAM/) IMAMURA T.

XX PA (TDIJ/) TEN DIJKE P.

XX PI Miyazono K, Imamura T, Ten Dijke P;

XX DR WPI; 2005-195280/20.

XX DR P-PSDB; ADY51876.

XX PT Determining if a substance inhibits binding of transforming growth

XX PT factor(TGF)-beta to Alk-1 comprises contacting a cell expressing an Alk-1

XX PT with the substance in the presence of TGF-beta.

XX PS Disclosure; SEQ ID NO 13; 59pp; English.

XX CC This invention relates to novel serine/ threonine receptor kinase nucleic

CC acids and the encoded proteins thereof. Specifically, it refers to
 CC receptor kinases identified as activin receptor like kinases (Alks) that
 CC are members of the transforming growth factor beta (TGF-beta)
 CC superfamily. The present invention describes a method for identifying TGF
 CC -beta inhibitors by determining whether a substance inhibits binding of
 CC TGF-beta to Alk-1, in particular where that substance is an antibody that
 CC binds to TGF-beta or the extracellular domain of Alk-1. The proteins
 CC having specific serine/ threonine receptor kinase activity can be used in
 CC therapy to modulate activin or TGF-beta activity and as such can be used
 CC to treat liver cirrhosis and pulmonary fibrosis, cancer, rheumatoid
 CC arthritis or glomerulonephritis. Accordingly, they exhibit hepatotropic,
 CC antiinflammatory, respiratory-Gen, cytosstatic, antirheumatic,
 CC antiarthritic and nephrotropic activities. This polynucleotide is the
 CC murine ALK cDNA sequence of the invention.

XX SQ Sequence 2070 BP; 592 A; 414 C; 480 G; 584 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,17e-292 Length: 2070
 Score: 2823.00 Matches: 526
 Percent Similarity: 99.81% Conservative: 5
 Best Local Similarity: 98.87% Mismatches: 1
 Query Match: 99.47% Indels: 0
 DB: 14 Gaps: 0

US-10-600-645-2 (1-532) x ADY51875 (1-2070)

Qy 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleSerHis 20
 Db 217 ATGACTCAGCTATACACTTACATCAGATTACTCGGAGCCCTGTCTGTTCATCATTTCTCAT 276
 Qy 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
 Db 277 GTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGGCAGTGTGTATGAATCAGACTGGAC 336
 Qy 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
 Db 337 CAGNAGAAGCCAGAAATGGAGTGACTTTTAGCACCAGAGAGATACCTTGCCTTTCTTAAAG 396
 Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
 Db 397 TGTATTGTCTCAGGACACTGCCAGATGATGCTATTATTAACACATGCATGCAATATGTC 456
 Qy 81 HisCysPheAlaIleIleGluGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
 Db 457 CATTTGCTTTGCCATTATAGAGAAGATGATCAGGGAGAACACACATTAACTTCTGGGTGT 516
 Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
 Db 517 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCGAAAGCCAGCTACGAGG 576
 Qy 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
 Db 577 ACAATAGAAATGTTGTTCGACCAATTTTGTGCAACACAGTATTTCGAGGCTACACTGCCCT 636
 Qy 141 ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
 Db 637 GTTGTATAGGTCGGTTCCTTGTATGCACATCCGATGGCTGTGTGTGCTCATTTCCATG 696
 Qy 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
 Db 697 GCTGCTGTATAGTTGCTATGATCATCTTCTCAGCTGCTTTTGTCTATAAGCATATTGT 756
 Qy 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
 Db 757 AAGAGTATCTCAAGCAGGGGTGCTTACACCGTGTATTTGGAACAGGATGAAGCATTTATT 816
 Qy 201 ProValGlyGluSerLeuLysPheLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
 Db 817 CCAGTAGGAGAAATCATTTGAAAGACCTGATTGACCATGCTCCCAAGCTCTGGGAGTGATCT 876
 Qy 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240

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Db      877  GGATTGCTTTATTGGTTTCAGCGAACTATTGCGAAACAGATTTCAGATGGTTTCGGCAGGTT  936
Qy      241  GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTyrPheArgGlyGluLysValalaVal  260
Db      937  GGTAAAGGCGCTATTCGAGAAGTATGGATGGGTAAATGGGTGAGTGGTGAAGTGGCTGTC  996
Qy      261  LysValPhePheThrThrGluGluAlaSerTyrPheArgGluThrGluIleTyrGlnThr  280
Db      997  AAAGTGTTTTTACCCTCAAGAGCTAGCTGTTTAGAGAAACAGAAATCACCAGAGC  1056
Qy      281  ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly  300
Db      1057  GTGTTAAATCGTCATGAAATATACTTTGTTTTATAGCTGCAGACATTAAGGCACTGGT  1116
Qy      301  SerTyrThrGlnLeuTyrIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe  320
Db      1117  TCCTGGACTCAGCTGTATTGTATTACTGATTACCATGAAATGGATCTCTATGACTTC  1176
Qy      321  LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys  340
Db      1177  CTGAATGTGCCACACTAGACACCGAGGCCCTACTCAAGTTAGCTTATTTCTGCTGTGT  1236
Qy      341  GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis  360
Db      1237  GGTCTGTGCCACTCCACACAGAAATTTATGTGTACCCAGGGAAGCCTGCAATGCTCAT  1296
Qy      361  ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp  380
Db      1297  CGAGACCTGAAGAGCAAAACATCTCTATTAAAGAAAAATGGAAGTTGCTGTATTGCTGAC  1356
Qy      381  LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr  400
Db      1357  CTGGGCTAGCTGTGTTAAATTCACAGTGATACAATGAAAGTTGACATCCCTTGAATACC  1416
Qy      401  ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn  420
Db      1417  AGGGTGGGCACCAAGCGGTACATGGCTCCAGAAGTGCTGATGAAAGCCTGATTAAGAAC  1476
Qy      421  HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet  440
Db      1477  CATTTCCAGCCCTACATCATCTATGCTGACATCTATAGCTTTTGGTTTGATCATTTGGGAAATG  1536
Qy      441  AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet  460
Db      1537  GCTCGTCGTGTATTACAGAGGAATCGTGGAGGAATATCAATTTACCATATTACAACTG  1596
Qy      461  ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg  480
Db      1597  GTGCCCAGTGACCCATCCTATGAGGACATGCGTGAGGTTGTGTGTGTAAGCGCTTGGCG  1656
Qy      481  ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet  500
Db      1657  CCAATCGTCTCTAACCGCTGGAACAGCGATGAATGCTTCGAGCAGTTTTTGAAGCTAATG  1716
Qy      501  SerGluCysTyrAlaHisProAlaSerArgLeuThrAlaLeuArgIleLysLysThr  520
Db      1717  TCAGATGTTGGGCCCATTAATCCAGCCTCCAGACTCACAGCTTTGAGATCAAGAAGACA  1776
Qy      521  LeuAlaLysMetValGluSerGlnAspValLysIle  532
Db      1777  CTTGCAAAATGGTTGAATCCACGAGTGTAAAGATT  1812
```

RESULT 11

```
AAQ90184
ID  AAQ90184 standard; DNA; 2402 BP.
XX
AC  AAQ90184;
XX
DT  25-MAR-2003 (revised)
DT  01-NOV-1995 (first entry)
XX
DE  BRK-1 DNA.
XX
```

BRK-1; BMP receptor kinase protein-1; bone morphogenetic protein; ds.

Mus sp.

Location/Qualifiers
11..1609
/*tag= a
sig_peptide 11..79
/*tag= b
mat_peptide 80..1606
/*tag= c

WO9514778-A2.

01-JUN-1995.

23-NOV-1994; 94WO-US013534.

24-NOV-1993; 93US-00158735.

(PROC) PROCTER & GAMBLE CO.

Cook JS, Correa PE, Koenig BB, Rosenbaum JS, Ting J;

WPI: 1995-206935/27.
P-PSDB; AAR74343.

New bone morphogenetic protein receptor kinase protein - used for identifying cpds. capable of binding it and for developing therapeutic cpds. and detection system(s).

Claim 3; Page 29-32; 49pp; English.

A cDNA library prepared from NIH3T3 poly-A RNA was screened with J159 PCR fragment to isolate clone BRK-1 (sequence given in AAQ90184) encoding full-length BMP receptor kinase protein (AAR74343). Vectors including the CC DNA were used to express recombinant BRK-1 in CHO and COS-7 hosts. CC (Updated on 25-MAR-2003 to correct PN field.)

Sequence 2402 BP; 676 A; 482 C; 540 G; 704 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,71e-292	Length:	2402
Score:	2823.00	Matches:	526
Percent Similarity:	99.81%	Conservative:	5
Best Local Similarity:	98.87%	Mismatches:	1
Query Match:	99.47%	Indels:	0
DB:	2	Gaps:	0

US-10-600-645-2 (1-532) x AAQ90184 (1-2402)

Qy 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20

Db 11 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCCTGCTCTTCATCATTTCTCAT 70

Qy 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValasp 40

Db 71 GTTCAAGGGCAGAAATCTAGATAGTATGCTCCTAGCTGGTATGAAATCAGACTTGGAC 130

Qy 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60

Db 131 CAGAAAGAGCCAGAAAATGGAGTGACTTTAGCACAGAGGATACCTTGCCTTTCTTAAG 190

Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80

Db 191 TGTATTGCTCAGGACACTGCCAGATGATGCTATTATAACACATGATCACTAATGTC 250

Qy 81 HisCysPheAlaIleIleGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100

Db 251 CATTGCTTTGCCATTATAGAAAGATGATCAGGGAGAAACACATTAATCTCTGGGTG 310

Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgA 120

Db 311 ATGAAGTATGAAGCTCTGATTTTCAATGCAAGGATTACCGAAGCCAGCTACGCAGG 370
Qy 121 ThrileGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
Db 371 ACATAGATGTTGTCGACCAATTTGTGCACAGTATTTGACAGCTACACTGCCCCCT 430
Qy 141 ValValileGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuileSerMet 160
Db 431 GTTGTTATAGTCCGTTCTTTGATGGCAGCATCCGATGGCTGTGTGTGCTCATTTCCATG 490
Qy 161 AlaValCysileValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
Db 491 GCTGTCTGTATAGTGTATGATCATCTCTCCAGCTGCTTTTGTCTATAAGCATATTGT 550
Qy 181 LysSerileSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
Db 551 AAGGTATCTCAAGCAGGGTCTGTACACCGTGATTTGGAACAGGATGAAGCATTTATT 610
Qy 201 ProValGlyGluSerLeuLysAspLeuileAspGlnSerGlnSerSerGlySerGlySer 220
Db 611 CCAAGTAGAGAAATCATTTGAAAGACCTGATTGACCAGTCCCAAGCTCTGGGAGTGATCT 670
Qy 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 671 GGATTCGCTTTATTGGTTTCAGCGAACTATTGCCAAACAGATTCAGATGGTTCCGCAAGTT 730
Qy 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
Db 731 GGTAAAGCCGCTATGGAGAAGATGATGGTAAATGGCGTGGTAAAGTGGCTGTC 790
Qy 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
Db 791 AAAGTGTTTTTTACCACCTGAAGAAGCTAGCTGGTTTAGAGAAACAGAAATCTACCAGCG 850
Qy 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaLysLeuLysGlyThrGly 300
Db 851 GTGTTAATGCTCATGAAATATATCTTGGTTTATAGCTGCAGACATTTAAAGCACTGGT 910
Qy 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db 911 TCTTGACTCAGCTGTATTGATTACTGATTACCATGAAATGGATCTCTCTATGACTTC 970
Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db 971 CTGAATGTCCACACTAGACACAGAGCCCTACTCAAGTTAGCTTATTCTGCTGTTGT 1030
Qy 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1031 GGTCTGTGCCACCTCCACACAGAAATTTATGGTACCAGGAAGCTGCAATGGTCTCAT 1090
Qy 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
Db 1091 CGAGACTGAAGAGCAAAACATCTCTATTAAAGAAATGGAAGTGTGCTGATTGCTGAC 1150
Qy 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db 1151 CTGGCCCTAGCTGTAAATTTCAACAGTGATACAAATGAAGTTGACATACCTTGAATACC 1210
Qy 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
Db 1211 AGGGTGGCCACCAAGCGGTACATGGCTCCAGAAAGTGTGATGAAAGCCCTGAAATAAAAC 1270
Qy 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
Db 1271 CATTTCCAGCCCTACATCATGGCTGACATCTATAGCTTTGGTTTGTATCATTTGGGAAATG 1330
Qy 441 AlaArgArgCysileThrGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db 1331 GCTCGTGTGTATTACAGAGAGGATCTGGAGGATATCAATTACCATATTACACATG 1390
Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db 1391 GTGCCAGTGACCCATCTATGAGGACATCGGTGAGGTTGTGTGTGAAACCGTTGCCG 1450

Qy 481 ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1451 CCATTCGTCTTAACCGCTGGAACAGCATGAATGCTTCGACGAGTTTTTGAAGCTAATG 1510
Qy 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
Db 1511 TCAGAATGTTGGCCCATTAATCCAGCTCCAGACTCACAGCTTTGAGAAATCAAGACACA 1570
Qy 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db 1571 CTTGCCAAAATGGTTGAATCCCAAGGATGTAAGATT 1606
RESULT 12
AAT27228
ID AAT27228 standard; cDNA; 2402 BP.
XX
AC AAT27228;
XX
DT 22-AUG-1996 (first entry)
XX
DE Bone morphogenetic protein type-I receptor kinase-1 gene.
XX
KW Mouse; bone morphogenetic protein receptor kinase-1;
KW bone morphogenetic protein receptor kinase-3; antibody; diagnostic;
KW bone disorder; osteogenic; bone morphogenetic protein-agonist;
KW drug screening; reporter gene; bone morphogenetic protein-antagonist;
KW hormone-responsive element; ds.
OS Mus musculus.
FH
FT Key
CDS 11..1609
FT /tag= a
FT /product= "Bone morphogenetic protein receptor kinase-1"
XX
PN W09614412-A2.
XX
PD 17-MAY-1996.
XX
PF 30-OCT-1995; 95WO-US014085.
XX
PR 04-NOV-1994; 94US-00334179.
XX
PA (PROC) PROCTER & GAMBLE CO.
XX
PI Rosenbaum JS, Nohno T;
XX
DR WPI; 1996-251762/25.
DR P-PSDB; AAR96201.
XX
PT Isolated bone morphogenic protein receptor kinase protein - used to
determine if a test cpd. is capable of binding to, or is (ant)agonist of
BMP receptor kinase protein transcription.
XX
PS Example 4; Page 61-63; 87pp; English.
XX
CC The sequence encodes mouse bone morphogenetic protein (BMP) receptor type
-I kinase-1 (BRK-1), which induces cellular differentiation in response
to BMP. The gene may be inserted in plasmid pJT4, to form plasmid pJT4-
J159F, and co-expressed with a type-II BRK-3 gene to study complex
formation between the 2 receptor types. The BRK-3 receptor and antibodies
against it may be used in diagnostic assays for BMP disorders, or in
therapy to bind or scavenge BMPs. In addition, expression of the BRK-3
gene along with a reporter gene under the control of a hormone-
responsive element in a cell culture may be used to screen compounds for
BRK-agonist or -antagonist activity, by monitoring reporter gene
expression
SQ Sequence 2402 BP; 676 A; 482 C; 540 G; 704 T; 0 U; 0 Other;
Alignment Scores: 2.71e-292 Length: 2402
Pred. No.:

Score:	2823.00	Matches:	526
Percent Similarity:	99.81%	Conservative:	5
Best Local Similarity:	98.87%	Mismatches:	1
Query Match:	99.47%	Indels:	0
DB:	2	Gaps:	0
US-10-600-645-2 (1-532) x AAT27228 (1-2402)			
QY	1	MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis	20
DB	11	ATGACTCAGCTATACACTTACATCAGATTACTGGGAGCGTCTGTTCATCTCAT	70
QY	21	ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetIleSerAspValAsp	40
DB	71	GTTCAGGGGAGAACTAGATAGTATGCTCCATGGCAGCTGGTATGAAATCAGACTTGGAC	130
QY	41	GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys	60
DB	131	CAGAAGAGCCAGAAATGGAGTGACTTTAGCACCCAGAGATACCTTGGCTTTCTTAAAG	190
QY	61	CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly	80
DB	191	TGCTATTGCTCAGGACACTGCCAGATGATGCTATTAAACACATGCATACTAATGGC	250
QY	81	HisCysPheAlaIleIleGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys	100
DB	251	CATTGCTTTGGCCATTATAGAAAGATGATCAGGGAGAAACACATTAACTTCTGGGTGT	310
QY	101	MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg	120
DB	311	ATGAAGTATGAGGCTCTGATTTTCAATGCAAGGATTCACCGAAGCCAGCTAGCGAGG	370
QY	121	ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro	140
DB	371	ACAATAGAATGTTGTCGGACCAATTTGTCAACACAGTATTTGCAGCCTACATGCCCCCT	430
QY	141	ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet	160
DB	431	GTGTGTATAGGTCGTTCTTGTATGGCAGCATCCGATGGCTGGTGTGCTCATTTTCCATG	490
QY	161	AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrIleHisTyrCys	180
DB	491	GCTGTCTGTATAGTGTCTATGATCATCTTCTCAGCTGCTTTTGTCTATNAGCATATTGT	550
QY	181	LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle	200
DB	551	AAGAGTATCTCAAGCAGGGGTGTTACAAACCGTGATTTTGGAAACAGGATGAAGCATTTATT	610
QY	201	ProValGlyGlnSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer	220
DB	611	CCAGTAGGAGAAATCATTTGAAAGACCTGATTTGACCAAGCTCCCAAGCTCTGGGAGTGGATCT	670
QY	221	GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal	240
DB	671	GAATTGCCCTTTATGTTTCAGGAACTATTTGCCAAACAGATTTCAGATGGTTCGGCAGGTT	730
QY	241	GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTyrArgGlyGluLysValAlaVal	260
DB	731	GGTAAAGGCCGCTATCGAGAAAGTATGGATGGGTAAATGGCGTGGTGAAGGCTGGCTGTC	790
QY	261	LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr	280
DB	791	AAAGTGTTTTTTACCCTCAAGAAAGCTAGCTGGTTTAGAGAAACAGAAATCTTACCAGAGC	850
QY	281	ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly	300
DB	851	GTGTTAATCGCTCATGAAATATATCTTGGTTTTTATAGCTGCAGACATTAAGGCACTGGT	910
QY	301	SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe	320
DB	911	TCCTGGACTCAGCTGTATTGATTACTGATTACCATGAAATGGATCTCTCTATGACTTC	970
QY	321	LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys	340

DB	971	CTGAAATGTGCCACACTAGACACCCAGACCCCTACTCAAGATTAGCTTATTCTCTGCTTGT	1030
QY	341	GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis	360
DB	1031	GGTCTGTGCCACCTCCACACAGAAATTTATGTTACCCCAAGGAGCCTGCAATTGCTCAT	1090
QY	361	ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysIleAlaAsp	380
DB	1091	CGACACCTGAAAGAGCAAAAACATCCTTATTAAAGAAAAATGGAAGTTGCTGTTATTCGTGAC	1150
QY	381	LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr	400
DB	1151	CTGGCCCTAGCTGTAAATTCACAGTGATACAAATGAAGTTGACATACCCCTTGAATACC	1210
QY	401	ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLysSerLysAsn	420
DB	1211	AGGGTGGGCACCAAGCGGTACATGGCTCCAGAAAGTCTGGATGAAAGCCTGAATAAAAAC	1270
QY	421	HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet	440
DB	1271	CATTTCCAGCCCTACATCATGGCTGACATCTATAGCTTTGGTTTGCATCATTTGGGAAATG	1330
QY	441	AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet	460
DB	1331	GCTCGTCTGTTGTTTACAGAGGAATCGTGAGGAATATCAATTACCATATTACCAACATG	1390
QY	461	ValProSerAspProSerTyrGluAspMetArgGluValValCysValIleArgLeuArg	480
DB	1391	GTGCCCACTGACCCATCCTATGAGGACATCGTGAGGTTGTGTGTGAAACGCTTGGCG	1450
QY	481	ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet	500
DB	1451	CCAAATCGTGTCTAAACCGCTGGAACAGCGATGAAATGCTTCGAGCAGTTTGAAGCTAATG	1510
QY	501	SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr	520
DB	1511	TCAGAAATGTTGGGCCCATTAATCCAGCCTCCAGACTCACAGCTTTGAGAATCAAGAAGACA	1570
QY	521	LeuAlaLysMetValGluSerGlnAspValLysIle	532
DB	1571	CTTGCAAAAATGTTGATCCAGGATGTAAGATT	1606
RESULT 13			
ID	AAT28021	standard; cDNA; 2402 BP.	
XX	XX	AAT28021;	
XX	XX	31-DEC-1996 (first entry)	
DE	XX	Mouse BMP type I receptor kinase (BRK-1) cDNA.	
XX	XX	BMP type II receptor kinase-3; BRK-3; bone morphogenetic protein;	
KW	XX	BMP type I receptor kinase; BRK-1; BMP receptor; ds.	
OS	XX	Mus sp.	
FH	XX	Key	Location/Qualifiers
FT	XX	CDS	11..1609
FT	XX		/*tag= a
XX	XX	WO9614579-A1.	
XX	XX	17-MAY-1996.	
PF	XX	30-OCT-1995; 95WO-US014027.	
XX	XX	04-NOV-1994; 94US-00334178.	
XX	XX	05-JUN-1995; 95US-00462467.	
PA	XX	(PROC) PROCTER & GAMBLE CO.	

PI Rosenbaum JS;
XX WPI; 1996-251887/25.
DR P-PSDB; AAR95225.
XX
XX Assays for bone morphogenetic protein activities - using complex of BMP
PT type I receptor kinase protein and BMP receptor kinase protein BRK-3.
XX
XX Claim 5; Page 64-66; 101pp; English.
XX
XX A cDNA clone (AAT28021) codes for full-length mouse bone morphogenetic
CC protein (BMP) type I receptor kinase protein-1 (BRK-1) (AAR95225), a
CC receptor capable of binding BMP and transducing a signal initiated by the
CC binding. Host cells co-transfected with vectors carrying full-length,
CC incomplete or soluble BMP type I receptor kinase protein cDNA and full-
CC length, incomplete, soluble or truncated BMP type II receptor kinase
CC protein-3 (BRK-3) cDNA (see also AAT28018-20 and AAT28022-30) express a
CC BMP receptor complex useful for screening cpds. for BMP receptor affinity
CC or for determining the concentration of a BMP receptor ligand in a
CC clinical sample
XX
SQ Sequence 2402 BP; 676 A; 482 C; 540 G; 704 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,71e-292 Length: 2402
Score: 2823.00 Matches: 526
Percent Similarity: 99.81% Conservative: 5
Best Local Similarity: 98.87% Mismatches: 1
Query Match: 99.47% Indels: 0
DB: 2 Gaps: 0

US-10-600-645-2 (1-532) x AAT28021 (1-2402)

Qy 1 MetThrClnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
Db 11 ATGACTCAGTATACACTTACATCAGATTACTGGAGCCGTCTGTTTCATCATTTCTCAT 70

Qy 21 ValGlnGlyGlnAenLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
Db 71 GTTCAAGGGCAGAAATCTAGATAGTGTCTCATGGCAGTGTGTATGAATCAGACTTGGAC 130

Qy 41 GlnLysProGluAenGlyValThrLeuAlaProGluAspThrLeuPropheLeuLys 60
Db 131 CAGAAGAAGCCAGAAATGAGTGACTTTAGCACCAGAGGATACCTTGGCTTTCTTAAAG 190

Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAenAsnThrCysIleThrAsnGly 80
Db 191 TGCTATTGTCTCAGGACACTGCCAGATGATGCTATTAAATACACATGCACTAATGGC 250

Qy 81 HisCysPheAlaIleIleGluGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 251 CATTTGCTTTGCCATTATAGAGAAGATGATCAGGGAGAAACCATTAATCTTCGGTGT 310

Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db 311 ATCAAGTATGAAGCTCTGATTTTCAATGCAAGGATTCACCGAAGCCAGCTACCGCAG 370

Qy 121 ThrIleGluCysCysArgThrAenLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
Db 371 ACAATAGAATGTTGTTCGACCAATTTGTGCAACAGTATTTCAGCCTACACTGCCCCCT 430

Qy 141 ValValIleGlyProPhePheAspGlySerValArgTyrLeuAlaValLeuIleSerMet 160
Db 431 GTTGTTATAGTCCTGTTTGTATGGCAGCATCCGATGGTGTGTGCTCAITTCATTCATG 490

Qy 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
Db 491 GCTGTCTGTATAGTGTGATGATCATCTTCTCCAGCTGCTTTTGCTATAAGCATATTCT 550

Qy 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluClnAspGluAlaPheIle 200
Db 551 AAGAGTATCTCAGCAGGGGTCGTTACAACCGGTGATTTGGAAACAGGATGAAGCATTTATT 610

Qy 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
Db 611 CCAGTAGGAGANTCATTTGAAAGACCTGATTGACCAAGTCCCNAAGCTCTGGAGTGGATCT 670

Qy 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 671 GGATTGCTCTTATTGTTTCAGCGCAATATTGCCAAACAGATTCAAGTGGTTCGGCAGGTT 730

Qy 241 GlyLysGlyArgTyrGlyGluValTyrMetGlyLysTyrPheArgGlyGlyLysValAlaVal 260
Db 731 GGTAAAGCCCGCTATGGAGAAAGTATGATGGGTAAATGGCGTGGTGAAGTGGCTGTC 790

Qy 261 LysValPhePheThrThrGluGluAlaSerTyrPheArgGluThrGluIleTyrGlnThr 280
Db 791 AAGTGTGTTTACCCTGGAAGAGTAGTGTGTTAGAGAAACAGAAATCTACCAAGC 850

Qy 281 ValLeuMetArgHisGluAenIleLeuGlyPheIleAlaAlaAepIleLysGlyThrGly 300
Db 851 GTGTTAATGCTCATGAAATATATCTGTTTATAGCTGCAGACATTAAGGCACCTGGT 910

Qy 301 SerTyrThrClnLeuTyrIleThrAspTyrHisGluAenGlySerLeuTyrAspPhe 320
Db 911 TCCTGGACTCAGCTGATTGTTGATTACTGATTACCATGAAATGGATCTCTCTATGACTTC 970

Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db 971 CTGAATGTGCCACACTAGACACAGAGCCCTACTCAAGTTAGCTTATTCTGCTGCTTGT 1030

Qy 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1031 GGTCTGTGCCACCTCCACACAGAAATTTATGTTACCAAGGAAAGCTGCAATGCTCAT 1090

Qy 361 ArgAspLeuLysSerLysAsnIleLeuLysLysAsnGlySerCysCysIleAlaAsp 380
Db 1091 CGAGACTCAGAGAGCAAAACATCTCTTATTAGAAAAATGGAAGTTGCTGTTATGCTGAC 1150

Qy 381 LeuGlyLeuAlaValLysPheAenSerAspThrAsnGluValAspIleProLeuAenThr 400
Db 1151 CTGGGCTAGCTGTTTAAATTTCAACAGTGATACAAATGAAGTTGACATACCCTTGAATACC 1210

Qy 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
Db 1211 AGGGTGGGCACCAAGCGGTACATGGCTCCAGAAAGTCTGGATGAAAGCCTGAATAAAAC 1270

Qy 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTyrGluMet 440
Db 1271 CATTTCCAGCCCTACATCATCTGCTGACATCTTAGCTTTGGTTGTATCTTTGGGAAATG 1330

Qy 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db 1331 GCTGCTGTTGTTATACAGAGGAATCGTGGAGGAATATCAATTACCATATTACACATG 1390

Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db 1391 GTGCCAGTGACCCCTCTATGAGGACATGCGTGGAGTGTGTGTGTGAAACCGCTTGGCG 1450

Qy 481 ProIleValSerAsnArgTyrPheAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1451 CCAATCGTGTCTAAACCGCTGGAACAGCGATGAATGTCTTCGAGCAGTTTTTGAAGCTAATG 1510

Qy 501 SerGluCysTyrAlaHisAenProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
Db 1511 TCAGAAATGTTGGGCCCATTAATCCAGCTCCAGACTCACAGCTTTTGAAGATCAAGAAGACA 1570

Qy 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db 1571 CTTGCCAAAAATGTTGAATCCCGAGGATGTAAGATT 1606

RESULT 14
AAV71972
ID AAV71972 standard; cDNA; 2402 BP.
XX
AC AAV71972;

XX 16-FEB-1999 (first entry)
 DT Mouse BMP receptor kinase protein (BRK)-1 encoding cDNA.
 DE Mouse BMP receptor kinase protein; BMP; BMP receptor kinase; ActRIIB receptor;
 DE BRK; receptor ligand; drug; ds.
 XX Mus sp.
 XX Key Location/Qualifiers
 XX CDS 11..1609
 FT /*tag= a
 FT /product= "mouse BRK-1 protein"
 XX WO9852038-A1.
 XX 19-NOV-1998.
 XX 13-MAY-1998; 98WO-US009519.
 XX 16-MAY-1997; 97US-0046768P.
 XX (PROC) PROCTER & GAMBLE CO.
 XX Rosenbaum JS;
 XX WPI; 1999-009930/01.
 XX P-PSDB; AAW86248.
 XX Screening method using bone morphogenetic protein receptor complex -
 PT which binds to potential drugs, and ActRIIB receptor used in the complex,
 PT also host cells transfected with DNA encoding the complex.
 XX Claim 2; Page 88-91; 110pp; English.
 XX This cDNA encodes a mouse BMP receptor kinase protein (BRK)-1. This can
 CC be used in the method of the invention of determining whether a compound
 CC can bind to a bone morphogenetic protein (BMP) receptor kinase protein
 CC complex. The method comprises allowing a compound in a sample to bind to
 CC the complex, where the complex is comprised of (i) a BMP; (ii) a BRK
 CC protein; (iii) an ActRIIB receptor. The method can be used to determine
 CC the concentration of a BMP receptor ligand in a sample by comparing the
 CC binding to a standard curve prepared with known concentrations of BMP
 CC ligand. The method can also be used to determine whether a test compound
 CC produces a signal on binding to a BMP receptor protein complex. The
 CC method is useful for determining whether a ligand, such as a known or
 CC putative drug, can bind to and/or activate the receptors
 XX Sequence 2402 BP; 676 A; 482 C; 540 G; 704 T; 0 U; 0 Other;
 SQ

Alignment Scores:
 Pred. No.: 2,71e-292 Length: 2402
 Score: 2823.00 Matches: 526
 Percent Similarity: 99.81% Conservative: 5
 Best Local Similarity: 98.87% Mismatches: 1
 Query Match: 99.47% Indels: 0
 DB: 2 Gaps: 0

US-10-600-645-2 (1-532) x AAV71972 (1-2402)

QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleSerHis 20
 DB 11 ATGACTCAGCTATACACTTACATCAGATTACTGGGAGCCTGTCTTCATCATCTTCAT 70
 QY 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
 DB 71 GTTCAAGGCGCAAACTAGATAGTATGCTCCATGGCAGCTGGTATGAAATCAGACTTGGAC 130
 QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
 DB 131 CAGAGAAGCCAGAAATGGAGTACTTTAGCACCAGAGGATACCTTGCCTTTCTTAAAG 190

QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
 DB 191 TGCTATTGCTCAGGACACTGCCAGATGCTATTATAACACATGATCATTAATATGTC 250
 QY 81 HisCysPheAlaIleIleGluGluAspGlnGlyGluThrThrLeuThrSerGlyCys 100
 DB 251 CATGCTTTGCCATTATAGAGAGATGATCAGGGAGAAACACACATTAACTTCGGGTGT 310
 QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
 DB 311 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCAACGAAAGCCAGCTACGAGG 370
 QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
 DB 371 ACAATAGAAATGTTGCGGACCAATTTGTGCAACCAAGTATTTGCAGCCTACACTGCCCT 430
 QY 141 ValValIleGlyProPhePheAspGlySerValArgTyrLeuAlaValLeuIleSerMet 160
 DB 431 GTTGTATAGTCCGTTCTTTGATGGCAGCATCCGATGGTGGTGTGCTCATTTCCATG 490
 QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
 DB 491 GCTGCTCTATAGTTGCTATGATCATCTTCTCCAGCTGCTTTTGTCTATAAGCATATTCT 550
 QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
 DB 551 AAGAGTATCTCAAGCAGGGGTGTTTACAAACCGTGATTTGGAAACAGGATGAAGCATTTAT 610
 QY 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
 DB 611 CCAGTAGAGAGATCATTTGAAGACCTGATTGACCAAGCTCCCAAGCTCTGGGAGTGGATCT 670
 QY 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
 DB 671 GGATTTGCCCTTTATTTGGTTTCAGCGAACTATTGCCAAACAGATTTCAGATGGTTCCGAGG 730
 QY 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
 DB 731 GGTAAAGCCCTATGGAGAAAGTATGGATGGTAAATGGCGTGGTGAAGAGTGGCTGTC 790
 QY 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
 DB 791 AAGTGTTTTACCACCTGAGAGAGCTAGCTGGTTTAGAGAAACAGAAATCTTACCAGAG 850
 QY 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
 DB 851 GTGTTAATGCTCATGAAATATATCTTGTTTTATAGCTGCAGACATTAAGGCACTGGT 910
 QY 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
 DB 911 TCCTGGACTCAGCTGTATTGATTACTTACCATTGAAATGGGATCTCTCTATGACTTC 970
 QY 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
 DB 971 CTGAAATGTGCCACACTAGACACAGCCCTACTCAAGTAGCTTATCTGCTGCTGTGT 1030
 QY 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
 DB 1031 GGTCTGTGCCACCTCCACACAGAAATTTATGGTACCCAAAGGAGCCCTGCAATTTGCTCAT 1090
 QY 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
 DB 1091 CGAGACCTGGAAGAGCAAAACATCCTTATTAGAAAAATGGAAAGTTGCTGTATTGCTGAC 1150
 QY 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
 DB 1151 CTGGCCCTAGCTGTTAAATTCACACAGTGTACAAATGAAGTTGACATACCTTGAATACC 1210
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 DB 1211 AGGTGGGCACCAAGCGGTACATGGCTCCAGAAAGTGTGGATGAAAGCTTGAATAAAG 1270
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Db 1271 CATTTCCAGCCCTACATCATGGCTGACATCTATAGCTTTGGTTTGATCATTTGGAAATG 1330
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Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
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RESULT 15

AAQ90183

ID AAQ90183 standard; DNA; 2056 BP.

XX AAQ90183;

AC AAQ90183;

DT 25-MAR-2003 (revised)

DT 01-NOV-1995 (first entry)

XX Truncated BRK-1.

XX BRK-1; BMP receptor kinase protein-1; bone morphogenetic protein; ds.

XX Mus sp.

XX Key Location/Qualifiers

FD CDS 291..1793

FT /*tag= a

FT sig_peptide 291..1359

FT /*tag= b

FT mat_peptide 360..1790

FT /*tag= c

XX W09514778-A2.

XX 01-JUN-1995.

XX 23-NOV-1994; 94WO-US013534.

XX 24-NOV-1993; 93US-00158735.

XX (PROC) PROCTER & GAMBLE CO.

XX Cook JS, Correa PE, Koenig BB, Rosenbaum JS, Ting J;

XX WPI; 1995-206935/27.

XX P-PSDB; AAR74342.

XX New bone morphogenetic protein receptor kinase protein - used for

XX identifying cpds. capable of binding it and for developing therapeutic

XX cpds. and detection system(s).

XX Claim 6; Page 25-28; 49pp; English.

XX PCR primers (given in AAQ90186-89) based on unique sequences present in

XX activin and Dap-1 receptor kinase domain VI were used to amplify cDNA

XX derived from NIH3T3 cells. A 300 bp PCR fragment obtd. was used to screen

XX a cDNA library prepd. from NIH3T3 cells in lambda ZapII to obtain clone

XX J159 containing DNA (AAQ90183) encoding truncated BRK-1 (AAR74342).

XX Vectors including the DNA were used to express recombinant tBRK-1 in CHO

CC and COS-7 hosts. (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 2056 BP; 573 A; 436 C; 506 G; 541 T; 0 U; 0 Other;
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Score: 2798.00 Matches: 526
Percent Similarity: 94.48% Conservative: 5
Best Local Similarity: 93.59% Mismatches: 1
Query Match: 98.59% Indels: 30
DB: 2 Gaps: 1

US-10-600-645-2 (1-532) x AAQ90183 (1-2056)

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Qy 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
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Qy 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
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Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
Db 471 TGTCTATTGCTCAGGACACTGCCAGATGATGCTATTAAATACACATGCACTAATAATGGC 530
Qy 81 HisCysPheAlaIleIleGluGluAspAspGlnGlyThrThrLeuThrSerGlyCys 100
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Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgAig 120
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Qy 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
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Qy 141 ValValIleGlyProPhePheAspGlySerValArgTyrLeuAlaValLeuLeuSerMet 160
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Qy 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
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Qy 181 LysSerIleSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
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1311 GGTCGTGTGCACCTCCACACAGAAATTTATGTTACCCAAAGGGAAGCCTGCAATTGCTCAT 1370
QY 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
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GenCore version 5.1.1.6
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SUMMARIES			
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2	2838	100.0 1813 3	US-09-874-628-1 Sequence 1, Appl1
3	2838	100.0 1813 6	PCT-US94-10080-1 Sequence 1, Appl1
4	2823	99.5 2070 3	US-09-382-256-13 Sequence 13, Appl1
5	2823	99.5 2070 3	US-09-395-115-13 Sequence 13, Appl1
6	2823	99.5 2070 3	US-08-436-265-13 Sequence 13, Appl1
7	2823	99.5 2070 3	US-09-679-187-13 Sequence 13, Appl1
8	2823	99.5 2070 3	US-09-267-963D-13 Sequence 13, Appl1
9	2823	99.5 2402 3	US-08-462-467B-11 Sequence 11, Appl1

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ALIGNMENTS

RESULT 1
US-08-123-934A-1
; Sequence 1, Application US/08123934A
; Patent No. 6291206
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, John
; APPLICANT: CELESTE, Anthony J.
; APPLICANT: THIES, R. Scott
; APPLICANT: YAMAJI, No. 6291206oru
; TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute Inc. - Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,934A
; FILING DATE: 17-SEP-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 876 1170

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; TELEFAX: 617 876 5851
; INFORMATION FOR SEQ ID NO. 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1813 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: CFK1-23a
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 61..1656
US-08-123-934A-1

Alignment Scores:
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US-10-600-645-2 (1-532) x US-08-123-934A-1 (1-1813)

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QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
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RESULT 2

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; Sequence 1, Application US/09874628
; Patent No. 6610513
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, John
; CELESTE, Anthony J.
; THIES, R. Scott
; YAMAJI, No. 6610513oru
; TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute Inc.- Legal Affairs
```

STREET: 87 CambridgePark Drive
 CITY: Cambridge
 STATE: MA
 COUNTRY: USA
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/874,628
 FILING DATE: 05-Jun-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/123,934
 FILING DATE: 17-SEP-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: LAZAR, Steven R
 REGISTRATION NUMBER: 32,618
 REFERENCE/DOCKET NUMBER: 5203
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617 876 1170
 TELEFAX: 617 876 5851

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1813 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

IMMEDIATE SOURCE:

CLONE: CPM1-23a

NAME/KEY: CDS

LOCATION: 61..1656

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-874-628-1

Alignment Scores:

Pred. No.:	1.28e-317	Length:	1813
Score:	2838.00	Matches:	532
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-10-600-645-2 (1-532) x US-09-874-628-1 (1-1813)

QY	1	MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyValaCysLeuPheIleIleSerHis	20
DB	61	ATGACTCAGCTATACACTTACATCAGATTACTGGGAGCCCTGCTGTTTCTCAT	120
QY	21	ValGlnGlycInAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValasp	40
DB	121	GTTCAAGGGCAGAACTCTAGATAGTATGCTCCATGGTACTGCTGATGAAATCAGACGTTGGAC	180
QY	41	GlnLysLysProGluAnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys	60
DB	181	CAGAAGAAGCCGGAAATGGAGTGAGCTTATGACACCCAGAGGACACCTTACCTTTCTTAAAA	240
QY	61	CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly	80
DB	241	TGCTATTGCTCAGACACACTGCCAGATGACGCTATTATTAACATGATCACTAATATGGC	300
QY	81	HisCysPheAlaIleIleGluGluAspGlnGlyThrThrLeuThrSerGlyCys	100
DB	301	CATTGCTTTGCCATTATAGAAGAAGATGATCAGGAGAAACCAACGTTAACTTCTGGTGT	360
QY	101	MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg	120
DB	361	ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCAAAAGCCAGCTTACGAGG	420

QY	121	ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro	140
DB	421	ACAATAGATGTTGTCGACCAATTTGTGCAACCAATATTTGCAGCCTACACCTCCCT	480
QY	141	ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet	160
DB	481	GTGCTTATAGGCCCATTTCTTGTATGGCAGCGTCGATGGCTGGCTGCTCATCTCTATG	540
QY	161	AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys	180
DB	541	GCTGTCTGTATTGTGCGCATGATCGTCTTCTCAGCTGCTTCTGTTTACAACATTTACTGT	600
QY	181	LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle	200
DB	601	AGAGTATCTCAAGCAGAGGTCGTTCACACCGTGACTTGGACAGGATGAAGCATTTATT	660
QY	201	ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer	220
DB	661	CCAGTAGGAGAACTCACTGAAAGACCTGATTGACAGTCACAAAGCTCTGGTAGTGATCT	720
QY	221	GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal	240
DB	721	GGATTACCTTTTATGGTTGAGCAACTATTGCCAAACAGATTGAGTGGTTCGACAGGT	780
QY	241	GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal	260
DB	781	GGTAAGGGCCGATATGAGAGATATGATGGGTAAATGGCTGGTGAANAAGTGGCTGTC	840
QY	261	LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr	280
DB	841	AAAGTATTTTACCACCTGAAGAAGCTAGCTGTTTATAGAGAAACAGAAATCTACCAGCG	900
QY	281	ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly	300
DB	901	GTGTTAATGCGTCATGAAATATATCTGTTTATAGCTGCACACATTAAGAAGCACCGGT	960
QY	301	SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe	320
DB	961	TCCTGGACTCAGCTGTTTGTATTGATTACTGATTACCATGAGATGGTCTCTCTATGACTTC	1020
QY	321	LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys	340
DB	1021	CTGAATATGTGCCACCTGACACACAGAGCCCTACTCAAGTTAGTATTCTGCTGCTGCTGT	1080
QY	341	GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis	360
DB	1081	GGTCTGTGCCACCTCCACACAGAAATTTATGGCACCAAGGCAAGCTGCAATTTGCTCAT	1140
QY	361	ArgAspLeuLysSerLysAsnIleLeuLysLysAsnGlySerCysCysIleAlaAsp	380
DB	1141	CGAGACCTGAGAGCAAAAACATCTCTTATTAGAAAAATGGTAGTTGCTGTATTGCTGAC	1200
QY	381	LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr	400
DB	1201	CTGGGCTAGCTGTTAAATTTCAACAGTGACACAAATGAAGTTGACATACCTTTGAACACC	1260
QY	401	ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn	420
DB	1261	AGGGTGGGACCCAGCGGTACATGGCTCCAGAAGTCTCGACGAGAGCCCTGAGTAAAAAC	1320
QY	421	HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet	440
DB	1321	CATTTCAGCCCTACATCATGCTGACATCTACAGCTTTGGTTTGTATCATTTTGGGAGATG	1380
QY	441	AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet	460
DB	1381	GCCCGCTCGTGTATTACAGGAGGAATCGTGGAGGAATAACAATACATATTACAACATG	1440
QY	461	ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg	480
DB	1441	GTGCTGTAGTGGCCCATCTTTATGAAGACATCGCTGAGGTGCTGTGTGTAACGCTTGGCG	1500
QY	481	ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet	500

Db 1501 CCAATGCTCTTAACCGCTGGACAGTGAATGCTCTCGAGCCGCTTTTGAAGCTGATG 1560
QY 501 SerGluCysTyrAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
Db 1561 TCAGAAATGCTGGGCCCAATATCCAGCATCCAGACTCCAGCTTTCAGAGTTCAGAGTCAAGAGACG 1620
QY 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db 1621 CTCGCAAGATGCTTGAATCCAGGATGTAAGATT 1656

RESULT 3

PCT-US94-10080-1
; Sequence 1, Application PC/TUS9410080
; GENERAL INFORMATION:
; APPLICANT: GENETICS INSTITUTE, INC.
; TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute Inc. - Legal Affairs
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10080
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/123,934
; FILING DATE: 17-SEP-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, Steven R
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5203-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8260
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1813 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: CFK1-23a
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 61..1656
PCT-US94-10080-1

Alignment Scores:

Pred. No.:	1,28e-317	Length:	1813
Score:	2838.00	Matches:	532
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-600-645-2 (1-532) x PCT-US94-10080-1 (1-1813)

QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuGlyAlaCysLeuPheIleIleSerHis 20
Db 61 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCCCTGCTGTTTCATCATTTCTCAT 120

QY	21	ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp	40
Db	121	GTTCAGGCGCAGAAATCTAGATAGTATGCTCCATGCTAGTGTGTAATAATCAGACGGGAC	180
QY	41	GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys	60
Db	181	CAGAGAGAGCCGAAAATGGAGTACGTTAGCACAGAGGACACCTTACCTTTCTTAAAA	240
QY	61	CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly	80
Db	241	TGCTATTGCTCAGGACACTGCCAGATGACGCTATTATAACACATGCAATAATAATGCG	300
QY	81	HisCysPheAlaIleIleGluLeuAspGlnGlyGluThrThrLeuThrSerGlyCys	100
Db	301	CATTGCTTTGCCATTATAGAGAAATGATCAGGAGAGAAACACCGTTAACTTCTGCGGTG	360
QY	101	MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgAtg	120
Db	361	ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCAAAAGCCAGCTACGCAG	420
QY	121	ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro	140
Db	421	ACAATAGAAATGTTGCGGACCAATTTGTCAACCAATATTTGCAGCCTACACTGCCCCCT	480
QY	141	ValValIleGlyProPheAspGlySerValArgTTPLeuAlaValLeuIleSerMet	160
Db	481	GTCGTTATAGGCCCAATCTTTGATGGCAGCGTCCGATGGCTGGCTGCTCATCTATG	540
QY	161	AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys	180
Db	541	GCTGCTGTATTTGTCGCCATGATCGTCTTCTCCAGCTGCTTCTGTACAAAACATTACTG	600
QY	181	LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle	200
Db	601	AAGAGTATCTCAAGCAGAGGTCGTTACAACCGTGACTTGGAAACAGGATGAAGCATTTAT	660
QY	201	ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerCysGlySerGly	220
Db	661	CCAGTAGGAGAAATCACTGAAAGACCTGATTGACCAGTCAAAAGCTCTGGTAGTGATCT	720
QY	221	GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal	240
Db	721	GGATTACCTTTATTTGTTTCAGCGAACTATTGCCAAACAGATTTCAGATGGTTCCGAGG	780
QY	241	GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal	260
Db	781	GCTAAGGCGCGTATGGAGAAAGTATGGATGGGTAATGGCGTGTGAAAAAGTGGCTGC	840
QY	261	LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr	280
Db	841	AAAGTATTTTATCCACTGAAGAGCTAGCTGGTTTAGAGAAACAGAAATCTACCAGCG	900
QY	281	ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly	300
Db	901	GTTTAAATGCGTCATGAAAATATATCTTGGTTTTATAGCTGCAGACATTTAAAGCCCGG	960
QY	301	SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe	320
Db	961	TCCTGGACTCAGCTGATTGTTGATTACTGATTACCATGAGATGGGTCTCTCTATGACTTC	1020
QY	321	LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys	340
Db	1021	CTGAAATGTGCCACCTCGACACCCAGAGCCCTACTCAAGATTAGCTTATTTCTGCTCGCTG	1080
QY	341	GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis	360
Db	1081	GGTCTGTGCCACCTCCACAGAAATTTATGGCAGCAAGGACGCACTGCAATTTGCTCAT	1140
QY	361	ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp	380
Db	1141	CGAGACCTGAAGAGAGCAAAACATCTTTATTAAGAAAAATGGTAGTTGCTGTTATGCTGAC	1200
QY	381	LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr	400

1201 CTGGCCCTAGCTGTAAATTCAACAGTGCACAAATGAAGTTGACATACCTTTGAACACC 1260
401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLeuAsn 420
1261 AGGTGGGACACAGCGGTACATGGCTCCAGAGTGTGGACGAGACCTGAGTAAAC 1320
421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleLeuTyrGluMet 440
1321 CATTTCCAGCCCTACATCATGGCTGACATCTACAGCTTTGGTTTGATCATTTGGGACATG 1380
441 AlaArgArgCysIleThrGlyGlyValValGluGluTyrGlnLeuProTyrTyrAsnMet 460
1381 GCCCGTGCCTGTATTACAGGAGGAATCGTGAGGAATATCAATTTACCATATTCAACATG 1440
461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLeuAspArg 480
1441 GTCCCTAGTGACCCATCTTATGAAGACATGCGTGAGGTGCTGTGTGAACCGCTTCCGG 1500
481 ProIleValSerAsnArgTTPAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
1501 CCAATCGTCTCTAACCGCTGAACAGTGTGATGCTTCCGACCGCTTTTGAAGCTGATG 1560
501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysThr 520
1561 TCAGATGCTGGGCCCAATAATCCAGCATCCAGACTCACAGCTTTGAGAATCAAGAGACG 1620
521 LeuAlaLysMetValGluSerGlnAspValIle 532
1621 CTCGCAAGATGGTTGAATCCAGGATGTAAGATT 1656

RESULT 4

US-09-382-256-13

Sequence 13, Application US/09382256A

Patent No. 6207814

GENERAL INFORMATION:

APPLICANT: MIYAZONO, Kohei

TEN DIJKE, Peter

FRANZEN, Petra

YAMASHITA, Hidetoshi

HELDIN, Carl-Henrik

TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS

HAVING SERINE THREONINE KINASE DOMAINS,

AND THEIR USE

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fulbright & Jaworski L.L.P.

STREET: 666 Fifth Avenue

CITY: New York City

STATE: New York

COUNTRY: USA

ZIP: 10103

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/382,256A

FILING DATE: 24-Aug-1999

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB93/02367

FILING DATE: No. 6207814ember 17, 1993

APPLICATION NUMBER: GB 9224057.1

FILING DATE: No. 6207814ember 17, 1992

APPLICATION NUMBER: GB 9304677.9

FILING DATE: March 8, 1993

APPLICATION NUMBER: GB 9304680.3

FILING DATE: March 8, 1993

APPLICATION NUMBER: 9311047.6

FILING DATE: May 28, 1993

APPLICATION NUMBER: 9313763.6

FILING DATE: July 2, 1993
APPLICATION NUMBER: 9316099.2
FILING DATE: August 3, 1993
APPLICATION NUMBER: 321344.5
FILING DATE: October 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 6207814man D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5298.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2070 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Mouse
FEATURE:
NAME/KEY: CDS
LOCATION: 217..1812
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-382-256-13

Alignment Scores:

Pred. No.:	1-2e-315	Length:	2070
Score:	2823.00	Matches:	526
Percent Similarity:	99.81%	Conservative:	5
Best Local Similarity:	98.87%	Mismatches:	1
Query Match:	99.47%	Indels:	0
DB:	3	Gaps:	0

US-10-600-645-2 (1-532) x US-09-382-256-13 (1-2070)

QY	1	MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleSerHis	20
DB	217	ATGACTCAGCTATACACTTACATCAGATTACTGGAGCCCTGCTGTTTCATCTTCAT	276
QY	21	ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp	40
DB	277	GTTCAGGGGAGAAATCTAGATAGTCTCCATGGCAGCTGGTATGAAATCAGACTTGGAC	336
QY	41	GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys	60
DB	337	CAGAGAAGCCAGAAATGGAGTGACTTTAGCACAGAGAGATACCTTGCCTTTCTTAAG	396
QY	61	CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly	80
DB	397	TGCTATTGCTCAGGACACTGCCAGATGATGCTATTATAAACACATGCACTAATAATGGC	456
QY	81	HisCysPheAlaIleIleGluAspAspGlnGlyThrThrThrLeuThrSerGlyCys	100
DB	457	CATTGCTTTGGCCATTATAGAAGAAGATGATCAGGAGAAACCCACATTAACTTCGGGTGT	516
QY	101	MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg	120
DB	517	ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCCAGAAAGCCAGCTACGAGG	576
QY	121	ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrIleGlnProThrLeuProPro	140
DB	577	ACAATAGAATGTTGTCGACCAATTTGTGCAACAGTATTTGCGAGCCTACACTGCCCCCT	636
QY	141	ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValIleSerMet	160
DB	637	GTGTGTTATAGTCCGCTTCTTTGATGGCAGCATCCGATGGCTGGTGTGCTCACTTCATG	696
QY	161	AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys	180

Db 697 GCTGCTGTATAGTCTGCTATGATCATCTCTCCAGCTGCTTTGCTATAGCATTTATGT 756
QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
Db 757 AAGAGTATCTCAAGCAGGGGTGCTTACAAACCGTGATTTGGAAACAGGATCAAGCATTTATT 816
QY 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
Db 817 CCAGTAGAGAAATCATTTGAAAGACCTGATTCACCACTCCCAAGCTCTGGGAGTGATCT 876
QY 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 877 GGATTCCTTTATGTTTCAGCGAATATTGCCAAACAGATTGAGATGTTGGCAGGTT 936
QY 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
Db 937 GGTAAAGGCCGCTATGGAGAAGTATGGATGGGTAAATGGGTGAAAGTGGCTGTC 996
QY 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
Db 997 AAGTGTGTTTTTACCACCTGAAGAAGCTAGCTGGTTTAGAGAAACAGAAAATCTACCAGAC 1056
QY 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db 1057 GTGTTAATGCGTCATGAAATATATCTTGGTTTTATAGCTGCAGACATTAAAGCACTGTT 1116
QY 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db 1117 TCCTGGACTCAGCTGATTTGATTACTGATTACCATGAAATGGATCTCTCTATGACTTC 1176
QY 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db 1177 CTGAAATGTGCCACACTAGACACAGAGCCCTACTCAAGTTAGCTTTATTCTGCTGCTGT 1236
QY 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1237 GGTCTGTGCCACTCCACAGAAATTTATGTATCCAGGAAAGCTGCAATGTCCTAT 1296
QY 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
Db 1297 CGAGACCTGAAGAGCAAAACATCCTATTAAAGAAAATGGAAGTTGCTGTATTGCTGAC 1356
QY 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db 1357 CTGGGCTAGCTGTTAAATTCACACGTGATACAAATGAAAGTTGACATACCCTTGAATACC 1416
QY 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
Db 1417 AGGCTGGGCACCACCGGTACATGGCTCCAGAAAGTCTGGATGAAAGCCTGAATAAAAC 1476
QY 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
Db 1477 CATTTCCAGCCCTACATCATGCTGACATCATAGCTTTGGTTTGATCATTTGGGAAATG 1536
QY 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db 1537 GCTCGCTGTTGTTATACAGAGGAATCGTGGAGGAATATCAATTACCATATTACACATG 1596
QY 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db 1597 GTGCCACGTACCCATCTCATAGGACATCGGTGAGGTTGTGTGTGAAACGCTTGGCG 1656
QY 481 ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1657 CCAATCGTGTCTAACCGCTGGAACAGCGATGAATGCTTCGAGCACTTTTGAAGCTAATG 1716
QY 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
Db 1717 TCAGAATGTTGGGCCCATTAATCCAGCCTCCAGACTCCAGACTTGTGAGATCAAGAAGACA 1776
QY 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532

Db 1777 CTTGCCAAAATGGTTGAATCCCGAGGTGTAAAGATT 1812
RESULT 5
US-09-395-115-13
; Sequence 13, Application US/09395115
; Patent No. 6271365
; GENERAL INFORMATION:
; APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
; APPLICANT: Fransen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/395,115
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,265
; FILING DATE: 30-October-1995
; APPLICATION NUMBER: PCT/GB93/02367
; FILING DATE: 17-No. 6271365ember-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9224057.1
; FILING DATE: 17-No. 6271365ember-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9304677.9
; FILING DATE: 8-March-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9304680.3
; FILING DATE: 8-March-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9311047.6
; FILING DATE: 28-May-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9313763.6
; FILING DATE: 2-July-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9136099.2
; FILING DATE: 3-August-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9321344.5
; FILING DATE: 15-October-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohlei, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: LUD 5298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2070 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; FEATURE:

NAME/KEY: CDS
LOCATION: 217..1812
US-09-395-115-13

Alignment Scores:

Pred. No.: 1,28-315 Length: 2070
Score: 2823.00 Matches: 526
Percent Similarity: 99.81% Conservative: 5
Best Local Similarity: 98.87% Mismatches: 1
Query Match: 99.47% Indels: 0
DB: 3 Gaps: 0

US-10-600-645-2 (1-532) x US-09-395-115-13 (1-2070)

QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuGlyAlaCysLeuPheIleSerHis 20
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DB 277 GTTCAAGGGCAGAAATCAGATGATGCTCCATGGCACTGGTATGAATCAGACTTCGAC 336
QY 41 GlnLysLysProGluAenGlyValThrLeuAlaProGluAaspThrLeuProPheLeuLys 60
DB 337 CAGAAGAAGCCAGAAATGGAGTGACTTTAGCACACAGAGGATACCTTGGCCTTCTTAAAG 396
QY 61 CysTyrCysSerGlyHisCysProAaspAaspAlaIleAenAenThrCysIleThrAenGly 80
DB 397 TGCATTGTCTCAGAGCACTGCCAGATGATGCTAATTAACACATGATCACTAATATGGC 456
QY 81 HisCysPheAlaIleIleGluGluAaspGlnGlyGluThrThrLeuThrSerGlyCys 100
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QY 101 MetLysTyrGluGlySerAaspPheGlnCysLysAaspSerProLysAlaGlnLeuArgArg 120
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QY 121 ThrIleGluCysArgThrAenLeuAenGlnTyrIleLeuGlnProThrLeuProPro 140
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QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
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QY 181 LysSerIleSerArgGlyArgTyrAenArgAaspLeuGlnAaspGluAlaPheIle 200
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QY 461 ValProSerAaspProSerTyrGluAaspMetArgGluValValCysValLysArgLeuArg 480
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QY 501 SerGluCysTrpAlaHisAenProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
DB 1717 TCAGATGTTGGGCCCATTAATCCAGCTCCAGACTCCAGCTTTCAGAAATCAAGAGACA 1776
QY 521 LeuAlaLysMetValGluSerGlnAaspValLysIle 532
DB 1777 CTTGCAAAAATGGTTGAATCCAGGATGTAAGATT 1812

RESULT 6

US-08-436-265-13
Sequence 13, Application US/08436265
Patent No. 6316217
GENERAL INFORMATION:
APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
APPLICANT: Yamashita, Hidetoshi; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins And Their Use
TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-October-1995

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/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/GB93/02367
/ FILING DATE: 17-NO. 6316217ember-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 9224057.1
/ FILING DATE: 17-NO. 6316217ember-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 9304677.9
/ FILING DATE: 8-March-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 9304680.3
/ FILING DATE: 8-March-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 9311047.6
/ FILING DATE: 28-May-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 9313763.6
/ FILING DATE: 2-July-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 9136099.2
/ FILING DATE: 3-August-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 9321344.5
/ FILING DATE: 15-October-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kohlei, Vineet
/ REGISTRATION NUMBER: 37,003
/ REFERENCE/DOCKET NUMBER: LUD 5298
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 688-9200
/ TELEFAX: (212) 838-3884
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2070 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: internal
/ ORIGINAL SOURCE:
/ ORGANISM: Mouse
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 217..1812
/ US-08-436-265-13

Alignment Scores:
Pred. No.: 1.2e-315 Length: 2070
Score: 2823.00 Matches: 526
Percent Similarity: 99.81% Conservative: 5
Best Local Similarity: 98.87% Mismatches: 1
Query Match: 99.47% Indels: 0
DB: 3 Gaps: 0

US-10-600-645-2 (1-532) x US-08-436-265-13 (1-2070)

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QY 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
DB 277 GTTCAAGGCGAGAATCTAGATAGTATGCTCCATGGCAGCTGGTATGAAATCAGACTTGGAC 336
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QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
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101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArg 120
517 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACGAAAGCCAGCTAGCAGG 576
121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuPro 140
577 ACAATAGAAATGTTGTCGGACCAATTTGTGCAACCAAGTATTTGCAGCCTACACTGCCCCCT 636
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637 GTTGTATAGGTCCGTTCTTGTATGGCAGCATCCGATGGCTGGTGTGCTCATTTCCATG 696
161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrIleHisTyrCys 180
697 GCTGTCTGTATAGTTGCTATGATCATCTTCTCCAGCTGCTTTGTCTATAAGCATATTATT 756
181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
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817 CCAGTAGGAGAATCATTTGAAAGACCTGATTGACCAAGTCCCAAGGCTCTGGGAGTGGATCT 876
221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
877 GGATTTGCCCTTTATTGGTTTCAGCGAACTATTGCAACACAGATTCAGATGGTTTCGGCAGGTT 936
241 GlyLysGlyArgTyrGlyGluValTyrMetGlyLysTyrArgGlyGluLysValAlaVal 260
937 GGTAAAGGCCCGCTATGGAGAGATGATGGTAAATGGCGTGGTGAAAGTGGCTGTC 996
261 LysValPhePheThrThrGluGluAlaSerTyrPheArgGluThrGluIleTyrGlnThr 280
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341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
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QY 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
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QY 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
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RESULT 8

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US-09-267-963D-13
; Sequence 13, Application US/09267963D
; Patent No. 6692925
; GENERAL INFORMATION:
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; APPLICANT: MIYAZONO, Kohei
; APPLICANT: IMAMURA, Takeshe
; APPLICANT: DEN DIJKE, Peter
; TITLE OF INVENTION: PROTEINS HAVING SERINE/THREONINE KINASE DOMAINS, CORRESPONDING
; FILE REFERENCE: LUD 5539.1 CIP
; CURRENT APPLICATION NUMBER: US/09/267,963D
; CURRENT FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/GB93/02367
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: US 09/039,177
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-267-963D-13
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Alignment Scores:

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Pred. No.: 1.2e-315 Length: 2070
Score: 2823.00 Matches: 526
Percent Similarity: 99.81% Conservative: 5
Best Local Similarity: 98.87% Mismatches: 1
Query Match: 99.47% Indels: 0
DB: 3 Gaps: 0
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US-10-600-645-2 (1-532) x US-09-267-963D-13 (1-2070)

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QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
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QY 81 HisCysPheAlaIleIleGluGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
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Qy 401 ArgValGlyThrArgAspTyrMetAlaProGluValLeuAspGluSerLeuLysAsn 420
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Qy 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db 1537 GCTCGCTGTTGTATTACAGAGGAATCGTGAGGAATATCAATTTACCATATTACAACATG 1596
Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db 1597 GTGCCCGTGCACCATCTCTATAGGACATCGGTGAGGTGTGTGTGGAACCTTGGCGG 1656
Qy 481 ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1657 CCAATCGTGTCTAACCGCTGAACAGCGATGAATGCTTCAGCAGCTTTTGAAGCTAATG 1716
Qy 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysThr 520
Db 1717 TCAGATGTTTGGGCCCATTAATCCAGCCCTCAGACTCAGACTTTTGAATCAAGAAGACA 1776
Qy 521 LeuAlaLysMetValGluSerGlnAsnValIle 532
Db 1777 CTTTGCAAAAATGTTTGAATCCAGGATGTAAAGATT 1812

RESULT 9
US-08-462-467B-11
; Sequence 11, Application US/08462467B
; Patent No. 6210899
; GENERAL INFORMATION:
; APPLICANT: Rosenbaum, Jan S
; TITLE OF INVENTION: The Use of a BMP Protein Receptor
; COMPLEX FOR SCREENING BONE METABOLISM ACTIVES AND CELLS
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; TITLE OF INVENTION: Co-Transfected With a Type II BMP Receptor and a Type I
; TITLE OF INVENTION: BMP Receptor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Procter & Gamble Company
; STREET: 11810 East Miami River Road
; CITY: Ross
; STATE: OH
; COUNTRY: USA
; ZIP: 45061
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,467B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hersko, Bart S.
; REGISTRATION NUMBER: 32,572
; REFERENCE/DOCKET NUMBER: 5474R
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (513) 627-0633
; TELEFAX: (513) 627-0260
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2402 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-462-467B-11

Alignment Scores:
Pred. No.: 1,54e-315 Length: 2402
Score: 2823.00 Matches: 526
Percent Similarity: 99.81% Conservative: 5
Best Local Similarity: 98.87% Mismatches: 1
Query Match: 99.47% Indels: 0
DB: 3 Gaps: 0

US-10-600-645-2 (1-532) x US-08-462-467B-11 (1-2402)

Qy 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
Db 11 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCCCTGCTGTTTCATCACTTCTCAT 70
Qy 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
Db 71 GTTCAAGGCGAGAATCTAGATAGTATGCTCCATGGCAGCTGGTATGAATCAGACTTGGAC 130
Qy 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
Db 131 CAGAGAAGCCAGAAATGAGTACTTTAGCACCAGAGAGTACCTTGGCTTTCTTAAG 190
Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
Db 191 TGTATTGTCTCAGGACACTGCCAGATGATGCTATTATAACACATGCACTAATAATGGC 250
Qy 81 HisCysPheAlaIleIleGluLysAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 251 CATTTGCTTTGCCATTATAGAAGAGATGATCAGGGAGAAACACCATTAATCTCTGGGTGT 310
Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db 311 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCGAAACCCAGCTACGAGG 370
Qy 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
Db 371 ACAATAGATGTTGTGGGACCAATTTGTGCAACCAAGTATTGTGAGCCTACACTGCCCCCT 430
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QY 141 ValValIleGlyPropPheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
DB 431 GTTGTTATAGGTCGGTCTTTGATGGCAGCATCCGATGGCTGGTGTGCTCATTTCCATG 490
QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrIlyshisTyrCys 180
DB 491 GCTGCTGTATAGTGTATGATCATCTCTCCAGCTGCTTTTGTATAAGCATATTATGT 550
QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGlnAlaPheIle 200
DB 551 AAGAGTATCTCAAGCAGGGGTGGTTACAAACCGGTGATTTGGAAACAGGATGAAGCATTTATT 610
QY 201 ProValGlyLysSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
DB 611 CCAGTAGGAGATCATTTGAAGACCTTGATGACCGTCCCAAGCTCTGGAGTGGATCT 670
QY 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
DB 671 GGATTGCCCTTTATGGTTCCAGCGAATATTGCCAAACAGATTCAGATGGTTCCGCCAGTT 730
QY 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
DB 731 GGTAAAGGCGGTATGGAAGATGATGGATGGGTAAATGGCTGGTCAAAAAGTGGCTGTC 790
QY 261 LysValPhePheThrThrGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
DB 791 AAGTGTGTTTTTACCCTGAAGAGCTAGCTGGTTAGAGAAACAGAAATCTACCAGAG 850
QY 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
DB 851 GTGTTAATCGCTCATGAAATATACTTGTGTTTATAGCTGCAGACATTAAGGCACTGGT 910
QY 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
DB 911 TCCTGGACTCAGCTGATTTGATTTACTGATTACCATGAAATGGATCTCTATGACTTC 970
QY 321 LeuLysCysAlaThrIleuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
DB 971 CTGAATGTGCCACACTAGACACAGAGCCCTACTCAAGTTAGCTTATTTCTGCTGCTGT 1030
QY 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
DB 1031 GGCTGTGTCACCTCCACACAGAAATTTATGGTACCCAGGAGCGCTCAATTTGCTCAT 1090
QY 361 ArgAspLeuLysSerLysAsnIleLeuLysLysAsnGlySerCysCysIleAlaAsp 380
DB 1091 CGAGACCTGAAGAGCAAAACATCCTTATTAAGAAAAATGGAAGTTGCTGTATTGCTGAC 1150
QY 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
DB 1151 CTGGGCTAGCTGTGTTAAATTCACAGTGATACAAATGAAGTTGACATACCTTGAATACC 1210
QY 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
DB 1211 AGGTGGGACCAAGCGGTACATGGCTCCAGAGTGTCTGGATGAAGCCTGGAATAAAC 1270
QY 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
DB 1271 CATTTCCAGCCCTACATCATGCTGACATCTATAGCTTTGGTTTGTATCATCTTTGGAAATG 1330
QY 441 AlaArgArgCysIleThrGlyIleValGluIleValGluTyrGlnLeuProTyrTyrAsnMet 460
DB 1331 GCTCGCTGTGTTATTCAGAGAGGAATCGTGGAGGAATATCAATTTACCATATTACAACTG 1390
QY 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
DB 1391 GTGGCCAGTGACCCCTCATGAGGACATCGCTGAGGTTGTGTGTGGAACGCTTGGCG 1450
QY 481 ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
DB 1451 CCAATCGTCTCAACCGCTGGAACAGCGATGAATGTTCTCGAGCAGTTTTTGAAGCTAATG 1510
QY 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysIleThr 520

DB 1511 TCAGNATGTTGGCCCATTAATCCAGCTTCACAGCTCCAGATTTGAGNATCAAGAGACA 1570
QY 521 LeuAlaLysMetValGluSerGlnAspValIlySile 532
DB 1571 CTTGCAAAAATGGTTGAATCCAGGATGTTAAAGATT 1606
RESULT 10
US-08-158-735A-3
; Sequence 3, Application US/08158735A
; Patent No. 6248554
; GENERAL INFORMATION:
; APPLICANT: COOK, JONATHAN S.
; APPLICANT: CORREA, PAUL E.
; APPLICANT: KOENIG, BETH B.
; APPLICANT: ROSENBAUM, JAN S.
; APPLICANT: TING, JERRY
; TITLE OF INVENTION: DNA SEQUENCE CODING FOR A BMP RECEPTOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE PROCTER & GAMBLE COMPANY
; STREET: 11810 EAST MIAMI RIVER ROAD
; CITY: ROSS
; STATE: OH
; COUNTRY: USA
; ZIP: 45061
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/158,735A
; FILING DATE: 24-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CORSTANJE, BRAHM J.
; REGISTRATION NUMBER: 34,804
; REFERENCE/DOCKET NUMBER: 5088
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (513) 627-2858
; TELEFAX: (513) 627-0260
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2402 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(11..1606)
US-08-158-735A-3
Alignment Scores:
Pred. No.: 1,54e-315 Length: 2402
Score: 2823.00 Matches: 526
Percent Similarity: 99.81% Conservative: 5
Best Local Similarity: 98.87% Mismatches: 1
Query Match: 99.47% Indels: 0
DB: 3 Gaps: 0
US-10-600-645-2 (1-532) x US-08-158-735A-3 (1-2402)
QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
DB 11 ATGACTCAGCTATACACTTACATCATGATTTACTGGAGCGCTGCTGTTTCATCATTTCTCAT 70
QY 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
DB 71 GTTCAAGGGCGAATCTAGATAGTAGTCTCCATGGCAGCTGGTATGAAATCAGACTGGAC 130
QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60

Db 131 CAGAAGAGCCAGAAAATGGAGTGACTTTAGCACCCAGAGGATACCTTGGCTTCTTTAAAG 190
Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
Db 191 TGCTATTGCTCAGGACACTCCAGATGATGCTATTAAATACACATGCATTAATATGGC 250
Qy 81 HisCysPheAlaIleIleGluGluAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 251 CATTTGCTTTGCCATTATAGAAGAAGATGATCAGGAGAAACCAACATTAACCTTCTGGGTGT 310
Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db 311 ATGAAGTATGAAGCTCTGATTTTCAATGCAAGATTCACCGAAAGCCAGCTACGACAG 370
Qy 121 ThrIleGluCysCysArgThrAsnLeuLeuAsnGlnTyrLeuGlnProThrLeuProPro 140
Db 371 ACAATAGAAATGTTGCGACCAATTTGTGCAACAGTATTTGCGAGCTACACTGCCCTT 430
Qy 141 ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
Db 431 GTTGTATTAGGTCGGTCTTTGATGGCAGCATCCGATGGCTGGTGTGCTCAITTTCCATG 490
Qy 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
Db 491 GCTGTCTGTATAGTTGCTATGATCATCTCTCCAGCTGCTTTTGTCTATAAGCAATTATTGT 550
Qy 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
Db 551 AAGAGTATCTCAAGCAGGGGTGCTTACACCGTGATTTTGGAAACAGGATGAAGCATTTATT 610
Qy 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
Db 611 CCAGTAGGAGAATCATTTAAAGACCTGATTGACCAAGTCCCAAGCTCTGGAGTGATCT 670
Qy 221 GlyLeuProLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 671 GGATTGCTTTATTTGTTAGCGCAACTATTGCGCAACAGATTGAGATGGTTTCGCGAGGTT 730
Qy 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
Db 731 GGTAAGGCGCTATGGAGAGATGGATGGTAAATGGCGTGGTGAAGAGTGGCTGTC 790
Qy 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
Db 791 AAAGTGTTTTTACCACCTGAAGAAGCTAGCTGTTTAGAGAAACAGAAATCTACACAGC 850
Qy 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db 851 GTGTTAATGCTCATGAAATATATCTTGGTTTTATAGCTGCAGACATTAAGGCACTGCT 910
Qy 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db 911 TCTGAGCTCAGCTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATT 970
Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db 971 CTGAATGTGCCACACTAGACACAGAGCCCTACTCAAGTTAGCTTATTCTGCTGCTTCT 1030
Qy 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1031 GGTCTGTGCCACCTCCACACAGAAATTTATGGTACCAAGGAAGCTGCAATTTGCTCAT 1090
Qy 361 ArgAspLeuLysSerLysAsnIleLeuIleLysAsnGlySerCysLysIleAlaAsp 380
Db 1091 CGAGAGCTGAAGAGCAAAACATCTTATTAAAGAAAATGGAAGTTGCTGATTGCTGAC 1150
Qy 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db 1151 CTGGGCTAGCTGTTAAATTTCAACAGTGATACAAATGAAGTTGACATACCTTGAATACC 1210
Qy 401 ArgValGlyThrArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
Db 1211 AGGGTGGGCACCAAGCGGTACATGGTCTCCAGAAAGTCTGGATGAAAGCCTGAATAAAAC 1270

Qy 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
Db 1271 CATTTCCAGCCCTACATCATGCTGACATCTATAGCTTTGGTTTGATCATTTGGGAAATG 1330
Qy 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db 1331 GCTGCTGCTGTATTACAGGAGGAATCGTGGAGGAATATCAATTACCATATTACAACATG 1390
Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db 1391 GTGCCAGTGACCCATCTATGAGGACATGCGGTGAGGTTGTGTGTGAACCGCTTGGCG 1450
Qy 481 ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1451 CCATTCGTCTTAACCGCTGGAACAGCGATGATGCTCTCGAGCAGCTTTGAAGCTAATG 1510
Qy 501 SerGluCysTyrAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
Db 1511 TCAGATGTTGGGCCCATTAATCCAGCTCCAGACTCACAGCTTTGAGAAATCAAGAAGACA 1570
Qy 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db 1571 CTTGCAAAAATGGTTGAATCCAGGATGTAAGATT 1606

RESULT 11

US-08-334-179A-11
; Sequence 11, Application US/08334179A
; Patent No. 6306622
; GENERAL INFORMATION:
; APPLICANT: ROSENBAUM, JAN S.
; APPLICANT: NOHNO, TSUTOMU
; TITLE OF INVENTION: CDNA ENCODING A BMP TYPE II RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSES: THE PROCTER AND GAMBLE COMPANY
; STREET: 11810 EAST MIAMI RIVER ROAD
; CITY: ROSS
; STATE: OH
; COUNTRY: US
; ZIP: 45061
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.30, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/334,179A
; FILING DATE: 04-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CORSTANJE, BRAHM J.
; REGISTRATION NUMBER: 34,804
; REFERENCE/DOCKET NUMBER: 5473
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 513-627-2858
; TELEFAX: 513-627-0260
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2402 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(11..1606)
US-08-334-179A-11

Alignment Scores: 1.54e-315 Length: 2402
Pred. No.: 2823.00 Matches: 526
Score: 99.81%
Percent Similarity: 99.81% Conservative: 5

Best Local Similarity: 98.87% Mismatches: 1
Query Match: 99.47% Indels: 0
DB: 3 Gaps: 0

US-10-600-645-2 (1-532) x US-08-334-179A-11 (1-2402)

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QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
DB 11 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCCCTGCTGTTCAATCTCTCAT 70
QY 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
DB 71 GTTCAAGGGCAGAACTAGATAGTATGCTCCATGGCAGCTGGTATGAATCAGACTTGGAC 130
QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
DB 131 CAGAAGAAGCCAGAAATGGAGTGACTTTAGCACCAGAGGATACCTTGCCCTTCTTAAAG 190
QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
DB 191 TGTATTGCTCAGGACACTGCCACAGATGCTATTATAACACACATGATAACTAATGGC 250
QY 81 HisCysPheAlaIleIleGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
DB 251 CATTGCTTTGCCATTATAGAAGAGATGATCAGGGAGAAACCACTTAACCTTCGGTGT 310
QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
DB 311 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCGAAAGCCAGCTAGCGAG 370
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DB 371 ACAATAGATGTTGTCGACCAATTTGTCACACAGTATTTGCAGCTACACTGCCCCCT 430
QY 141 ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
DB 431 GTTGTATTAGGTCGTTCTTGATGGCAGCATCCGATGGCTGGTGTGCTCATTTCCATG 490
QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
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QY 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
DB 671 GGATTTGCCCTTATTGTTTTCAGCGAACTATTGCGCAACAGATTCAGATGGTTCCGCGAGTT 730
QY 241 GlyLysGlyArgTyrGlyValTrpMetGlyLysTrpArgGlyGlyLysValAlaVal 260
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QY 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
DB 791 AAAGTGTTTTTTACCACCTGAAGAGCTAGCTGGTTTAGAGAAACAGAAATCTACCAGAGC 850
QY 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
DB 851 GTGTTAATCGCTCATGAAATAATATCTTGGTTTTATAGCTGCAGACATTAAGGCGACTGGT 910
QY 301 SerTrpThrGlnLeuTyrIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
DB 911 TCTTGACTCAGCTGATTGTGATTTACTGATTACCATGAAATGGATCTCTATGACTTC 970
QY 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaCys 340
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QY 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
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QY 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
DB 1091 CGAGACCTGAGAGCAAAACACATCTTATTAAAGAAATGGAAGTTGCTGTATTGCTGAC 1150
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DB 1151 CTGGCCCTAGCTGTATAATTCAACAGTATACAAATGAAGTTGACATACCCCTTGAATACC 1210
QY 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLysSerLysAsn 420
DB 1211 AGGTGGGCACCAAGCGGTACATGGCTCCAGAAAGTCTGGATGAAAGCCTGAATAAAAAC 1270
QY 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
DB 1271 CATTTCCAGCCCTACATCATGCTGACATCTATAGCTTTGGTTTGATCATTTGGGAAATG 1330
QY 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
DB 1331 GCTCGTCTGTGTTATTACAGGAGGAATCGTGAGGAATATCAATTACCATATTACAACATG 1390
QY 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
DB 1391 GTGCCAGTAGTACCCATCTTATGAGGACATGCGTGAGGTGTGTGTGTAACCGCTTGGCG 1450
QY 481 ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
DB 1451 CCATTCGTGCTTAACCGCTGGAAACAGCATGATGATCTTCGAGCAGATTTTGNAGCTAATG 1510
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DB 1511 TCAGAAATGTTGGGCCATAATCCAGCCTCCAGACTCACAGCTTTGAGAATCAAGAAGACA 1570
QY 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
DB 1571 CTTGCAAAATGGTTGAATCCAGGATGTAAAGATT 1606

RESULT 12
US-08-158-735A-1
; Sequence 1, Application US/08158735A
; Patent No. 6248554
; GENERAL INFORMATION:
; APPLICANT: COOK, JONATHAN S.
; APPLICANT: CORREA, PAUL E.
; APPLICANT: KOENIG, BETH B.
; APPLICANT: ROSENBAUM, JAN S.
; APPLICANT: TING, JERRY
; TITLE OF INVENTION: DNA SEQUENCE CODING FOR A BMP RECEPTOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE PROCTER & GAMBLE COMPANY
; STREET: 11810 EAST MIAMI RIVER ROAD
; CITY: ROSS
; STATE: OH
; COUNTRY: USA
; ZIP: 45061
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/158,735A
; FILING DATE: 24-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CORSTANJE, BRAHM J.
; REGISTRATION NUMBER: 34,804
; REFERENCE/DOCKET NUMBER: 5088
```

TELECOMMUNICATION INFORMATION:

; TELEPHONE: (513) 627-2858
 ; TELEFAX: (513) 627-0260
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2056 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: join(291...1790)
 ; US-08-158-735A-1

Alignment Scores:

Pred. No.: 9.23e-313 Length: 2056
 Score: 2798.00 Matches: 526
 Percent Similarity: 94.48% Conservative: 5
 Best Local Similarity: 93.59% Mismatches: 1
 Query Match: 98.59% Indels: 30
 DB: 3 Gaps: 1

US-10-600-645-2 (1-532) x US-08-158-735A-1 (1-2056)

Qy 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
 Db 291 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCCTGTCTGTTTCATCATTTCTCAT 350
 Qy 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetIysSerAspValAsp 40
 Db 351 GTTCAAGGGCAGAACTTAGATAGTATGCTCCATGGCACCTGGTATGAATCAGACTTGGAC 410
 Qy 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
 Db 411 CAGAGAGCCAGAAATGGAGTGACTTTAGCACCAGAGGATACCTTGCCTTCTTTAAAG 470
 Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
 Db 471 TGCTATTGCTCAGGACACTGCCCCAGATGATGCTATTATTAACACATGCATACTAATGCG 530
 Qy 81 HisCysPheAlaIleIleGluAspGlnGlyValThrThrLeuThrSerGlyCys 100
 Db 531 CATTTGCTTTGCCATTATAGAAGAAGATGATCAGGAGAAACCACTTAACCTTCCTGGGTGT 590
 Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
 Db 591 ATGAAGTATGAAGCTCTGATTTTCAATGCAAGATTCACGAAAGCCAGCTACGCAGG 650
 Qy 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrIleLeuGlnProThrLeuProPro 140
 Db 651 ACAATAGATGTTGTCGGACCAATTTGTGCAACAGTATTTGCGAGCTACACTGCCCCCT 710
 Qy 141 ValValIleGlyProPheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
 Db 711 GTTGTATAGTCCGTTCTTTGATGGCAGCATCCGATGGCTGGTGTGCTCATTTCCATG 770
 Qy 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrIysHisTyrCys 180
 Db 771 GCTGTCTGATAGTGTATGATCATCTTCTCAGCTGCTTTTGTGATAGCATTAATGT 830
 Qy 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
 Db 831 AAGAGTATCTCAGCAGGGGTCTTACACCGTGATTTGGACAGGATGAGCATTTAT 890
 Qy 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
 Db 891 CCAAGTAGGAATCATTTGAAGACCTGATTGACAGCTCCCAAGAGCTCTGGGAGTGATCT 950
 Qy 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
 Db 951 GGATTCCTTTATTGGTTAGCCAACTATTGCCAAACAGATTACAGATGTTGGCAGGTT 1010
 Qy 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260

Db 1011 GGTAAAGGCGCTATTCGAGAAGTATGCATGGGTAAATGCGTGGTAAAAAGTGGCTGTC 1070
 Qy 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
 Db 1071 AAAGTGTGTTTTTACCACCTGAAGAAGCTAGCTGGTTTTAGAGAAACAGAAATCTACACGACG 1130
 Qy 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
 Db 1131 GTGTTAATGGTCATGAANAATATACCTGGTTTTATAGCTGCAGACATTAAGGCACTGGT 1190
 Qy 301 SerTrpThrGlnLeuTyrIleLeuThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
 Db 1191 TCCTGGACTCAGCTGATTTGATTACTGATTACCATGAAATGGAATGCTCTCTATGACTTC 1250
 Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaLysSerAlaAlaCys 340
 Db 1251 CTGAAATGTGCCACACTACAGACCAGACCCCTACTCAAGTTAGCTTATTCTGCTGCTGT 1310
 Qy 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
 Db 1311 GGTCTGTGCCACTCCACACAGAAATTTATGGTACCAGAGGAGGCTGCATTTGCTCAT 1370
 Qy 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
 Db 1371 CGAGACCTGAAGAGCAAAAACATCCTTATTAAGAAAAATGGAAGTTGCTGTATGCTGAC 1430
 Qy 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAanThr 400
 Db 1431 CTGGGCCCTAGCTGTGTTAAATTCACAGTGTATACAAATGAAGTTGACATACCCCTTGAATACC 1490
 Qy 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuLysAsn 420
 Db 1491 AGGTTGGGACCAAGCGGTACATGCTCCAGAAAGTCTGGATGAAGCCCTGATATAAAC 1550
 Qy 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
 Db 1551 CATTTCCAGCCCTACATCATGCTGACATCTATAGCTTTGGTTTGATCATTTGGGAAATG 1610
 Qy 441 AlaArgArgCysIleThrGlyIleValGluGlyThrGlnLeuProTyrTyrAsnMet 460
 Db 1611 GCTGCTGCTGTATTACAGAGGAATCGTGGAGGAATATCAATTTACCATATTAACAACATG 1670
 Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
 Db 1671 GTGCCAGTGAACCCATCTCTATGAGGACATGCTGAGGTGTGTGTGTGAACGCTTGGCG 1730
 Qy 481 ProfileValSerAsnArgTrpAsnSerAspGlu----- 491
 Db 1731 CCAATCGTCTTAACCGCTGGAACAGCATGAAGTGAAGTTGGAGCAAGTCCCTGCTAAAG 1790
 Qy 491 ----- 491
 Db 1791 TGATGAGTGAGTCCGAGTTACTCTGTGCTCACACACTCTGTTTTCATTTATTTCTCTT 1850
 Qy 492 ---CysLeuArgAlaValLeuLysLeuMetSerGluCysTrpAlaHisAsnProAlaSer 510
 Db 1851 TAGTGTCTCGAGCAGTTTGAAGCTAATGTCAGAAATGTTGGGCCCATTAATCAGCCTCC 1910
 Qy 511 ArgLeuThrAlaLeuArgIleLysLysThrLeuAlaLysMetValGluSerGlnAspVal 530
 Db 1911 AGACTCAGACCTTTGAGAATCAAGAAGACACTTGCAAAAATGTTGTAATCCCGAGATGTA 1970
 Qy 531 LysIle 532
 Db 1971 AAGATT 1976

RESULT 13

US-08-481-337A-5
 ; Sequence 5, Application US/08481337A
 ; Patent No. 5863738
 ; GENERAL INFORMATION:
 ; APPLICANT: TEN DIJKE, Peter

APPLICANT: HELDIN, Carl-Henrik
APPLICANT: MIYAZONO, Kohei
APPLICANT: SAMPATH, Kuber T.
TITLE OF INVENTION: Morphogenic Protein-Specific Cell
TITLE OF INVENTION: Surface Receptors and Uses Therefor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,337A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, Thomas C.
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: CRP-097CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2932 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 310..1905
OTHER INFORMATION: /product= "Human ALK3"

US-08-481-337A-5

Alignment Scores:

Pred. No.:	3,68e-309	Length:	2932
Score:	2769.00	Matches:	517
Percent Similarity:	98.50%	Conservative:	7
Best Local Similarity:	97.18%	Mismatches:	8
Query Match:	97.57%	Indels:	0
DB:	2	Gaps:	0

US-10-600-645-2 (1-532) x US-08-481-337A-5 (1-2932)

QY	1	MetThrGlnLeuTyrThrTyrileArgLeuLeuGlyAlaCysLeuPheileileSerHis	20
DB	310	ATGACTCAGCTATACATTACATCAGATTATTGGAGCCTATTGTTTCATCATTTCTCGT	369
QY	21	ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetCysSerAspValasp	40
DB	370	GTTCAAGGACAGAATCTGGATAGTATGCTTCATGGCAGCTGGGATGAAATCAGACTCCGAC	429
QY	41	GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys	60
DB	430	CAGAAAAAGTCAGAAAATGGAGTAACCTTAGCACCAGAGGATACCTTGCTTTTAAAG	489
QY	61	CysTyrCysSerGlyHisCysProAspAspAlaileAsnAsnThrCysilethrAsnGly	80
DB	490	TGCTATTGCTCAGGCAGCTGTCAGATGATGCTATTATAACACATGATCAATAATGGA	549
QY	81	HisCysPheAlailelleGluAspAspGlnGlyThrLeuThrSerGlyCys	100
DB	550	CATTGCTTTGCCATCATAGAAGAAGATGACCAGGGAGAAACACATTAGCTTCAGGGTGT	609
QY	101	MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArg	120

Db	610	ATGAATATGAAGGATCTGATTTTCAGTGCAGAAAGATTCTCCAAAAGCCAGCTACGCCGG	669
QY	121	ThrileGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro	140
DB	670	ACAATAGAATGTTGTCGGACCAATTTATGTAAACAGATATTTGCAACCCACACACTGCC	729
QY	141	ValValilleGlyProPhePheAspGlySerValArgTyrLeuAlaValleSerMet	160
DB	730	GTTGTCAATAGGTCGGTTTTTGTATGGCAGCATTCGATGGCTGCTGCTCATTTCTATG	789
QY	161	AlaValCysilleValAlaMetilleValPheSerSerCysPheCysTyrLysHisTyrCys	180
DB	790	GCTGTCTGCATAATTTGCTATGATCATCTTCCACAGCTGCTTTTGTACAAACATTTATGC	849
QY	181	LysSerilleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheille	200
DB	850	AAGAGCATCTCAAGCAGACGTCGTTTACAAATCGTGATTTTGGAAACAGATGAACATTTAT	909
QY	201	ProValGlyGluSerLeuLysAspLeuileAspGlnSerGlnSerSerGlySerGlySer	220
DB	910	CCAGTTGGAGAAATCACTAAAAGACCTTATTGACCAGTCAAAAGTTCTGGTAGTGGTCT	969
QY	221	GlyLeuProLeuLeuValGlnArgThrilleAlaLysGlnilleGlnMetValArgGlnVal	240
DB	970	GGACTACCTTTATTGGTTTCAGGAACTATTGCCAAACAGATTTCAGATGTCGCGCAAT	1029
QY	241	GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTyrPargGlyGlyLysValAlaVal	260
DB	1030	GGTAAAGGCCGATATGGAGAAAGTATGGATGGCAATGGCGTGGCGAAAAAGTGGCGTG	1089
QY	261	LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluileTyrGlnThr	280
DB	1090	AAAGTATTCTTTTACCACCTGAAAGAACCCAGCTGGTTTCGAGAAACAGAAATCTTACCA	1149
QY	281	ValLeuMetArgHisGluAsnilleLeuGlyPheilleAlaAlaAspilleLysGlyThrGly	300
DB	1150	GTGCTAATGGCCCATGAAACATATCTTGGTTTCATAGCGGCAGACATTAAGGTACAGGT	1209
QY	301	SerTrpThrGlnLeuTyrLeuileThrAspTyrHisGluAsnGlySerLeuTyrAspPhe	320
DB	1210	TCCTGGAGCTCAGCTCTATTTCATTACTGATTACCATGAAATGGATCTCTCTATGACTTC	1269
QY	321	LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys	340
DB	1270	CTGAAATGTGTACACTGGACACAGACCCCTGCTTAAATTTGGCTTATTTCAGCTGCCTGT	1329
QY	341	GlyLeuCysHisLeuHisThrGluileTyrGlyThrGlnGlyLysProAlaileAlaHis	360
DB	1330	GCTCTGTGCCACCTGACACAGAAATTTATGGACCCCAAGGAAGCCCGCAATTTGCTCAT	1389
QY	361	ArgAspLeuLysSerLysAsnilleLeuileLysLysAsnGlySerCysCysileAlaAsp	380
DB	1390	CGAGACCTAAAGAGCAAAACATCTCATCAAGAAAAATGGAGTTGCTGCATTCCTGAC	1449
QY	381	LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspilleProLeuAsnThr	400
DB	1450	CTGGCCCTTGCTGTATAATTTCAACAGTGACACAAATGAAGTTGATGTCCTTGAATACC	1509
QY	401	ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn	420
DB	1510	AGGTGGGCACCAACCGCTACATGGCTCCCAAGTGTGGAGCAAGAGCTGAACAAAAAC	1569
QY	421	HisPheGlnProTyrilleMetAlaAspilleTyrSerPheGlyLeuileileTrpGluMet	440
DB	1570	CACITCCAGCCCTACATCATGCTGACATCTACAGCTTCGCGCTTAATCATTTGGGAGATG	1629
QY	441	AlaArgArgCysilleThrGlyGlylleValGluGluTyrGlnLeuProTyrTyrAsnMet	460
DB	1630	GCTCGTCTGTATACAGAGGGATCGTGAAGAATAACCAATTTGCCATATTACAAACATG	1689
QY	461	ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg	480

Db 1690 GTACCGAGTATCCGTATACGAAGATATGCGTGAGGTTGTGTGTGTCACAAACGTTTCGG 1749
Qy 481 ProileValSerAenArgTtpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1750 CCAATTGCTCTAATCGGTGGAACAGTGAATGCTCTACAGCAGTTCCTTTGAAGCTAATG 1809
Qy 501 SerGluCysTrpAlaHisAenProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
Db 1810 TCAGAATGCTGGGCCCAATCCAGCCTCCAGACTCACAGCAATTGAGAAATTAAGAGACG 1869
Qy 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db 1870 CTTGCCCAAGATGGTTGAATCCCAAGATGTAAAAATC 1905

RESULT 14
US-09-382-256-5
Sequence 5, Application US/09382256A
Patent No. 6207814
GENERAL INFORMATION:
APPLICANT: MIYAZONO, Kohei
TEN DIJKE, Peter
FRANZEN, Petra
YAMASHITA, Hidetoshi
HELDIN, Carl-Henrik
TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS
HAVING SERINE THREONINE KINASE DOMAINS,
AND THEIR USE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/382,256A
FILING DATE: 24-Aug-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: No. 6207814ember 17, 1993
APPLICATION NUMBER: GB 9224057.1
FILING DATE: No. 6207814ember 17, 1992
APPLICATION NUMBER: GB 9304677.9
FILING DATE: March 8, 1993
APPLICATION NUMBER: GB 9304680.3
FILING DATE: March 8, 1993
APPLICATION NUMBER: 9311047.6
FILING DATE: May 28, 1993
APPLICATION NUMBER: 9313763.6
FILING DATE: July 2, 1993
APPLICATION NUMBER: 9316099.2
FILING DATE: August 3, 1993
APPLICATION NUMBER: 321344.5
FILING DATE: October 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 6207814man D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5298.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2932 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown

TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 310..1905
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-382-256-5
Alignment Scores:
Pred. No.: 3 68e-309 Length: 2932
Score: 2769.00 Matches: 517
Percent Similarity: 98.50% Conservative: 7
Best Local Similarity: 97.18% Mismatches: 8
Query Match: 97.57% Indels: 0
DB: 3 Caps: 0
US-10-600-645-2 (1-532) x US-09-382-256-5 (1-2932)
Qy 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleSerHis 20
Db 310 ATGACTCAGCTATACATTTACATCAGATTATTGGGAGCCTATTATTGTTTCATCATTTCTCGT 369
Qy 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
Db 370 GTTCAAGSAGAGAATCTGGATAGTATGCTTTCATGGCACTGGGATGAAATCAGATCCGAC 429
Qy 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
Db 430 CAGAAAAGTCAGAAAATGGAGTAACCTTAGCACCCAGAGAGATACCTTGCTTTTAAAG 489
Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
Db 490 TGCTATTGCTCAGGCACTGTCAGATGATGCTATTATAACACATGATCACTAATGGA 549
Qy 81 HisCysPheAlaIleIleGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 550 CATTGCTTTGCCATCATAGAAGAAGATGACCAAGGAGAAACCAATAGCTTCAGGCTGT 609
Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db 610 ATGAATATGAAGGATCTGATTTTCAGTGCRAAGATTCTCCAAAAGCCAGCTACGCCGG 669
Qy 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
Db 670 ACAATAGATGTTGTCGGACCAATTTATGTAACCAAGTATTTGCAACCCACACTGCCCCCT 729
Qy 141 ValValIleGlyProPhePheAspGlySerValArgTrrPleuAlaValLeuIleSerMet 160
Db 730 GTTGTATAGGTCGGCTTTTTCATGGCAGCATTCGATGCTGTTTGTCTATTTCTATG 789
Qy 161 AlaValCysIleValAlaMetIleValPheSerCysPheCysTyrLysHisTyrCys 180
Db 790 GCTGCTGCATTAATTGCTATGATCATCTTCTCAGCTGCTTTTGTACAAACATTATTGC 849
Qy 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
Db 850 AAGAGCATCTCAAGCAGACGCTGTTTACATCTGTTTGGAAACAGGATGAAGCATTTATT 909
Qy 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
Db 910 CCAGTTGGAGAAATCACTAAAGACCTTATTGACCAAGCTTCAAAAGTTCTCGTAGTGGTCT 969
Qy 221 GlyLeuProLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 970 GGACTACCTTTATTGGTTCAGCAACTATTGCAAAACAGATTTCAGATGTTCCGGCAAGTT 1029
Qy 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260

1030 GGTAAGGCGCATATGGAGAAGTATGGATGGGCAAAATGGTGGCGCAAAAAGTGGCGGTG 1089
Qy LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
Db AAGATATCTTTTACCACCTGAAGAGCGCAGTGGTTTCGAGAAACAGAAATCTACCAAACT 1149
Qy ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db GTGCTAATGGCCATGAAACATACTTGGTTTCATAGCGGCAGACATTAAGGTACAGGT 1209
Qy SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db TCTGTGACTCAGCTCTATTGATTACTGATTACCATGAAATGGATCTCTCTATGACTTC 1269
Qy LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db CTGAAATGTGCTACACTGACACACAGAGCCCTGCTTAAATTTGGCTTTATTTCAGCTGCTGT 1329
Qy GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db GTCTGTGCGCACCTGCACACAGAAATTTATGGACCCCAAGGAAAGCCCAATTTGCTCAT 1389
Qy ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysIleAlaAsp 380
Db CGAGACCTTAAGAGAGCAAAACATCTCTCATCAAGAAAAATGGGAGTTTGTGCTGCTGAC 1449
Qy LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db CTGGGCTTGTGCTTAAATTTCAACAGTGCACACAAATGAAAGTTGATGTGCGCTTGAATACC 1509
Qy ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
Db AGGTGGGACCAACACGCTACATGGCTCCGAGTCTCGAGCGAAGCCCTGACAAAAAC 1569
Qy HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
Db CACTTCCAGCCCTTACATCATGCTGCTGACATCTACAGCTTCGGCTTAATCATTTTGGGAGATG 1629
Qy AlaArgArgCysIleThrGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db GTCTGCTGTGTATCATCAGAGGGATCGTGGAGAAATACCAATTTGCCATATTACAACTG 1689
Qy ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db GTACCGAGTGATCCGTCATACGAAGATATCGGTAGGTGTGTGTGTCAAACTTTGGCG 1749
Qy ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db CCAATTGTCTTAATCGGTGGAACAGTGTATGAATGTCTACGAGCAGTTTTTGAAGCTAATG 1809
Qy SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
Db TCAGATGTGTGGCCACAAATCCAGCTCCAGACTCACAGCATTTGAGAAATTAAGAAGAGC 1869
Qy LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db CTGCCAAGATGGTTGAATCCCAAGATGTAATAATC 1905

RESULT 15

US-09-395-115-5
; Sequence 5, Application US/09395115
; Patent No. 6271365
; GENERAL INFORMATION:
; APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
; APPLICANT: Franzen, Petra; Yamashita, Hidekoshi; Heldin, Carl-Henrik
; TITLE OF INVENTION: Activin Receptor-Like Kinase, proteins
; TITLE OF INVENTION: Having Serine Threonine Kinase Domains And Their Use
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York

Alignment Scores:

Pred. No.:	3.68e-309	Length:	2932
Score:	2769.00	Matches:	517
Percent Similarity:	98.50%	Conservative:	7
Best Local Similarity:	97.18%	Mismatches:	8
Query Match:	97.57%	Indels:	0
DB:	3	Gaps:	0

US-10-600-645-2 (1-532) x US-09-395-115-5 (1-2932)

Qy 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleSerHis 20
Db 310 ATGACTCAGCTATACATTACATCAGATTATTGGAGCGCTATTTTTCATCATTTCTCGT 369

ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/395,115
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-October-1995
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. 6271365ember-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6271365ember-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9304680.3
FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9311047.6
FILING DATE: 28-May-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9136099.2
FILING DATE: 3-August-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-October-1993
ATTORNEY/AGENT INFORMATION:

NAME: Kohlei, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD 5298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2932 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 310..1905
US-09-395-115-5

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Qy 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
Db 370 GTTCAAGGACAGAACTCGTAGTAGTCTTCATGGCACTGGGATGAATCAGACTCCGAC 429
Qy 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
Db 430 CAGAAAAAGTGCAGAAAAAGTGAAGTAACTTTAGCACCAGAGGATACCTTTGCGCTTTTAAAG 489
Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnThrCysIleThrAsnGly 80
Db 490 TGCTATTGCTCAGGCGCACTGTCAGATGATGCTATTATAACACATGCATAACTAATGGA 549
Qy 81 HisCysPheAlaIleIleGluGluAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 550 CATTGCTTTGCCATCATAGAGAAGATGACCCAGGAGAAACCACTTAGCTTCAGGGTGT 609
Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db 610 ATGAAATATGAAGGATCTGATTTTCAGTGCAGAAAGATTCCTCAAAAGCCAGCTACGCCGG 669
Qy 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrIleuGlnProThrLeuProPro 140
Db 670 ACAATAGATGTTGCGACCAATTTATGTAACCAAGTATTTCGAACCCACACTGCCCCCT 729
Qy 141 ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
Db 730 GTTGTCATAGTTCGGTTTTGTATGGCAGCAATCGATGGCTGGTTTTGCTCATTTCTATG 789
Qy 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
Db 790 GCTGCTGCATAATTGCTATGATCATCTCTCCAGCTGCTTTTGTACAAACATTTATTC 849
Qy 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
Db 850 AAGAGCATCTCAAGCAGACGTCGTACAAATCGTGAATTTGGAACAGGATGAAGCATTTATT 1909
Qy 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySer 220
Db 910 CCAGTTGGAGATCACTAANAAGACCTTATTGACCAGTCACANAAGTTCTGGTAGTGGGTCT 969
Qy 221 GlyLeuProLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 970 GGACTACCTTTATTGGTTTCAGCGAACTATTGCCAAACAGATTCAGATGGTCCGCGAAGTT 1029
Qy 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
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Db 1150 GTGCTAATGCCCATGAAACATACTTGGTTTCATAGCGGCAGACATTAAGGTACAGGT 1209
Qy 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
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Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db 1270 CTGNAATGTCTACACTGGACACAGAGCCCTGCTTAAATTTGGCTTATTTCAGCTGCTGT 1329
Qy 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1330 GTTCTGTGCCACCTGCACACAGAAATTTATGGCACCCAGGAAAGCCGCAATTGCTCAT 1389
Qy 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
Db 1390 CGAGACCTAAGAGCAAAAAATCCTCATCAAGAAAAAATGGGAGTTGCTGCATTGCTGAC 1449
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Job Time: 1.249 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 9, 2005, 22:23:06 ; Search time 152 Seconds
(without alignments)

1308.491 Million cell updates/sec

Title: US-10-600-645-2

Perfect score: 2838

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Scoring table: BLOSUM62

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Fgapop 10.0, Fgapext 0.5

Delop 6.0, Delext 7.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100
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Database : Published Applications_NA_New:

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10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	561.5	19.8	2090	6	US-10-420-192-7
2	280	9.9	3527	6	US-10-770-726-35
3	248	8.7	2505	7	US-11-186-283-3
4	248	8.7	3025	7	US-11-186-283-1
5	242	8.5	2505	7	US-11-186-283-9
6	242	8.5	3026	7	US-11-186-283-7
7	241.5	8.5	3105	7	US-11-021-441-3
8	230.5	8.1	1383	6	US-10-990-276-2
					Sequence 7, Appli
					Sequence 35, Appl
					Sequence 3, Appli
					Sequence 1, Appli
					Sequence 9, Appli
					Sequence 7, Appli
					Sequence 3, Appli
					Sequence 2, Appli

9	230	8.1	1542	6	US-10-990-276-4	Sequence 4, Appli
10	226	8.0	6058	6	US-10-770-726-17	Sequence 17, Appl
11	224	7.9	1437	7	US-11-021-441-19	Sequence 19, Appl
12	222	7.8	1254	7	US-11-021-441-16	Sequence 16, Appl
13	222	7.8	1254	7	US-11-021-441-17	Sequence 17, Appl
14	222	7.8	1382	7	US-11-021-441-40	Sequence 40, Appl
15	222	7.8	1716	7	US-11-021-441-25	Sequence 25, Appl
16	222	7.8	1737	7	US-11-021-441-21	Sequence 21, Appl
17	222	7.8	1737	7	US-11-021-441-23	Sequence 23, Appl
18	222	7.8	2778	7	US-11-021-441-39	Sequence 39, Appl
19	212.5	7.5	2981	6	US-10-949-720-399	Sequence 399, App
20	212.5	7.5	3955	6	US-10-821-234-349	Sequence 349, App
21	212.5	7.5	4235	6	US-10-949-720-392	Sequence 392, App
22	211	7.4	3805	6	US-10-510-524-2	Sequence 2, Appli
23	211	7.4	3805	6	US-10-955-054A-144	Sequence 144, App
24	211	7.4	4234	6	US-10-955-054A-133	Sequence 133, App
25	209.5	7.4	951	7	US-11-137-315A-3	Sequence 3, Appli
26	209.5	7.4	2042	6	US-10-770-726-12	Sequence 12, Appl
27	206.5	7.3	2197	6	US-10-750-185-35470	Sequence 35470, A
28	203.5	7.2	3890	6	US-10-821-234-269	Sequence 269, App
29	202.5	7.1	1082144	7	US-11-117-187-211	Sequence 211, App
30	199	7.0	1866	6	US-10-955-054A-5	Sequence 5, Appli
31	195.5	6.9	2328	6	US-10-770-726-7	Sequence 7, Appli
32	195.5	6.9	4034	7	US-11-115-086-5	Sequence 5, Appli
33	195	6.9	1611	7	US-11-186-284-114	Sequence 114, App
34	195	6.9	2820	7	US-11-112-908-2	Sequence 2, Appli
35	194	6.8	4989	7	US-11-090-351-3	Sequence 3, Appli
36	193.5	6.8	3711	7	US-11-115-086-3	Sequence 3, Appli
37	193.5	6.8	4975	6	US-10-770-726-19	Sequence 19, Appl
38	193	6.8	717	7	US-11-115-086-1	Sequence 1, Appli
39	193	6.8	1224	6	US-10-523-477-2	Sequence 2, Appli
40	193	6.8	1224	6	US-10-770-726-40	Sequence 40, Appl
41	193	6.8	1224	7	US-11-136-815A-4	Sequence 4, Appli
42	191.5	6.7	5484	6	US-10-955-054A-86	Sequence 86, Appl
43	188.5	6.6	3052	6	US-10-770-726-34	Sequence 34, Appl
44	186	6.6	1888	6	US-10-770-726-25	Sequence 25, Appl
45	186	6.6	2838	6	US-10-770-726-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1

US-10-420-192-7
; Sequence 7, Application US/10420192
; Publication No. US20050260579A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Herbert Y.
; APPLICANT: Wang, Xiao-Fan
; APPLICANT: Weinberg, Robert A.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: TGF-Beta Type Receptor cDNAs Encoded Products and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 0399.1086-022
; CURRENT APPLICATION NUMBER: US/10/420,192
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US 09/584,929
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 08/446,936
; PRIOR FILING DATE: 1995-05-23
; PRIOR APPLICATION NUMBER: US 08/311,703
; PRIOR FILING DATE: 1994-09-23
; PRIOR APPLICATION NUMBER: US 07/786,063
; PRIOR FILING DATE: 1991-10-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2090
; TYPE: DNA
; ORGANISM: genomic
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (336) ... (2038)
US-10-420-192-7

Alignment Scores:
Pred. No.: 3,52e-55 Length: 2090
Score: 561.50 Matches: 144
Percent Similarity: 50.20% Conservatives: 104
Best Local Similarity: 29.15% Mismatches: 195
Query Match: 19.79% Indels: 51
DB: 6 Gaps: 13

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DB 534 TGCATGAGCAATGCG-----AGCATCACTCCATCTGTGAGAGCCACAGGAAGTC 584

QY 82 CysPheAlaIleleuGluAspAspGlnGlyGluThrLeuThrSerGlyCys--- 100
DB 585 TGTGTGGCTGTATGGAGAAAGATGACGAG---AACATAACACTAGAGACAGTTTGCCAT 641

QY 101 ---MetLysTyxGluCysSerAspPheGlnCysLysAsp-----SerProLysAlaGln 117
DB 642 GACCCCAAGCTCCCTTACCATGACTTTATTCTGGAGATGCTGCTTCTCCAAAGTGCATT 701

QY 118 LeuArgArgThrIleGlu-----CysCysArgThrAsnLeu 129
DB 702 ATGAGGAAAAAAGAAAGCTGGTGAGACTTCTTCATGTCTCTGTAGCTCTCATGAG 761

QY 130 CysAsnGlnTyLeu-----GlnProThrLeuProPro 140
DB 762 TGCATGACAAACATCATCTTCTCAGAAAGATATAACACCAGCAATCCTGACTTGTGCTA 821

QY 141 ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
DB 822 GTCATATTT-----CAAGTGACAGGCATCAGCTCTCTGCCACCACTG 863

QY 161 AlaValCysIleValAlaMetIleValPheSerCysPheCysTyryLysHisTyCys 180
DB 864 GGAGTGCCATATCTGTCAATCATCTTC-----TACTGC 899

QY 181 LysSerIleSerSerArgGlyArgTyArgAsnArgAspLeuGlu-----GlnAspGluAla 198
DB 900 TACCGGTTTAACCGGAGCAGAGAGCTGAGTTCAACCTGGGAAACCGGCAAGCGGGAAG 959

QY 199 PheIleProValGlyCysLeuLysAspLeuIleAspGlnSerGlnSerSerGlySer 218
DB 960 CTCATGGAGTTGAGCGGACACTGTGCTCATCTCTGGAAGATGACCGCTCTGACATCAGC 1019

QY 219 GlySerGlyLeuProLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArg 238
DB 1020 TCCAGTGTGCCAACACATCAACCAACACAGAGCTGCTGCCCATGTAGCTGGACACC 1079

QY 239 GlnValGlyLeGlyArgTyGlyGluValTrpMetGlyLysTrpArgGly----- 255
DB 1080 CTGGTGGGAAAGGTCGCTTGTCTGAGGTCATATAAGGCCAAGCTGAAGCAGAAACACTTCA 1139

QY 256 -----GluLysValAlaValLysValPhePheThrThrGluGluAlaSerTrpPhe 272
DB 1140 GAGCAGTTTGAGACAGTGGCAGTCAAGATCTTTTCCCTATGAGGAGTATGCTCTTTGGAAG 1199

QY 273 ArgGluThrGluIleTyGlnThrValLeuMetArgHisGluAsnIleLeuGlyPheIle 292
DB 1200 ACAGAGAGGAGCATCTTCTCAGACATCAATCTGAGCATGAGAAACATCTCAGTTCTCG 1259

QY 293 AlaAlaAspIleGlySerThrGlySerTrpThrGlnLeuTyThrLeuIleThrAspTyHis 312
DB 1260 ACGGCTGAGGAGCGGAAGCGGAGTTGGGAAACAATACTGCTGATCACCGCTTCCAC 1319

QY 313 GluAsnGlySerLeuTyTrpPheLeuLysCysAlaThrLeuAspThrArgAlaLeu 332
DB 1320 GCCAAGGGCAACCTACAGAGTACCTGACGCGGCATGTCTATCAGCTGGAGGACCTGCGC 1379

QY 333 LysLeuAlaTySerAlaAlaCysGlyLeuCysHisLeuHisThrGluIleTyGlyThr 352
DB 1186 CGGCACTAC-----AAGATCTGGCGGCGTTCGCGGGGCGCGCTGCACCTGAAACGAGCG 1239

DB 1380 AAGTGGGCGAGCTCCCTCGCCGGGGGATTGCTCACCTCCACAGTGAT---CACACTCCA 1436

QY 353 GlnGlyLysPro-----AlaIleAlaHisArgAspLeuLysSerLysAsnIleLeuIle 370
DB 1437 TGTGGAGGCCCAAGATGCCATCGTCACAGGAGCTCAAGAGCTCCAATATCTCGTG 1496

QY 371 LysLysAsnGlySerCysCysIleAlaAspLeuGlyLeuAlaValLysPheAsnSerAsp 390
DB 1497 AAGAACGACCTAACCTGCTGCTGTGTGACTTTGGGCTTTCCCTCGCTTGACCCCTACT 1556

QY 391 ThrAsnGluValAspIleProLeuAsnThrArgValGlyThrArgTyTrpMetAlaPro 410
DB 1557 CTGCTGTGGATGACCTGGCTAACAGTGGGAGGTGGGAACCTGCAAGATACATGCTCCA 1616

QY 411 GluValLeuAspGluSerLeuSerLysAsnHisPheGlnProTyTrpIleMetAlaAspIle 430
DB 1617 GAAGTCCTAGATCCAGGATGAATTTGGAGAATGCTGAGTCTCTCAAGCAGACCGCATGTC 1676

QY 431 TyrSerPheGlyLeuIleIleTrpGluMetAlaArgArgCysIleThrGlyGlyIleVal 450
DB 1677 TACTCCATGGCTGTGCTCTCTGGGAATGACATCTCGCTGTAAATGCAATGCGAGTGGGAAGTA 1736

QY 451 GluGluTyGlnLeuProTyTrpAsnMetValProSerAspProSerTyTrpGluAspMet 470
DB 1737 AAAGATTATGAGCTCCATTTGGTTCCAAAGGTGGGAGACCCCTGTGTGCAAGCATG 1796

QY 471 ArgGluValValCysValLysArgLeuArgProIleValSerAsnArgTrpAsnSerAsp 490
DB 1797 AAGCAACAAGTGTGAGAGATCGAGGGCGACAGAAATTCAGCTTCTGGCTCAACCAC 1856

QY 491 GluCysLeuArgAlaValLeuLysLeuMetSerGluCysTrpAlaHisAsnProAlaSer 510
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QY 511 ArgLeuThrAlaLeuArgIleLysLysThrLeuAlaLysMet 524
DB 1917 CGTTCACAGCCAGTGTGTGGCAGAACGCTTCAGTGAGCTG 1958

RESULT 2
US-10-770-726-35
; Sequence 35, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 3527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-35

Alignment Scores:
Pred. No.: 1,33e-21 Length: 3527
Score: 280.00 Matches: 99
Percent Similarity: 43.85% Conservatives: 65
Best Local Similarity: 26.47% Mismatches: 116
Query Match: 9.87% Indels: 94
DB: 6 Gaps: 18

US-10-600-645-2 (1-532) x US-10-770-726-35 (1-3527)

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DB 1186 CGGCACTAC-----AAGATCTGGCGGCGTTCGCGGGGCGCGCTGCACCTGAAACGAGCG 1239

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Qy 197 GluAlaPheLeProValGlyGluSerLeuLysAspLeuLeuLeuSerGlnSer 216
Db 1240 GTGTCCTTCTC-----AGCTGCCGAGCTTGTGAACACACAGGCCGAC 1287
Qy 217 GlySerGlySerGlyProLeuLeuValGln----- 227
Db 1288 AGCCTGTCCACCGGCTTGGCTGGCGCGCCCTGCCGSAAGCAGCAGCCTGAGCCCTG 1347
Qy 228 -----ArgThrIleAlaLysGlnIleGlnMetValArgGlnValGly 241
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Qy 242 LysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGlu-----LysValAlaVal 260
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Qy 292 IleAlaAlaAspLeuLysGlyThrGlySerTrpThrGlnLeuTyrLeuIleThrAspTyr 311
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Qy 312 HisGluAsnGlySerLeuTyrAspPheLeuLysCysAla-----ThrLeuAspThr 328
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Qy 329 ArgAlaLeuLysLeuAlaTyrSerAlaAlaCysGlyLeuCysHisLeuHisThrGlu 348
Db 1672 TCGAGCTGTGACATCGCTCGCAGTGGCTGAGGGCATGTGTACCTGGAGTGGCAG 1731
Qy 349 IleTyrGlyThrGlnGlyLysProAlaIleAlaHisArgAspLeuLysSerLysAsnIle 368
Db 1732 AATTAC-----ATCCACCGGGACCTGGCGCGCCAGGACATC 1767
Qy 369 LeuIleLysLysAsnGlySerCysIleAlaAspLeuGlyLeuAlaValLysPheAsn 388
Db 1768 CTGCTGGGGAAACACCTCTCAAGTTGGGGACTTCGGGTAGCCAGGCTTATCAAG 1827
Qy 389 SerAsp-----ThrAsnGluValAspIleProLeuAsnThrArgValGlyThrArg 405
Db 1828 GAGAGCTCTACCTCTCCCATGACCAATATCCCTAC----- 1866
Qy 406 ArgTyrMetAlaProGluValLeuAspGluSerLysSerLysAsnHisPheGlnProTyr 425
Db 1867 AAGTGGAGGCCCT-----GAAGCGCTCTCCGAGGCCATTACTCC----- 1908
Qy 426 IleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMetAlaArgCysIle 445
Db 1909 ACCAAATCCGACGCTGTGCTCTTGGGATTTCTCTGCATGAGATGTTTCAGCAGG----- 1962
Qy 446 ThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMetValProSerAspPro 465
Db 1963 -----GTCCAGGTGCCCTAC-----CCAGGCATGTCC 1989
Qy 466 SerTyrGluAspMetArgGluValValCysValLysArgLeuArg-----ProIleValSer 484
Db 1990 AACCATGAGGCTTCTGAGGTGGACCGCGGTACCGCATGCGCTGCCCTCTG----- 2043
Qy 485 AsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMetSerGluCysTrp 504
Db 2044 -----GAGTCCCGCCCGCGGTGCACAAAGTGTATGCTGATGTCATGCTG 2085
Qy 505 AlaHisAsnProAlaSerArg-----LeuThrAlaLeuArg 516
Db 2086 TGCAGGAGACCCCGAGCAGACCTGCTTCAAGGCCCTCGCG 2127
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RESULT 3

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US-11-186-283-3
; Sequence 3, Application US/11186283
; Publication No. US20050255520A1
; GENERAL INFORMATION:
; APPLICANT: Raju, Jeyaseelan
; TITLE OF INVENTION: NOVEL CARC PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MNI-068CP2
; CURRENT APPLICATION NUMBER: US/11/186, 283
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/626, 173
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: US/09/947, 199A
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/111, 938
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 09/291, 839
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/458, 457
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2505)
US-11-186-283-3
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Score:	248.00	Matches:	96
Percent Similarity:	44.32%	Conservative:	68
Best Local Similarity:	25.95%	Mismatches:	132
Query Match:	8.74%	Indels:	74
DB:	7	Gaps:	21

US-10-600-645-2 (1-532) x US-11-186-283-3 (1-2505)

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Qy 177 LysHisTyr-----CysLysSerIleSerSerArgGlyArg 188
Db 1204 AAGCATTTAAGAGACCAACAGATGAATGGCTGTGAATGAATATTTCTCAGCCTGGA--- 1260
Qy 189 TyrAsnArgAspLeuGlnAspGluAlaPheIleProValGlyGluSerLeuLysAsp 208
Db 1261 -----GGAGATGGCTCTCTATGTCTGTTCATCACCCTTTGGGGAAG 1302
Qy 209 LeuIleAspGlnSerGlnSerSerGlySer-----GlySerGlyLeuProLeu 224
Db 1303 ATTAAAGCATGACAAAGAGAGGAGGAGATATTTCTCTCTAAGAGCTGGATTGCTTCA 1362
Qy 225 LeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnValGlyLysGlyArg 244
Db 1363 CATTTCCATCTTCCAGCTCTCA---GAAATTGAGTTCCATGAGATTTATTGGCTCAGGTCT 1419
Qy 245 TyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaValLys----- 261
Db 1420 TTTGGGAAGATATATAAAGGACGATGCAGAAATAAATAGTGGCTATAAAACGTTATCGA 1479
Qy 262 -----ValPhePheThrThrGluGluAlaSerTrpPhe---ArgGluThrGluIleTyr 278
Db 1480 GCCAATACCTACTGCTCCCAAGTCAGATGGATATGTTTGGCAGAGGTGTCATT--- 1536
Qy 279 GlnThrValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGly 298
Db 1537 ----CTCTGCGAGCTCAATCATCTCCCGTAATTTCAGTTTGTGGGTCTTGTGTAATGAT 1593
Qy 299 ThrGlySerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyr 318
Db 1594 CCC-----AGCCAGTTTGGCATTTGTCACTCAATACATATCAGGGGGTCTCTGTTC 1644
```

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QY 319 AspPheLeu-----LysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyr 336
Db |||||
Db 1645 TCCTCTTCATGACGACAGAGGATCTTGATTTGCAGTCTAAATTAATTATTCAGTA 1704
QY 337 SerAlaAlaCysGlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysPro 356
Db |||||
Db 1705 GATGTGCGCAAGGACGATGAGTACCTTCACAACCTG-----ACACAG----- 1746
QY 357 AlaIleAlaHisArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCys 376
Db |||||
Db 1747 CCAATTATACATCGTGACTGGAACAGCTCACAATATTTCTCTATGAGGATGGCATGCT 1806
QY 377 CysIleAlaAspLeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIle 396
Db |||||
Db 1807 GTGGTGGCAGATTTGGGAATCA---AGATTCTACAGTCTCTGGATGAAGACAAC--- 1860
QY 397 ProLeuAsnThrArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSer 416
Db |||||
Db 1861 ---ATGACAAACAAACCTGGGAACCTCCGTTGGATGGCTCTTGAGGTGTTACGCGAGTGC 1917
QY 417 LeuSerLysAsnHisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIle 436
Db |||||
Db 1918 ACTCGGTACACC-----ATCAAGCAGATGTCTTCAGCTATGCTCTGTGT 1962
QY 437 IleTrpGluMetAlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuPro 456
Db |||||
Db 1963 CTGTGGGAAATT-----CTCACTGGC-----GAAATTCCA 1992
QY 457 TyrTyrAsnMetValPro-----SerAspProSerTyrGluAspMetArgGlu 472
Db |||||
Db 1993 TTGCTCATCTCAAGCCAGCGGTGGCGCAGCAGCATGGCTTACCACCACATCAGACCT 2052
QY 473 ValValCysValLysArgLeuArgProIleValSer-----AsnArgTrpAsnSer 489
Db |||||
Db 2053 CCAATTGGCTATTCCATTCCCAAGCCCATATCTCTCTGATACGAGGTTGGAACGCA 2112
QY 490 -----AspGluCysLeuArgAlaValLeuLysLeuMetSerGluCysTrp 504
Db |||||
Db 2113 TGTCCTGAAGGAGACCCCAATTTCTGAAGTTGTCATGAAGTTA---GAAGAGTGTCTC 2169
QY 505 AlaHis-----AsnProAlaSer 510
Db |||||
Db 2170 TGCAACATTGAGCTGATGCTCTCTGCATCA 2199
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RESULT 4

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US-11-186-283-1
; Sequence 1, Application US/11186283
; Publication No. US20050255520A1
; GENERAL INFORMATION:
; APPLICANT: Raju, Jayaselan
; TITLE OF INVENTION: NOVEL CARP PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MNI-068CP2
; CURRENT APPLICATION NUMBER: US/11/186,283
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/626,173
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: US/09/947,199A
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/111,938
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 09/291,839
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/458,457
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3025
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
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; LOCATION: (48)..(2552)
US-11-186-283-1
Alignment Scores:
Pred. No.: 6,2e-18 Length: 3025
Score: 248.00 Matches: 96
Percent Similarity: 44.32% Conservative: 68
Best Local Similarity: 25.95% Mismatches: 132
Query Match: 8.74% Indels: 74
DB: 21
Gaps: 21
US-10-600-645-2 (1-532) x US-11-186-283-1 (1-3025)
QY 177 LysHisTyr-----CysLysSerIleSerSerArgGlyArg 188
Db |||||
Db 1251 AAGCATTTAAGACAGACCAAGATGAATGGCTCTGAATGAATATTCACGCTCGA--- 1307
QY 189 TyrAsnArgAspLeuGluGlnAspGluAlaPheIleProValGlyGluSerLeuLysAsp 208
Db |||||
Db 1308 -----GGAGATGGCTCCTATGTGTCTGTTCATCACCTTGGGGAAG 1349
QY 209 LeuIleAspGlnSerGlnSerSerGlySer-----GlySerGlyLeuProLeu 224
Db |||||
Db 1350 ATTAAAGCATGACAAAAGAGAGACGATATTCCTCTTAAGAGCTGGATTGCTTCA 1409
QY 225 LeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnValGlyLysGlyArg 244
Db |||||
Db 1410 CATTTCATCTTCAGCTCTCA---GAAATTGAGTTCCATGATTTTGGCTCAGGTCT 1466
QY 245 TyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaValLys----- 261
Db |||||
Db 1467 TTTGGGAAGTATATAAAGGACGATGCAGAAATAAATAGTGGCTATAAAGCTTATCGA 1526
QY 262 -----ValPhePheThrGluGluAlaSerTrpPhe---ArgGluThrGluIleTyr 278
Db |||||
Db 1527 GCCAATACCTACTGTCTCAAGTCAGATGTGATATGTTTTCGAGAGGTGTCCATT--- 1583
QY 279 GlnThrValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGly 298
Db |||||
Db 1584 ---CTCTCCAGCTCAATATCCCTGCGTAATTCAGTTTGTGGTGTCTTGAATGAT 1640
QY 299 ThrGlySerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyr 318
Db |||||
Db 1641 CCC-----AGCCAGTTTGCCTACTCAATACATATCAGGGGTTCTCTGTTC 1691
QY 319 AspPheLeu-----LysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyr 336
Db |||||
Db 1692 TCCTCTCTTCATGACGACAGAGGATCTTGATTTGCAGTCTAAATTAATTATTCAGTA 1751
QY 337 SerAlaAlaCysGlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysPro 356
Db |||||
Db 1752 GATGTGCGCAAGGACGATGAGTACCTTCACAACCTG-----ACACAG----- 1793
QY 357 AlaIleAlaHisArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCys 376
Db |||||
Db 1794 CCAATTATACATCGTGACTTGAACAGTCACAATATTTCTCTCTATGAGATGGGATGCT 1853
QY 377 CysIleAlaAspLeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIle 396
Db |||||
Db 1854 GTGTGGCGAGATTTGGGAATCA---AGATTCTACAGTCTCTCGATGAAGACAAC--- 1907
QY 397 ProLeuAsnThrArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSer 416
Db |||||
Db 1908 ---ATGACAAACAAACCTGGGAACCTCCGTTGGATGGCTCTCTGAGGTGTTACGCGAGTGC 1964
QY 417 LeuSerLysAsnHisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIle 436
Db |||||
Db 1965 ACTCGGTACACC-----ATCAAGCAGATGTCTTCAGCTATGCTCTGTGT 2009
QY 437 IleTrpGluMetAlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuPro 456
Db |||||
Db 2010 CTGTGGGAAATT-----CTCACTGGC-----GAAATTCCA 2039
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QY 394 ValAspIleProLeuAsnThrArgValGlyThrArgArgTyrMetAlaProGluValLeu 413
DB 2506 GCAGATGATCCCATC-----CGCTGACCGCCCGAGGCCATT 2544
QY 414 AspGluSerLeuSerLysAsnHisPheGlnProTyrIleMetAla--AspIleTyrSer 432
DB 2545 TCC-----TACCGGAAGTTCACTCTGCCAGCAGCGTGTGGAGC 2583
QY 433 PheGlyLeuIleIleTyrGluMetAlaArgCysIleThrGlyGlyIleValGlu 452
DB 2584 TTTCGCAATTGTCATGTGGAGGTG-----ATGACCTATGGC----- 2619
QY 453 TyrGlnLeuProTyrTyrAsnMetValProSerAspProSerTyrGluAspMetArgGlu 472
DB 2620 ---GAGCGGCCCTACTGGAGTTG-----TCCAAACGAGGATGATGAAGCC 2664
QY 473 ValValCysValLysArgLeu--ArgProIleValSerAsnArgTyrAsnSerArgGlu 491
DB 2665 ATCAATGATGGTTCGGCTCCCGCTCCCAACACCATG-----GAC 2700
QY 492 CysLeuArgAlaValLeuLysLeuMetSerGluCysTyrPheAlaHisAsnProAlaSerArg 511
DB 2701 TGCCCTCGCCCATCTACAGCTCATGATGCAGTCTGCAGCAGGAGCGTCCCGCCGC 2760
QY 512 LeuThrAlaLeuArgIleLysLysThrLeuAlaLysMetValGluSerGlnAsp 529
DB 2761 CCCAAGTTGCTGACATCGTCAGCATCTCTGGACAAGCTCAATTCGTGCCCTGAC 2814
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RESULT 8

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US-10-990-276-2
; Sequence 2, Application US/10990276
; Publication No. US2005025549A1
; GENERAL INFORMATION:
; APPLICANT: Wesche, Holger
; APPLICANT: Li, Shyun
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
; FILE REFERENCE: 018781-003910US
; CURRENT APPLICATION NUMBER: US/10/990,276
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US/09/759,595
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 60/176,395
; PRIOR FILING DATE: 2000-01-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1383
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human IL-1 receptor-associated kinase 4 (IRAK-4)
; FEATURE:
; OTHER INFORMATION: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1383)
; OTHER INFORMATION: human IRAK-4
US-10-990-276-2
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Alignment Scores:
Pred. No.: 2,07e-16 Length: 1383
Score: 230.50 Matches: 87
Percent Similarity: 44.12% Conservative: 48
Best Local Similarity: 28.43% Mismatches: 118
Query Match: 8.12% Indels: 53
DB: 6 Gaps: 12
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US-10-600-645-2 (1-532) x US-10-990-276-2 (1-1383)

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QY 239 GlnValGlyLysGlyArgTyrGlyGluValTyrMetGlyLysTyrArgGlyGluLysVal 258
DB 571 AAAATGGGAGGAGGAGTTGGAGTTGTTATATAAAGGCTACGTAATAACACACTGTG 630
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QY 259 AlaValLys-----ValPhePheThrThrGluGluAlaSerTrpPheArg 273
DB 631 GCAGTGAAGAAGCTTTCAGCAATGGTTGACATTACTACTGAAGAAGCTGAAACAGCAGTTT 690
QY 274 GluThrGluIleTyrGlnThrValLeuMetArgHisGluAsn-----IleLeuGly 290
DB 691 GATCAAGAAATAAAGTAATGGCAAGGTGTCACATGAATACTTAGTAGAACTACTTGGT 750
QY 291 PheIleAlaAlaAspIleLysGlyThrGlySerTrpThrGlnLeuTyrLeuIleThrAsp 310
DB 751 TTC-----TCAAGTGATGGAGATGACCTCTGCTTGGATGGTACTCCACCAT 789
QY 311 TyrHisGluAsnGlySerLeuTyrAspPheLeuLysCys-----AlaThrLeu 326
DB 790 TACATGCTAATGGTTTCATTCGTACAGACAGACTCTCTGCTTGGATGGTACTCCACCAT 849
QY 327 AspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCysGlyLeuCysHisLeuHis 846
DB 850 TCTTGGCACATGAGATGCAAGATTGCTCAGGTGCAGCTAATGGCATCAATTTTCTACAT 909
QY 347 ThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHisArgAspLeuLysSerLys 366
DB 910 GAAATCATCAT-----ATTCATAGAGATATTAAAGTGCA 945
QY 367 AsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAspLeuGlyLeuAlaValLys 386
DB 946 AATATCTTACTGGATGAAGCTTTTACTGCTGCTAAAAATATCTGACTTTGGCCTTGACGGCT 1005
QY 387 PheAsnSerAspThrAsnGluValAspIleProLeuAsnThrArgValGlyThrArg 406
DB 1006 -----TCTGAGAAGTTTGGCCAGACAGCTCATGACTAGCAGAAATGTGGGAACAACAGCT 1059
QY 407 TyrMetAlaProGluValLeuAspGluSerLeuSerLysAsnHisPheGlnProTyrIle 426
DB 1060 TATATGGCACAGAAAGCTTTGCTGGAGAAATACACCCAAA-----1101
QY 427 MetAlaAspIleTyrSerPheGlyLeuIleIleTyrGluMetAlaArgCysIleThr 446
DB 1102 ---TCTGATATTTACAGCTTTGGTGTGTTTTTACTAGAAATA-----ATAACT 1146
QY 447 Gly---GlyIleValGluTyrGlnLeuProTyrTyrAsnMetValProSerAspPro 465
DB 1147 GGACTTCAGCTGTGGATGAACACCGTGAACCTCAGTTATTGCTA-----1191
QY 466 SerTyrGluAspMetArgGluValVal-----CysValLysArgLeuArgProIleVal 483
DB 1192 -----GATATTAAAGAAGAAATTCAGATGAAGAAAGACAAATTGAAGATTATATT 1242
QY 484 SerAsnArgTrpAsnSerAspGlu-----CysLeuArgAlaValLeuLysLeuMetSer 501
DB 1243 GATAAAAGATGAATGATGTCTGATTCCACTTCAGTTGAAGCTATCTACTCTGCTGCTAGT 1302
QY 502 GluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThrHis 527
DB 1303 CAATGCTGTGATGAAAGAAAAATAAGAGACCAGACATTAAAGAGGTTCAACAGCTGCTG 1362
QY 522 AlaLysMetValGluSer 527
DB 1363 CAAGAGATGACAGCTTCT 1380
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RESULT 9
US-10-990-276-4
; Sequence 4, Application US/10990276
; Publication No. US2005025549A1
; GENERAL INFORMATION:
; APPLICANT: Wesche, Holger
; APPLICANT: Li, Shyun
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
; FILE REFERENCE: 018781-003910US
; CURRENT APPLICATION NUMBER: US/10/990,276
; CURRENT FILING DATE: 2004-11-15

Qy	379	AlaAspLeuGlyLeuAlaValIysPheAsnSerAspThrAsnGluValAspIleProLeu	398
Db	1144	TCTGACTTTGGGCTTGCA-----CGGGCTTCGGCAAGGCTAGCGCAGACGGTCA	1194
Qy	399	AsnThrArg---ValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeu	417
Db	1195	ACACAGCCGAATCGTGGGCACACCGCTTACATGGCACCCGAAGCTTTTGGCGGAGAAATA	1254
Qy	418	SerLysAsnHisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIle	437
Db	1255	ACACCCAAA-----TCTGACATCTACAGCTTCGGCGTGGTCTG	1293
Qy	438	TrpGluMetAlaArgArgCysIleThrGly---GlyIleValGluGluTyrGlnLeuPro	456
Db	1294	TTGAGACTG-----ATAACGGGCTGGCGGCTGTGGATGAAACCGTGAACCT	1341
RESULT 10			
US-10-770-726-17			
; Sequence 17, Application US/10770726			
; Publication No. US20050266409A1			
; GENERAL INFORMATION:			
; APPLICANT: Wyeth			
; APPLICANT: Brown, Eugene			
; APPLICANT: Liu, Wei			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND			
; TITLE OF INVENTION: CANCERS			
; FILE REFERENCE: AM101079 (031896-010000)			
; CURRENT APPLICATION NUMBER: US/10/770,726			
; CURRENT FILING DATE: 2004-02-04			
; NUMBER OF SEQ ID NOS: 48640			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 17			
; LENGTH: 6058			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-770-726-17			
Alignment Scores:			
	Pred. No.:	7.37e-15	Length: 6058
	Score:	226.00	Matches: 99
	Percent Similarity:	40.80%	Conservative: 74
	Best Local Similarity:	23.35%	Mismatches: 137
	Query Match:	7.96%	Indels: 114
	DB:	6	Gaps: 21
US-10-600-645-2 (1-532) x US-10-770-726-17 (1-6058)			
Qy	140	ProValValIleGlyProPheAspGlySerValArgTrpLeuAlaValLeuIleSer	159
Db	1642	CCACTCATCATCGGCTTCCTCGCGCGCTGGCTGTCTTCTCATTTGCTGGTTGTGATC	1701
Qy	160	MetAlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrIysHisTyr	179
Db	1702	GCATCGTGTGT-----	1713
Qy	180	CysLysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPhe	199
Db	1714	-----AACAGAAGCGGGGTTTGAGCGTCTGACTCG---	1746
Qy	200	IleProValGlyGluSerLeuIysAspLeuIleAspGlnSerGlnSerSerGlySerGly	219
Db	1747	---GAGTACACGGACAAGCTGCAACATCTCTCTGTGTCAAATTGACGAGGTGTC	1782
Qy	220	-----SerGlyLeuProLeuLeuValGln-----	227
Db	1783	CACATGACCCAGGCATGAAGATCTACATCGATCTTTTACCTACGAGGACCCCAACGAG	1842
Qy	228	-----ArgThrIleAlaLysGlnIleGlnMet-----ValArgGlnVal---	240
Db	1843	GCAGTCGGGAGTTTGCCAAAGAAATTGACATCTCTCTGTGTCAAATTGACGAGGTGATC	1902
Qy	241	GlyLysGlyArgTyrGlyGluValTrpMetGly-----LysTrpArgGlyGluLys---	257

Db	1903	GGAGCAGGGGAGTTTGGCGAGGCTCTGCAGTGGCCCACTGAAGCTGCAGGCACAGAGAGAG	1962
Qy	258	-----ValAlaValLysValPhe-----PhetrThrGluGluAlaSerTrpPhe	272
Db	1963	ATCTTTGTGGCCCAAGACGCCTCAAGTFCGGCTACACGGGAAGCAG	2010
Qy	273	ArgGluThrGluLeuTyrGlnThrValLeuMet-----ArgHisGluAsnLeuLeu	289
Db	2011	CGCGGAGACTTCCTCGAGCGAAGCCCTCCATCATGGCCGAGTTCGACCATCCCAACGTCA	2070
Qy	290	GlyPheLeuAlaAlaAspIleLysGlyThrClySerTrpThrGlnLeuTyrLeuLeuThr	309
Db	2071	CACCTGGAGGTGTCGTACCAAGAGC-----ACACGTGTGATGATCATCACC	2118
Qy	310	AspTyrHisGluAsnGlySerLeuTyrAspPheLeuLys-----CysAlaThrLeuAsp	327
Db	2119	GAGTTCATGGAGATGGCTCCTCGGACTCCTTCCTCGGCAAAACGATGGCGAGTTCACA	2178
Qy	328	ThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCysGlyLeuCysHisLeuHisThr	347
Db	2179	GTCAATCAGCTGGTGGGCATCTCTGGGGCATCGCAGCTGCATGAAGTACCTTGGCAGAC	2238
Qy	348	GluLeuTyrGlyThrGlnGlyLysProAlaIleAlaHisArgAspLeuLysSerLysAsn	367
Db	2239	ATGAACATAT-----GTTCAACGTGACCTGGCTGCCGCCAAC	2274
Qy	368	IleLeuIleLysLysAsnGlySerCysCysIleAlaAspLeuGlyLeuAlaValLysPhe	387
Db	2275	ATCTCTGTCACACGACACCTGGTCTGCAAGGTGTCGAGCTTGGGCTCTCACGCTTCTA	2334
Qy	388	AsnSerAspThrAsnGluValAspIleProLeuAsnThrArgValGlyThrArg-----	405
Db	2335	GAGGACGATACCTCA-----GACCCCACTACACAGTCCTGGCGGAAAGATCCCC	2388
Qy	406	---ArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsnHisPheGlnPro	424
Db	2389	ATCCGCTGGACGAGCCCGGAAGCCATC-----CAGTACCCGGAAG	2427
Qy	425	TyrIleMetAla---AspIleTyrSerPheGlyLeuIleIleTrpGluMetAlaArgArg	443
Db	2428	TTCACTCGGCCAGTGAATGTGTGAGTACCGCATTTGTCATGTGGAG-----	2475
Qy	444	CysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMetValProSer	463
Db	2476	-----GTGAUTCTCTATGGGAGGCGCCCTACTGGGACATGATCCAAACCAG	2520
Qy	464	AspProSerTyrGluAspMetArgLuuValValCysValLysArgLeuArgProIleVal	483
Qy	484	SerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMetSerGluCys	503
Db	2569	-----GATGCCGAGCGCCCTGCACCAACTCATGCTGGACTGT	2607
Qy	504	TrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThrLeuAlaLys	523
Db	2608	TGGCAGAGGACCCCAACCCGCCCCAAGTTCGGCCCAANTTGTCAACACGCTAGACNAG	2667
Qy	524	MetValGluSer	527
Db	2668	ATGATCCGCAAT	2679

	Db	GGCCAGTTGCCACCAACAATCATCGCGCTAGAGGCGTCATCTCCAATAACAGCCC	570
		:::::	
511		LeuTyrLeuIleThrAspTyrHisgluaHengLySerLeuTyrAspPheLeu----	Lys 3222
305	Qy	: :: : :: : :: : :: : :: : :: : :: : :: :	
		ATGATGATCATCATTGATGCATGTGAGAATGGGCCCTGGACAAAGTCTCTCGGSGAAG	630
571	Db	CysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCySgLyLeu	342
323	Qy	:::::::::::	
		GATGGCGAGTTGAGCGTGCTGCAGCTGTTGGGCATGCTCGGGGGCATCGCACGTGGCATG	690
631	Db	CysHisLeuHisThrGluiIeTrGlyThrGlnGlyLysProAlaileAlahisArzAgsp	362
343	Qy		

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Db 691 AAGTACCTGCCCAACATGAATAT-|||
Qy 363 LeuLysSerLysAsnIleLeuLysAsnGlySerCysValleAlaAspLeuGly 382
Db 727 CTGGCTGCCCGCAACATCTCTGCAAGCACTGTGTGCAAGGTGTCTGACTTTGGC 786
Qy 383 LeuAlaValLysPheAsnSerAsp-|||
Db 787 CTGTCCCGCTGTGGAGGACGACCCCGAGGCCACCTACACCAGCTGGCGCAAGATC 846
Qy 397 ProLeuAsnThrArgValGlyThrArgArgTyMetAlaProGluValLeuAspGluSer 416
Db 847 CCCATC-|||
Qy 417 LeuSerLysAsnHisPheGlnProTyIleMetAla-AspIleTySerPheGlyLeu 435
Db 880 -TACCGAAGTTTCACTCTGCCAGCGAGCTGTGGAGCTTTGGCATT 924
Qy 436 IleIleTrpGluMetAlaArgCysIleThrGlyIleValGluGluTyGlnLeu 455
Db 925 GTCATGTGGAGGTG-ATGACCTATGGC-|||
Qy 456 ProTyTyTrpAsnMetValProSerAspProSerTyGluAspMetArgGluValValCys 475
Db 958 CCCTACTGGGAGTTG-TCCCAACACGAGGTGATGAAGCCATCAATGAT 1005
Qy 476 ValLysArgLeu-ArgProIleValSerAsnArgTrpAsnSerAspGluCysLeuArg 494
Db 1006 GGCTTCGGCTCCCCACACCATG-|||
Qy 495 AlaValLeuLysLeuMetSerGluCysTrpAlaHisAsnProAlaSerArgLeuThra 514
Db 1042 GCATCTACAGCTCATGTCAGTGTGGCAGCAGGAGCGTCCCGCGCCCAAGTTC 1101
Qy 515 LeuArgIleLysLysThrLeuAlaLysMetValGluSerGlnAsp 529
Db 1102 GGTGACATCGTCAGCATCTCTGGACAAGCTCATTCGTGCGCCCTGCAC 1146
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RESULT 12

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US-11-021-441-16
; Sequence 16, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKY, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A., Jr.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 282172003900
; CURRENT APPLICATION NUMBER: US/11/021,441
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/616,750
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/615,287
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US 60/599,377
; PRIOR FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: PCT/US2004/23881
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US 10/883,599
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/556,744
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-021-441-16
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Score: 222.00 Matches: 89
Percent Similarity: 41.53% Conservative: 63
Best Local Similarity: 24.32% Mismatches: 146
Query Match: 7.82% Indels: 68
DB: 17 Gaps: 17

US-10-600-645-2 (1-532) x US-11-021-441-16 (1-1254)

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Qy 204 GluSerLeuLysAspLeu-----IleAspGlnSerGlnSerSerGlySerGlySer 220
Db 64 GAACAACTGAAGCCCTGAAGACATACGTGGAGCCCCACACATATGAGGACCCCAACCCAG 123
Qy 221 GlyLeuProLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 124 GCTGTGTTGAAGTTCACTACCGAGATCCATCTCTGTCTACTCGGAGAAAGGTGATC 183
Qy 241 GlyLysGlyArgTyGlyGluValTrpMetGly-----LysTrpArgGlyGluLysVal 258
Db 184 CGAGCAGGAGAGTGTGGGAGGTGTACAAGGGCATCTCAAGACATCTCGGGGGAAGAAG 243
Qy 259 AlaValLysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTy 278
Db 244 GAGGTGCGGTGGCCCATCAAGACGCTGAAAGCGGTAC-----ACAGAGAAGCAG 294
Qy 279 GlnThrValLeuMetArgHisGluAsnIleLeuGlyPheIleAla-----Ala 294
Db 295 CGAGTGGAGCTTCTCGCGCGCGCCGATCATGGCCAGTTTACGCCACCAACATCATC 354
Qy 295 AspIleLysGlyThr---GlySerTrpThrGlnLeuTyLeuIleThrAspTyHisGlu 313
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Qy 314 AsnGlySerLeuTyAspPheLeu-----LysCysAlaThrLeuAspThrArgAlaLeu 331
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Qy 332 LeuLysLeuAlaTySerAlaAlaCysGlyLeuCysHisLeuHisThrGluIleTyGly 351
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Qy 352 ThrGlnGlyLysProAlaIleAlaHisArgAspLeuLysSerLysAsnIleLeuLys 371
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Qy 372 LysAsnGlySerCysCysIleAlaAspLeuGlyLeuAlaValLysPheAsnSerAsp--- 390
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Qy 391 -----ThrAsnGluValAspIleProLeuAsnThrArgValGlyThrArg 405
Db 631 GAGGCCACTACACCAGCTGGCGCAAGATCCCATC-----TACCGGAAGTTC 669
Qy 406 ArgTyMetAlaProGluValLeuAspGluSerLeuSerLysAsnHisPheGlnProTy 425
Db 670 CGCTGGACCGCCCGGAGGCCATTTCC-----TACCGGAAGTTC 708
Qy 426 IleMetAla---AspIleTySerPheGlyLeuIleIleTrpGluMetAlaArgCys 444
Db 709 ACCTCTGCCAGCGAGCTGTGGAGCTTTGGCATTGTGATGTGGAGGTG----- 756
Qy 445 IleThrGlyGlyIleValGluGluTyGlnLeuProTyTyTrpAsnMetValProSerAsp 464
Db 757 ATGACCTATGGC-----GAGCGGCCCTACTGGGAGTTG----- 789
Qy 465 ProSerTyGluAspMetArgGluValValCysValLysArgLeu---ArgProIleVal 483
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 9, 2005, 19:17:20 ; Search time 4008 Seconds

(without alignments)

6210.261 Million cell updates/sec

Title: US-10-600-645-2

Perfect score: 2838

Sequence: 1 MTQLTYIRLLGACLFISH.....TALRIKKTAKWVESQDKVI 532

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-Q=/cgn2/USPTO.spool/US1060645/runat_02122005_103605_23292/app_query.fasta_1.711

-DB=EST -QFMT=fastap -SUFFIX=rest -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0

-UNITG=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45

-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL

-OUTFMT=pco -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000

-USER=US1060645_@CGN_1_1_4015@runat_02122005_103605_23292 -NCPU=6 -ICPU=3

-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG

-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*

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2: gb_est2:*

3: gb_est3:*

4: gb_hic:*

5: gb_est4:*

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7: gb_est6:*

8: gb_est7:*

9: gb_gss1:*

10: gb_gss2:*

11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2640	93.0	1532	10	AY411156 Homo sapi
3	1992	70.2	1532	10	AY411157 Pan trogl
4	1942	68.4	1511	4	AK086130 Mus muscu
5	1941	68.4	1509	10	AY418113 Homo sapi
6	1933.5	68.1	1509	10	AY418115 Mus muscu
7	1795	63.2	1509	10	AY418114 Pan trogl

8	1626.5	57.3	1121	3	BM473726
9	1501	52.9	874	1	AU124197
10	1432	50.5	826	1	DR156725
11	1384.5	48.8	842	8	CX204646
12	1353	47.7	779	6	CK638737
13	1342	47.3	783	6	CF744610
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15	1332	46.6	763	7	CV557698
16	1299	45.8	849	6	CD244444
17	1295	45.6	978	3	BI767168
18	1285.5	45.3	1073	7	CN643937
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22	1267	44.6	775	6	CD352514
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25	1255	44.2	773	1	AU123612
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29	1234	43.5	708	7	CN457827
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31	1224	43.1	736	6	CA749455
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35	1199	42.2	1713	4	AK015337
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37	1189	41.9	1409	11	DQ031141
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39	1185	41.8	677	7	CV558110
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41	1182	41.6	1427	10	AY417400
42	1179.5	41.6	3295	4	AK053428
43	1179	41.5	1427	10	AY417401
44	1164	41.0	817	6	CD352073
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ALIGNMENTS

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DEFINITION	Genomic survey sequence.				
ACCESSION	AY411158				
VERSION	AY411158.1	GI:39767126			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	1 (bases 1 to 1521)				
AUTHORS	Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 1521)				
AUTHORS	Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering				

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them based on alignment.
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Score:                 2648.50         Conservative: 5
Percent Similarity:    99.02%          Mismatches:  2
Best Local Similarity: 98.04%          Indels:      4
Query Match:          93.32%          Gaps:        1
DB:                   10

US-10-600-645-2 (1-532) x AY411156 (1-1521)

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QY   44  ProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLysCysTyrCys 63
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QY   64  SerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGlyHisCysPhe 83
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Db   123  TCAGACACTGCCAGATGATGCTATTATAACACATGATCAATTAAGCCATTGCGCTT 182

QY   84  AlaIleIleGluAspAspGlnGlyThrThrLeuThrSerGlyCysMetLysTyr 103
    |||
Db   183  GCCATTATAGAAGAGATGATCAGGAGAAACCAATTAACTTCTGGGTGATGAAGTAT 242

QY   104  GluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgThrIleGlu 123
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QY   124  CysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProValValIle 143
    |||
Db   303  TGTTGTCGACCAATTTGTGCAACCAAGTATTTGACGCTTACACTGCCCTCTGTTTATA 362

QY   144  GlyProPheAspGlySerValArgTrpLeuAlaValLeuIleSerMetAlaValCys 163
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QY   164  IleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCysLysSerIle 183
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QY   184  SerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIleProValGly 203
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QY   204  GluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySerGlyLeuPro 223
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QY   224  LeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnValGlyLysGly 243
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QY   264  PheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThrValLeuMet 283
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QY   364  LysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAspLeuGlyLeu 383
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QY   384  AlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThrArgValGly 403
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Db   1083  GCTGTAAATTTCAACAGTGATACAAATGAAGTTGACATACCTTGAATACACAGGTTGGC 1142

QY   404  ThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsnHisPheGln 423
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Db   1143  ACCAAGCGGTACATGGCTCCAGAAAGTGTGATGAAGCCCTGAATATAAAACCATTTCCAG 1202

QY   424  ProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTyrGluMetAlaArgArg 443
    |||
Db   1203  CCTACATCATGGCTGACATCTATAGCTTTGGTTTGATCATTTGGGAAATGGCTGCTGT 1262

QY   444  CysIleThrGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMetValProSer 463
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Db   1263  T-----GGAATCGTGGAGGAATATCAATTTACCATATTAACAATGGTGGCCAGT 1311

QY   464  AspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArgProIleVal 483
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QY   484  SerAsnArgTyrAsnSerAspGluCysLeuArgAlaValLeuLysLeuMetSerGluCys 503
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ACCESSION AY411156
VERSION   AY411156.1  GI:39767124
KEYWORDS  GSS.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
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REFERENCE 1 (bases 1 to 1532)
           Clark,A.G., Ghanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
           Todd,W.A., Tanenbaum,D.M., Clivello,D.R., Lu,F., Murphy,B.,
           Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
           Adams,M.D. and Cargill,M.
           Inferring nonneutral evolution from human-chimp-mouse orthologous
           gene trios
           Science 302 (5652), 1960-1963 (2003)
JOURNAL

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14671302
PUBMED
2 (bases 1 to 1532)
REFERENCE
AUTHORS
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sminsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE
JOURNAL
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Best Local Similarity: 96.66% Mismatches: 10
Query Match: 93.02% Indels: 0
DB: 10 Gaps: 0
US-10-600-645-2 (1-532) x AY411156 (1-1532)
QY 24 GlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAspGlnLysLys 43
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RESULT 3
AY411157
LOCUS
DEFINITION
Pan troglodytes BMPRIA gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY411157
VERSION
AY411157.1
KEYWORDS
GSS.
SOURCE
Pan troglodytes
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pan.
1 (bases 1 to 1532)
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 1532)
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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Percent Similarity: 77.41% Conservative: 8
Best Local Similarity: 75.83% Mismatches: 115
Query Match: 70.19% Indels: 0
DB: 10 Gaps: 0
US-10-600-645-2 (1-532) x AY411157 (1-1532)
QY 24 GlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValaAspGlnLysLys 43
Db 3 CAGATCTGGATAGTATGTTTCATGGCACTGGATGAAATCAGATCTCCACCGAAGAAAG 62
QY 44 ProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLysCysTyrCys 63
Db 63 TCAGAAATGGAGTAACCTTAGCACAGAGGATACCTTGGCTTTTAAAGTGCTATTGC 122
QY 64 SerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGlyHisCysPhe 83
Db 123 TCAGGNGACTGCCNNNGATGCTATTATAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 182
QY 84 AlaIleLeuGluAspAspGlnGlyGluThrThrLeuThrSerGlyCysMetLysTyr 103
Db 181 NNN 242
QY 104 GluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgThrIleGlu 123
Db 243 NNN 302
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Db 363 GGTCCGTTTTTGTGGCAGCAATTCATGGCTGGTGGTTCATTTCTATGGCTGCTGTC 422
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RESULT 4

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LOCUS       1911 bp      mRNA      linear      HTC 03-APR-2004
DEFINITION Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched
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            receptor, type 1B, full insert sequence.
ACCESSION   AK086130
VERSION     AK086130.1 GI:26351960
KEYWORDS    Mus musculus (house mouse)
SOURCE      Mus musculus
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS     Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE       High-efficiency full-length cDNA cloning
JOURNAL     Mech. Enzymol. 303, 19-44 (1999)
PUBLISHED  10349636
REFERENCE   2
AUTHORS     Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE       Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL     Genome Res. 10 (10), 1617-1630 (2000)
PUBLISHED  11042159
REFERENCE   3
AUTHORS     Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,
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            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Hashiwa,K.,
            Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsumura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE       RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
JOURNAL     Genome Res. 10 (11), 1757-1771 (2000)
PUBLISHED  11076861
REFERENCE   4
AUTHORS     The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
TITLE       Functional annotation of a full-length mouse cDNA collection
JOURNAL     Nature 409, 685-690 (2001)
PUBLISHED  11076861
REFERENCE   5
AUTHORS     The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
TITLE       Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
JOURNAL     Nature 420, 563-573 (2002)
PUBLISHED  11076861
REFERENCE   6
AUTHORS     Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,M.,
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            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
TITLE       Direct Submission
JOURNAL     Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
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prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
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QY 348 GluIleTyrGlyThrGlnGlyLysProAlaIleAlaHisArgAspLeuLysSerLysAsn 367
|||
|||
|||
952 GAAATCTTTAGTACTCAAGGCAAAACAGCAATTTGCCATCGAGATCTGAAAGTAAAC 1011
|||
|||
|||
QY 368 IleLeuLysLysAsnGlySerCysCysIleAlaAspLeuGlyLeuAlaValLysPhe 387
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|||
|||
1012 ATTTCTGGTGAAGAAAAATGGAACCTTGTCTGTTGCTGACCTGGCGCTGTTAAATTT 1071
|||
|||
|||
```

```
QY 388 AsnSerAspThrAsnGluValAspIleProLeuAsnThrArgValGlyThrArgArgTyr 407
|||
|||
|||
1072 ATTAGTGATACAAATGAAGTTGCATACACCACTAACACTCGAGTTGGCACCACCGCTAT 1131
|||
|||
|||
QY 408 MetAlaProGluValLeuAspGluSerLeuSerLysAsnHisPheGlnProTyrIleMet 427
|||
|||
|||
1132 ATGCTCTCCAGAAAGTGTGGCAGAGACTTGAACAGAAATCACTTCCAGCTTACATCATG 1191
|||
|||
|||
QY 428 AlaAspIleTyrSerPheGlyLeuIleIleTyrGluMetAlaArgCysIleThrGly 447
|||
|||
|||
1192 GCTGACATGATATAGTTTGGCCCTCATCCTTGGAGGTTGCTAGGAGATGTATCAGGA 1251
|||
|||
|||
QY 448 GlyIleValGluGluTyrGlnLeuProTyrTyrAsnMetValProSerAspProSerTyr 467
|||
|||
|||
1252 GGTATAGTGAAGATACACAGCTTCTTATCATGACCTAGTGCACAGTACCCTCTTAT 1311
|||
|||
|||
QY 468 GluAspMetArgGluValValCysValLysArgLeuArgProIleValSerAsnArgTyr 487
|||
|||
|||
1312 GAGGACATCAGGAGATTTGTGCATCAAGAAAGTTACGCCCTCATTTCCCAAAACCGGTGG 1371
|||
|||
|||
QY 488 AsnSerAspGluCysLeuArgAlaValLeuLysLeuMetSerGluCysTyrAlaHisAsn 507
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1372 AGCAGTGTAGTGTCTTAAGGCANNTGGGAAACTCATGACANATGCTGGGCTCACAAT 1431
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|||
|||
QY 508 ProAlaSerArgLeuThrAlaLeuArgIleLysLysThrLeuAlaLysMetValGluSer 527
|||
|||
|||
1432 CTGTGATCAAGCTGACAGCCCTCGCGGTTAAGAAACACTTGCCTGAGAGTCC 1491
|||
|||
|||
QY 528 GlnAspValLysIle 532
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|||
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1492 CAGGACATTAACATC 1506
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|||
|||
RESULT 8
BM473726
LOCUS
DEFINITION
5', mRNA
1121 bp mRNA linear EST 05-FEB-2002
AGENCOURT_6466656 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5562094
Sequence.
BM473726
BM473726.1 GI:18522768
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 (bases 1 to 1121)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM12290 row: 0 column: 23
High quality sequence stop: 679.
Location/Qualifiers
1. .1121
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5562094"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 88"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site 1: Not1; Site 2: Sal1; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
```

Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 3,976-173 Length: 1121
Score: 1626.50 Matches: 316
Percent Similarity: 92.02% Conservative: 7
Best Local Similarity: 90.03% Mismatches: 23
Query Match: 57.31% Indels: 5
DB: 3 Gaps: 1

US-10-600-645-2 (1-532) x BM473726 (1-1121)

```
QY 37 SerAspValAspGlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeu 56
DB 2 TCAGACTCCGACGACAGAAAAGTCAGAAAATGGAGTAACCTTAGCACCAGAGGATACCTTG 61

QY 57 ProPheLeuLysCysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCys 76
DB 62 CTTTTTNAAGTGCTATTGCTCAGGCACTGTCAGATGATGCTATTATTAACACATGC 121

QY 77 IleThrAsnGlyHisCysPheAlaIleIleGluGluAspAspGlnGlyGluThrThrLeu 96
DB 122 ATAACCTAATGGACATTTGCTTCCATCATAGAAGAAGATGACGAGGAGAAACACATTA 181

QY 97 ThrSerGlyCysMetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAla 116
DB 182 GCTTCAGGGTGATGAATATATGAAGATCTGATTTTCAGTGGAAAGATTTCTCAAAAGCC 241

QY 117 GlnLeuArgThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnPro 136
DB 242 CAGCTACGGCGGACATAGAAATGTTGTCGACCAATTTATGTAAACAGTATTGGCAACC 301

QY 137 ThrLeuProProValIleGlyProPheAspGlySerValArgTrpLeuAlaVal 156
DB 302 ACACATGCCCCCTGTTGTCATAGTCCGTTTTTTGATGGCAGCATTCGATGGCTGTTTG 361

QY 157 LeuIleSerMetAlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyr 176
DB 362 CTCATTCTCAGGCTGTCGCAATATGCTATGATCATCTCTCCAGCTGCTTTGTTTAC 421

QY 177 LysHisTyrCysLysSerIleSerArgGlyArgTyrAsnArgAspLeuGlnAsp 196
DB 422 AAACATATTGCAAGAGCATCTCAGCAGACGCTGTTCAATCGTATTTGGAACAGAT 481

QY 197 GluAlaPheIleProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSer 216
DB 482 GAAGCATTTATCCAGTTGGAGAATCACTAAAAGACCTTTATTGACCAGTCACAAAGTTCT 541

QY 217 GlySerGlySerGlyLeuProLeuValGlnArgThrIleAlaLysGlnIleGlnMet 236
DB 542 CGTAGTGGGTCCTGGACTACTCTTTATTGGTTTCAGCGAACTATTGCCAAAACAGATTCAGATG 601

QY 237 ValArgGlnValGlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGlu 256
DB 602 GTCCGCAAGTTGGTAAAGCCGATATGGAGAAGTATGGATGGCAAAATGGCGTGGCGAA 661

QY 257 LysValAlaValLysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGlu 276
DB 662 AAAGTGGCGGTGAAAGTATCTTTACCACCTGAAGAAGCCAGCTGTTTCGAGAAAACAGAA 721

QY 277 IleTyrGlnThrValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIle 296
DB 722 ATCTACCAAACTGTGCTAATGCGCCATGAAAACATACCTGTTTTCATAGCGGCAGACAT 781

QY 297 LysGlyThrGlySerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySer 316
DB 782 AAAGTACAGGTTCTCTGGACTCACTCTATTGTTGATTGATTACATTCATGAAAATGGATCT 841

QY 317 LeuTyrAsp-PheLeuLysCysAlaThrIleuAspThrArgAlaLeuLeuLysLeuAla 336
DB 842 CTCATGAACCTTCCTGAAATGTGTACACTGGACACACAGAGCCCTGCTTAAATGGCTTA 901
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QY 336 rSerAla-AlaCysGlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLys- 355
DB 902 TCAGCTGGCTGGGNGCTGGCCACCTGCCCCCAAGAAATTTATGGGCCCCCAAGAAAAG 961

QY 356 --ProAlaIleAlaHisArgAspLeuLysSerLysAsnIleLeuIle-LysLysAsn-GI 374
DB 962 CCCCAGCATGGCTCTCCGAAACCTTAAGGAGCAAAACATCTCTTCCAAAAAATGGG 1021

QY 374 ySerCysCysIleAlaAspLeuGly 382
DB 1022 AGATTGCTGCATTGCTGAACCGG 1046

RESULT 9
AUI24197
LOCUS AUI24197 NT2RM2 Homo sapiens cDNA clone NT2RM2001814 5', mRNA
DEFINITION sequence.
ACCESSION AUI24197
VERSION AUI24197.1 GI:10948913
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
MAMMALIA: Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo
REFERENCE 1 (bases 1 to 874)
AUTHORS Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J.,
Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
Isogai,T.
TITLE HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S.,
Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T.,
Suzuki,Y., Sugano,S., Isogai,T.)
JOURNAL Unpublished (2000)
COMMENT Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
Location/Qualifiers
source
1..874
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RM2001814"
/cell_type="teratocarcinoma"
/cell_lines="NT2"
/clone_lib="NT2RM2"
/notes="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal
precursor cells"

ORIGIN
Alignment Scores:
Pred. No.: 4,756-159 Length: 874
Score: 1501.00 Matches: 279
Percent Similarity: 98.62% Conservative: 6
Best Local Similarity: 96.54% Mismatches: 4
Query Match: 52.89% Indels: 0
DB: 1 Gaps: 0

US-10-600-645-2 (1-532) x AUI24197 (1-874)

QY 98 SerGlyCysMetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGln 117
DB 3 TCAGGGTGATGAAATATGAAGGATCTGATTTTCAGTCAAAAGATTTCTCCAAAGCCAG 62

QY 118 LeuArgArgThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThr 137
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Db 63 CTACGCCGACAAATAGAAATGTTGCGACCAATTTATGTAACCAAGTATTGCAACCCACA 122
Qy 138 LeuProValValIleGlyProPheAspGlySerValArgTrpLeuAlaValLeu 157
Db 123 CTGCCCCCTGTTGTCATAGTCCGTTTTTGTATGGCAGCATTCATGGCTGGTTTGCTC 182
Qy 158 IleSerMetAlaValCysIleValAlaMetIleValPheSerCysPheCysTyrLys 177
Db 183 ATTTCTATGGCTGTCTGCATAAATGCTATGATCATCTCTCCAGCTGCTTTGTTACAAA 242
Qy 178 HisTyrCysLysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGlu 197
Db 243 CATTTATGCAAGAGCATCTCAAGCAGACGTCGTTACAAATCGTATTTGGAACAGGATGAA 302
Qy 198 AlaPheIleProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGly 217
Db 303 GCATTTATTCAGTTGGAGAAATCACTAAAGACCTTATTGACCGTCCACAAAGTTCTGGT 362
Qy 218 SerGlySerGlyLeuProLeuValGlnArgThrIleAlaLysGlnIleGlnMetVal 237
Db 363 AGTGGGTCTGGACTACCTTTATTGGTTTCAGCAACTATTGCCAAACAGATTTCAGATGTC 422
Qy 238 ArgGlnValGlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLys 257
Db 423 CGCAAGTTGGTAAAGGCCGATATGGAGAAAGTATGGATGGGCAATGGCGTGGCAAAA 482
Qy 258 ValAlaValLysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIle 277
Db 483 GTGGCGGTGAAGTATTTCTTACCTGAAGATGCCAGCTGGTTTCGAGAAACAGAAATC 542
Qy 278 TyrGlnThrValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLys 297
Db 543 TACCAAACTGTGCTAATGCCCAATGAAACATACCTTGGTTTCATCGCGCAGACATTAA 602
Qy 298 GlyThrGlySerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeu 317
Db 603 GGTACAGGTTCCTGGACTCAGCTATTTGATTACTGATTTACCATGAAATGGATGCTCTC 662
Qy 318 TyrAspPheLeuLysCysAlaThrLeuAspThrArgAlaLeuLysLeuAlaTyrSer 337
Db 663 TATGACTTCTGAAATGTGCTACACTGGACACAGAGCCCTGCTTAAATTTGGCTTATCA 722
Qy 338 AlaAlaCysGlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAla 357
Db 723 GCTGCTGTGTCTGTGCTGCTGCACAGAAATTTATGCCACCCAGAGAAAGCCGCA 782
Qy 358 IleAlaHisArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCys 377
Db 783 ATTTGCTCATCGAGACCTTAAGAGCAAAACATNCTCATCAAGAAAAATGGGAATGCTGC 842
Qy 378 IleAlaAspLeuGlyLeuAlaValLys 386
Db 843 ATTTGCTGACCTGGGCTTGTGTTAA 869

RESULT 10
DR156725
LOCUS
DEFINITION
HESC2_69_D09.g1_A035_NIH_MGC_258 Homo sapiens cDNA clone
IMAGE:7965451.5", mRNA sequence.
DR156725
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 826)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
```

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FEATURES
source
1..826
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7965451"
/sex="male"
/tissue_type="human embryonic stem cells differentiated to
an early endodermal cell type"
/cell_type="human embryonic stem cells"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="NIH MGC_258"
/notes="Vector: pExpress-1; Site 1: NotI; Site 2: EcoRV;
RNA obtained from human embryonic stem cells isolated from
the inner cell mass of blastocyst stage embryos and
differentiated to an early endodermal cell type. Cell line
id and NIH Registry designation is BG01. Positive for
GATA4, MIXL1, Mex1, HNF4alpha expression; negative for AFP
expression. Passage number 40. cDNA primed using oligo-dT
primer: 5'-pGACTAGTCTAGATCGGCGGCCCT(T)25-3' and
cloned into the EcoRV/NotI sites of pExpress-1. This
primary library is non-normalized (normalized primary
library is NIH MGC 259). It was constructed by Express
Genomics (Frederick, MD). Sequence ends have been trimmed
to exclude vector and regions below Phred quality 16.
Three-prime sequences are presented as their reverse
complement and have been trimmed to exclude polyA. Note:
this is a Mammalian Gene Collection library."
ORIGIN
Alignment Scores:
Pred. No.: 2,97e-151 Length: 826
Score: 1432.00 Matches: 268
Percent Similarity: 98.91% Conservative: 4
Best Local Similarity: 97.45% Mismatches: 3
Query Match: 50.46% Indels: 0
DB: Gaps: 0
US-10-600-645-2 (1-532) x DR156725 (1-826)
Qy 118 LeuArgArgThrIleGluCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThr 137
Db 1 CTACGCCGACAAATAGAAATGTTGCGACCAATTTATGTAACCAAGTATTGCAACCCACA 60
Qy 138 LeuProValValIleGlyProPheAspGlySerValArgTrpLeuAlaValLeu 157
Db 61 CTGCCCCCTGTTGTCATAGTCCGTTTTTGTATGGCAGCATTCATGGCTGGTTTGCTC 120
Qy 158 IleSerMetAlaValCysIleValAlaMetIleValPheSerCysPheCysTyrLys 177
Db 121 ATTTCTATGGCTGTCTGCATAAATGCTATGATCATCTCTCCAGCTGCTTTGTTACAAA 180
Qy 178 HisTyrCysLysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGlu 197
Db 181 CATTTATGCAAGAGCATCTCAAGCAGACGTCGTTACAAATCGTATTTGGAACAGGATGAA 240
Qy 198 AlaPheIleProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGly 217
```

National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Brasagen, Inc.
cDNA Library Preparation: Express Genomics, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Laboratory for Genomics and Bioinformatics,
University of Georgia
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM 17072 row: g column: 17
Seq primer: JENREV (CAGGAACAGCTATGACC)
High quality sequence stop: 826.

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Db 241 GCATTATTCCAGTTGGAGAACTCACTAAAGACCTTATTGACCAGTCACAAAGTTCTGGT 300
Qy 218 SerGlySerGlyLeuProLeuValGlnArgThrIleAlaIysGlnIleGlnMetVal 237
Db 301 AGTGGGCTCTGGACTACCTTATTGGTTCAGCGAACTATTGCCAAACAGATTCCAGATGGTCTC 360
Qy 238 ArgGlnValGlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLys 257
Db 361 CGCGAAGTTGGTAAAGCCGATATGGAAGATGATGATGGGCAATGGCGTGGCGAAAAA 420
Qy 258 ValAlaValLysValPheThrThrGluGluAlaSerTrpPheArgGluThrGluIle 277
Db 421 GTGGCGGTGAAGATCTCTTACCAGTGAAGAGCCAGCTGGTTCGAGAAACAGAAATC 480
Qy 278 TyrGlnThrValLeuMetArgHisGluAenIleLeuGlyPheIleAlaAlaAspIleLys 297
Db 481 TACCAAACTGTGTAATGCCCATGAAACATACACTTGGTTTCATAGCGGCAGACATTAAA 540
Qy 298 GlyThrGlySerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAenGlySerLeu 317
Db 541 GGTACAGGTTCTCGAGCTCAGCTCTATTATTTGATTACTGATTACCATGAAATGGATCTCTC 600
Qy 318 TyrAspPheLeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSer 337
Db 601 TATGACTTCTGAAATGTCTACACTGGACACCCAGAGCCCTGCTTAAATTGCTTATTCA 660
Qy 338 AlaAlaCysGlyLeuCysHisIleuHisThrGluIleTyrGlyThrGlnGlyLysProAla 357
Db 661 GCTGCCTGTGGTCTGTGCCACCTGCACACAGAAATTTATGGCACCCAGGAAAGCCGCA 720
Qy 358 IleAlaHisArgAspLeuLysSerLysAenIleLeuIleLysLysAenGlySerCysCys 377
Db 721 ATTGCTCATCGAGACTTAAGAGCAAAACATCCTCATCAAGAAATGGAGTTGCTGC 780
Qy 378 IleAlaAspLeuGlyLeuAlaValLysPheAenSerAspThrAsn 392
Db 781 ATTGCTGACCTGNGCCTTCTGTTAAATTTCAACAGTCGACACAAAT 825

RESULT 11
CX204646 842 bp mRNA linear EST 29-DEC-2004
LOCUS MNS07540 Mouse Neurosphere Normalized cDNA library Mus musculus
DEFINITION cDNA 5', mRNA sequence.
ACCESSION CX204646
VERSION CX204646.1 GI:56859818
SOURCE EST.
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 842)
AUTHORS Williams,C., Wirta,V., Lundberg,J. and Friese,J.
TITLE Expressed sequence tags of cDNA clones from murine neurospheres
JOURNAL Unpublished (2005)
COMMENT Contact: Williams, C.
Molecular Biotechnology
Institution of Biotechnology
Albion University Center, KTH-Royal Institute of Technology, 106
91 Stockholm, Sweden
Tel: +46855378332.
Fax: +46855378481.
Email: cecilia.williams@biotech.kth.se
Seq primer: M3REW.
FEATURES
Location/Qualifiers
1..842
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/sex="MALE"
/tissue_type="Lateral wall of lateral ventricle"
/cell_type="Early passage neurosphere"
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/dev_stage="Adult"
/clone_lib="Mouse Neurosphere Normalized cDNA library"
/note="Organ: Adult brain; Vector: pCMVSPORT6.0; A cDNA
library was constructed in pCMVSPORT6.0 from RNA isolated
from neurospheres of adult male and female mice. Custom
normalized cDNA library by Invitrogen/ResGen"

ORIGIN
Alignment Scores: 7.59e-146 Length: 842
Pred. No.: 1384.50 Matches: 268
Score: 1384.50 Conserv: 4
Percent Similarity: 98.19% Mismatches: 5
Best Local Similarity: 96.75% Indels: 3
Query Match: 48.78% Gaps: 0
DB: 8
US-10-600-645-2 (1-532) x CX204646 (1-842)

Qy 91 GlnGlyGluThrThrLeuThrSerGlyCysMetLysTyrGluGlySerAspPheGlnCys 110
Db 3 CAGGAGAAACCCACATTAACTTCTGGGTGTATGAAGTATGAAGGCTCTGATTTTCAATGC 62
Qy 111 LysAspSerProLysAlaGlnLeuArgArgThrIleGluCysCysArgThrAsnLeuCys 130
Db 63 AAGGATTCCACGAAAGCCAGCTACGCAGGACAATAGAAATGTTGTCGAGCCAATTTGTGC 122
Qy 131 AenGlnTyrLeuGlnProThrLeuProProValValIleGlyProPhePheAspGlySer 150
Db 123 AACCAAGTATTTCAGCCTACACTGCCCTCTGTTATAGGTCCCTTCTTGTATGGCAGC 182
Qy 151 ValArgTrpLeuAlaValLeuIleSerMetAlaValCysIleValAlaMetIleValPhe 170
Db 183 ATCCGATGGCTGGTGTGCTCATTTCCATGGCTGCTGTATAGTTGCTATGATCATCTTC 242
Qy 171 SerSerCysPheCysTyrLysHisTyrCysLysSerIleSerSerArgGlyArgTyrAsn 190
Db 243 TCCAGCTGCTTTTGCATATAAGCAATTATTGTAAGAGTATCTCAAGCAGGGTCTGTACAC 302
Qy 191 ArgAspLeuGluGlnAspGluAlaPheIleProValGlyGluSerLeuLysAspLeuIle 210
Db 303 CGTGATTGGAAACAGCATGAAGCAATTTATTCAGTAGGAGAATCATGAAAGACCTGATT 362
Qy 211 AspGlnSerGlnSerSerGlySerGlySerGlyLeuProLeuValGlnArgThrIle 230
Db 363 GACCAGTCCCAAAGCTCTGGAGTGGATCTGATTTGCCCTTTTATTGTTTACGCGAACTATT 422
Qy 231 AlalysGlnIleGlnMetValArgGlnValGlyLysGlyArgTyrGlyValTrpMet 250
Db 423 GCCAAACAGATTCCAGATGTTTCGGCAGCTTGGTAAAGCCCGCTATGGAGAGTATGGATG 482
Qy 251 GlyLysTrpArgGlyGluLysValAlaValLysValPhePheThrThrGluGluAlaSer 270
Db 483 GGTAAATGGCGTGGTGAATAAGAGTGGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 542
Qy 271 TrpPheArgGluThrGluIleTyrGlnThrValLeuMetArgHisGluAenIleLeuGly 290
Db 543 TGGTTTAGAGAAACAGAAATCTTACAGACGGGTGTTAATGCGTCATGAAATATATCTTGT 602
Qy 291 PheIleAlaAlaAspIleLysGlyThrGlySerTrpThrGlnLeuTyrLeuIleThrAsp 310
Db 603 TTTATAGCTGCAGACATTAAAGGCACTGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 662
Qy 311 TyrHisGluAenGlySerLeuTyrAspPheLeuLysCysAlaThrLeuAspThrArgAla 330
Db 663 TACCATGAAATGGATCTCTCTATGACTTCTGAAATGTCGACACTAGACACAGAGCC 722
Qy 331 LeuLeuLysLeuAlaTyrSerAlaAlaCysGlyLeuCysHisLeuHisThrGluIleTyr 350
Db 723 CTACTCAAGTTAGCTTATTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 781
Qy 351 GlyThrGlnGlyLysProAlaIleAlaHisArgAspLeuLysSerLysAsn 367
Db 782 GGTACCCA-GGGAAGCCTGC-ATTGCTCATCGAGACCTGAAAGCAACAT 830
```

```

RESULT 12
CK638737
LOCUS
DEFINITION
  CK638737 779 bp mRNA linear EST 28-JAN-2004
  IMAGE:30644216 5', mRNA sequence.
ACCESSION
CK638737
VERSION
CK638737.1 GI:41364603
KEYWORDS
  EST.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
  1 (bases 1 to 779)
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-remail.nih.gov
  Tissue Procurement: Dr. James Lin University of Iowa
  cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Distribution information can be found at
  http://genome.uiowa.edu/distribution/mousefl.html
  This clone was contributed by the Brain Molecular Anatomy Project
  (BMAP)
  Seq primer: pyX-5.
  Location/Qualifiers
  1. 779
    /organism="Mus musculus"
    /mol_type="mRNA"
    /strain="C57BL/6"
    /db_xref="taxon:10090"
    /clone="IMAGE:30644216"
    /tissue_type="Upper Head"
    /dev_stage="9.5-10.5 dpc"
    /lab_hosts="DH10B (TI phage resistant)"
    /clone_lib="NIH_BMAP_HO0"
    /notes="Organ: Head; Vector: pyX-Asc; Site 1: EcoR I;
    Site 2: Not I; The library was constructed according
    Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
    1996. Denatured RNA was size fractionated on a 1% agarose
    gel. First strand cDNA synthesis was primed with oligo-dT
    primer containing a Not I site. Double strand cDNA was
    size selected according to mRNA size fraction, ligated
    with EcoR I adaptor, digested with NotI and then cloned
    directionally into pyX-Asc vector. The library tag
    is CGAAGTGAAT. This library was created for the University
    Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
    Developing Mouse Nervous System', supported by National
    Institute of Mental Health (NIMH)."
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ORIGIN

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Alignment Scores:
Pred. No.: 2,53e-142 Length: 779
Score: 1353.00 Matches: 253
Percent Similarity: 99.22% Conservative: 2
Best Local Similarity: 98.44% Mismatches: 2
Query Match: 47.67% Indels: 0
DB: 7 Gaps: 0

US-10-600-645-2 (1-532) x CK638737 (1-779)

QY 88 GluAspAspGlnGlyThrThrLeuThrSerGlyCysMetLysThrGluGlySerAsp 107
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Db 1 GAAGATGATCAGGAGAAACCAATTACTTCGGGTGATGAAGTATGAAGCTCTGAT 60
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QY 108 PheGlnCysLysAspSerProLysAlaGlnLeuArgThrIleGluCysCysArgThr 127
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Db 61 TTTCAATGCAAGGATTCCAGGAAGCCAGCTACGAGGACCAATAGAAATGTTGCGACC 120
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QY 128 AsnLeuCysAsnGlnTyrLeuGlnProThrLeuProProValValIleGlyProPhePhe 147
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Db 121 AATTTGTGCAACAGATATTGAGCCCTACACTGCCCTCTGTTTATAGTTCGTTCTTT 180
  |||||

QY 148 AspGlySerValArgTrpLeuAlaValLeuLysSerMetAlaValCysIleValAlaMet 167
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Db 181 GATGGCAGCATCGATGGCTGGTGTGCTCATTTTCCATGGCTGCTCTGTATAGTTGCTATG 240
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QY 168 IleValPheSerSerCysPheCysTyrLysHisTyrCysLysSerLysSerSerArgGly 187
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Db 241 ATCATCTTCTCCAGCTGCTTTTCTGCTATAAGCATTTATTGTAAGAGTATCTCAAGCAGGGT 300
  |||||

QY 188 ArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIleProValGluSerLeuLys 207
  |||||
Db 301 CGTTACACCGTGATTTGGACAGGATGAAGCAATTTATCCAGTAGAGAGTATGTAAGAA 360
  |||||

QY 208 AspLeuIleAspGlnSerGlnSerSerGlySerGlySerGlyLeuProLeuLeuValGln 227
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Db 361 GACCTGATTGACCACTCCCAAGCTCTGGAGTGGATCTGGATTGCTTTATTGTTTCAG 420
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QY 228 ArgThrIleAlaLysGlnIleGlnMetValArgGlnValGlyLysGlyArgTyrGlyGlu 247
  |||||
Db 421 CGAACTATTGCCAAACAGATTCAGATGGTTCCGACAGTGGTAAAGGCCCGCTATGGAGAA 480
  |||||

QY 248 ValTrpMetGlyLysTrpArgGlyGluLysValAlaValLysValPheThrThrGlu 267
  |||||
Db 481 GTATGGATGGTAAATGGCGTGGTGAAGAGTGGCTGTCAAAGTGTTTTTCACCTGAA 540
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QY 268 GluAlaSerTrpPheArgGluThrGluIleTyrGlnThrValLeuMetArgHisGluAsn 287
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Db 541 GAAGCTAGCTGGTTTAGAGAAACAGAAATCTACCACAGGTGTTTATGGCTCATGAAT 600
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QY 288 IleLeuGlyPheIleAlaAlaAspIleLysGlyThrGlySerTrpThrGlnLeuTyrLeu 307
  |||||
Db 601 ATACTTGGTTTATAGCTGCAGACATTAAGGACACTGGTTCTCTGGACTCAGCTGTATTG 660
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QY 308 IleThrAspTyrHisGluAsnGlySerLeuTyrAspPheLeuLysCysAlaThrLeuAsp 327
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Db 661 ATTACTGATTACCATGAAGTGGATCTCTCTATGACTTCTGAAATGTGCCACTAGAC 720
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QY 328 ThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCysGlyLeuCysHis 344
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Db 721 ACCAGAGCCCTACTCAAGTTAGCTTAATCTGCTGCTGTGCTGTGCTGCTGCTGCTG 771
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CF744610 783 bp mRNA linear EST 10-OCT-2003
UI-M-GVO-clt-q-20-0-UI.r1 NIH_BMAP_GVO Mus musculus cDNA clone
IMAGE:30617467 5', mRNA sequence.
CF744610
CF744610.1 GI:37640950
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
  1 (bases 1 to 783)
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-remail.nih.gov
  Tissue Procurement: Dr. James Lin, University of Iowa
  cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Distribution information can be found at
  http://genome.uiowa.edu/distribution/mousefl.html
  This clone was contributed by the Brain Molecular Anatomy Project
  (BMAP)
  Seq primer: pyX-5.
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FEATURES

source

Location/Qualifiers

1..783
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:30617467"
 /tissue_type="whole brain"
 /dev_stage="1,5, and 15 days newborn"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH_BMAP_GVO"
 /note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I. The library was constructed according to Bonafide, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAAGTGAAT. This library was created for the University of Iowa Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:

Pred. No.: 4,53e-141 Length: 783
 Score: 1342.00 Matches: 253
 Percent Similarity: 98.46% Conservative: 2
 Best Local Similarity: 97.68% Mismatches: 3
 Query Match: 47.29% Indels: 1
 DB: 6 Gaps: 0

US-10-600-645-2 (1-532) x CF744610 (1-783)

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 QY 106 rSepPheGlnCysLeuAspSerProlyeAlaGlnLeuArgArgThrIleGluCysCysAr 126
 Db 62 TGATTTTCAATGAAGGATTCACCGAAGCCAGCTACGACGACAAATAGATGTTGTCG 121
 QY 126 gThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProValValIleGlyProPh 146
 Db 122 GACCAATTTGTGCAACAGATTTTGCAGCCTACACTGCCCTGTTGTTATAGGTCGGTT 181
 QY 146 ePheAspGlySerValArgTrpLeuAlaValIleSerMetAlaValCysIleValAl 166
 Db 182 CTTTGATGCGAGCATCCGATGGTGGTGTGCTCATTTCCATGGCTGTCTGTATAGTTGC 241
 QY 166 aMetIleValPheSerSerCysPheCysTyrLysHisTyrCysLysSerIleSerSerAr 186
 Db 242 TATGATCATCTCTCCAGCTGCTTTGCTATAGCAATTTATTGAAGATGATCTCAAGCAG 301
 QY 186 gGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIleProValGlyGlySerLe 206
 Db 302 GGGTCGTTACACCGTGATTTGGAACAGGATGAGCATTTATTCAGTAGGAGATCATTT 361
 QY 206 ulysAspLeuIleAspGlnSerGlnSerSerGlySerGlySerGlyLeuProLeuLeuVa 226
 Db 362 GAAAGACCTGATTTGACAGCTCCCAAGCTCTGGAGTGGATCTGGATTCCTTTATTTGGT 421
 QY 226 lGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnValGlyLysGlyArgTyrGl 246
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 QY 246 yGluValTrpMetGlyLysTrpArgGlyGlyLysValAlaValLysValPhePheThrPh 266
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QY 266 rGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThrValLeuMetArgHisGl 286
 Db 542 TGAAGAAGCTAGCTGGTTTAGAGAAACAGAAATCTACCAGACGGTGTAAATCGGTCATGA 601
 QY 286 uAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGlySerTrpThrGlnLeuTy 306
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 QY 306 rLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPheLeuLysCysAlaThrIle 326
 Db 662 TTTGATTAATGATTAACCATGAAATGGAATCTCTCTATGACTCTCTGATGATGTCACACT 721
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RESULT 14
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 DEFINITION AUI24052 NT2RM2 Homo sapiens cDNA clone NT2RM2001576 5', mRNA sequence.
 ACCESSION AUI24052
 VERSION AUI24052 GI:56201134
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 807)
 AUTHORS Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki, Y., Sugano, S. and Isogai, T.
 TITLE HRI human cDNA project (Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki, Y., Sugano, S., Isogai, T.)
 JOURNAL Unpublished (2000)
 COMMENT On Oct 23, 2000 this sequence version replaced gi:55779243.
 CONTACT: Takao Isogai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
 The reason of remaining 5'-end 'N': This sequence was generated from 5'-end region of cDNA insert including about 20 base of the sequence before 'N'. This cDNA was obtained from oligo-capped cDNA library by which method 5'-end of mRNA was efficiently cloned. Therefore remaining 5'-end 'N' is important for a detection of transcription start site of this mRNA.
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 Percent Similarity: 98.14% Conservative: 3


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Best Local Similarity: 97.03%
Query Match: 47.29%
DB: 1
Gaps: 0
Indels: 2
Mismatches: 4
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US-10-600-645-2 (1-532) x AU124052 (1-807)

139	Qy	PhelIleProValGlyGlySerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySer	218
4	Db	TTTTATTCCAGTTGGAGAAATCACTAAAAGACCTTTATTGACCAAGTCACAAAGTTCTCGTAGT	63
219	Qy	GlySerGlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArg	238
54	Db	GGGCTCGACTACCTTTATTGGTTACAGCAACTATTGGCCAAACAGAAATTCAGATGGTCGG	123
239	Qy	GlnValGlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysVal	258
124	Db	CAAGTTGGTAAGGCCGATATGAGAAAGTATTGATGGCAATGGCGTGGCGAAAGAGTG	183
259	Qy	AlaValLysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyr	278
184	Db	CGGGTGAAGATTCTTTTACCACTGAAGAAGCAGCTGGTTTCGAGAAACAGAAATCTAC	243
279	Qy	GlnThrValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGly	298
244	Db	CAAACTGTGCTAATGGCCCATGAATAACATACTTGGTTTCATCGCGCAGACATTAAGGT	303
299	Qy	ThrGlySerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyr	318
304	Db	ACAGGTTCTCGACTCAGCTCTATTTCGATTACTGATTACCATGAAATGGATCTCTCTAT	363
319	Qy	AspPheLeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAla	338
364	Db	GACTCTCCTGAATATGTCTACCTGGACACAGAGCCCTGCTTAAATGGCTATTTCAGCT	423
339	Qy	AlaCysGlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIle	358
424	Db	GCCTGTGCTCTGTGCCACCTGCACACAGAAATTTATGGCACCCAGAAAGCCCGCAATT	483
359	Qy	AlaHisArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysIle	378
484	Db	GCTCATCGAGACCTTAAAGAGCAAAACATCCTCATCAAGAAAAATGGGAGTTGCTGCATT	543
379	Qy	AlaAspLeuGlyLeuAlaValLysPheAsnSerAspThrAsnGlnValAspIleProLeu	398
544	Db	GCTGACCTGGGCCCTGTCTGTAAATTCACACAGTGACACAAATGAAGTTGATGGCCCTTG	603
399	Qy	AsnThrArgValGlyThrArgTyrMetAlaProGluValLeuAspGluSerLeuSer	418
604	Db	AATACCAGNTGGGCCACCAACGCTACATGGCTCCCCGAAGTGTGGACGAAAGCCTGAAC	663
419	Qy	LysAsnHisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrp	438
664	Db	AAAAACCACTTCCAGCCCTACATCATGGCTTGACATCTACAGCTTCGGCCCTAATCATTTGG	723
439	Qy	GluMetAlaArg-ArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTy	458
724	Db	GAGATGGCTCGTCGCTGTATCACANGANGATCGTGGAGAAATACCAATTGCCATN-TA	782
458	Qy	rAsnMetValProSerAspProSer	466
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RESULT 15	CV557698	763 bp	mRNA	linear	EST 22-OCT-2004
LOCUS	UI-M-H2O-ctc-n-16-0-UI.r1	NIH_BMAP_H2O	Mus musculus	cdna clone	
DEFINITION	IMAGE:30695271 5', mRNA sequence.				
ACCESSION	CV557698				
VERSION	CV557698.1	GI:54443523			
KEYWORDS	EST.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 763)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arranged by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
This clone was contributed by the Brain Molecular Anatomy Project
(RWAP)

Seq primer: pYX-5.

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/dev_stage="newborn 1,5,"	
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/clone_lib="NIH_BMAP_H20"	
/note="Organ: Eye; Vector: Site 2: Not I; The library"	
Bonaldo, Lennon and Soar	
1996. Denatured RNA was	
gel.First strand cDNA syn	
primer containing a Not I	
size selected according t	
with EcoR I adaptor, dige	
directionally into pYX-A	
sequence located between	
is AATAATTAGC. This libr	
Iowa Brain Anatomy Proje	
Developing Mouse Nervous	
Institute of Mental Heal	

ORIGIN

Alignment Scores:		
Pred. No.:	8.11e-139	Length:
Score:	1322.00	Matches:
Percent Similarity:	99.21%	Conservative:
Best Local Similarity:	98.42%	Mismatches:
Query Match:	46.58%	Indels:
DB:	7	Gaps:

US-10-600-645-2 (1-532) x CV557698 (1-763)

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294	AlaAspIleLeuGlyThrGlySerTyrThrGlnLeuTyRLeuIleThrAspTyrHisGlu	313
63	GCAGACATTAAAGGCACCTGGTCTCGGACTCAGCTGTATTGTTACTGATTACCATGAA	122
314	AsnGlySerLeuTyRAspPheLeuLeuLysCysAlaThrLeuAspThrArgAlaIleLeuLys	333
123	AATGGATCTCTCTATGACTTCCCTGAAATGTGCCACACTAGACACCAAGAGCCCTTACTCAAG	182
334	LeuAlaTyRSerAlaAlaCysGlyLeuCysHisLeuHisThrGluIleTyRLeuGln	353
183	TTAGCTTATTCTGCTGCTGTGTGTGTGCCACTCTCACACAGAAATTTATGGTACCCAA	242
354	GlyLysProAlaIleAlaHisArgAspLeuLysSerLysAsnIleLeuIleLysLysAsn	373
243	GGGAAGCTCGCAATTGCTTCATCAGACCTGAAGAGCAAAAATCATCTTATTAGAAAAAT	302

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QY 394 ValAspIleProLeuAsnThrArgValGlyThrArgATGTyrMetAlaProGluValLeu 413
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QY 414 AspGluSerLeuSerLysAsnHisPheGlnProTyrIleMetAlaAspIleTyrSerPhe 433
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QY 434 GlyLeuIleIleTrpGluMetAlaArgArgCysIleThrGlyGlyIleValGluGluTyr 453
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QY 474 ValCysValLysArgLeuArgProIleValSerAsnArgTrpAsnSerAspGluCysLeu 493
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QY 494 ArgAlaValLeuLysLeuMetSerGluCysTrpAlaHisAsnProAlaSerArgLeuThr 513
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QY 514 AlaLeuArgIleLysLysThrLeuAlaLysMetValGlu 526
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Search completed: December 9, 2005, 22:23:00
Job time : 4028 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: December 9, 2005, 21:16:39 ; Search time 805 Seconds
(without alignments)
5464.980 Million cell updates/sec

Title: US-10-600-645-2
Perfect score: 2838
Sequence: 1 MTQLTYIRLGLACLFISH.....TALRIKTKLAKMVESQDVKI 532

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
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6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2838	100.0	1813	3	US-09-874-628-1
2	2838	100.0	1813	7	US-10-600-645-1
3	2838	100.0	3003	6	US-10-463-190-121
4	2838	100.0	3003	9	US-10-868-497-90
5	2838	100.0	3167	6	US-10-463-190-119
6	2838	100.0	3167	6	US-10-463-190-120
7	2838	100.0	3167	9	US-10-868-497-88
8	2838	100.0	3167	9	US-10-868-497-89

9	2823	99.5	2070	3	US-09-903-068-13	Sequence 13, Appl
10	2823	99.5	2070	9	US-10-739-413-13	Sequence 13, Appl
11	2823	99.5	2402	3	US-09-742-153-11	Sequence 11, Appl
12	2798	98.6	2056	7	US-10-641-319-3	Sequence 3, Appl
13	2769	97.6	1599	9	US-10-745-237-307	Sequence 307, App
14	2769	97.6	2623	5	US-10-153-217-1	Sequence 1, Appl
15	2769	97.6	2932	3	US-09-903-068-5	Sequence 5, Appl
16	2769	97.6	2932	3	US-09-982-543A-5	Sequence 5, Appl
17	2769	97.6	2932	6	US-10-286-152A-37	Sequence 37, Appl
18	2769	97.6	2932	6	US-10-463-190-116	Sequence 116, App
19	2769	97.6	2932	9	US-10-739-413-5	Sequence 5, Appl
20	2769	97.6	2932	9	US-10-868-497-85	Sequence 85, Appl
21	2769	97.6	2932	9	US-10-492-380-37	Sequence 37, Appl
22	2769	97.6	2932	9	US-10-450-763-22861	Sequence 22861, A
23	2769	97.6	2932	10	US-11-098-889-5	Sequence 5, Appl
24	2635.5	92.9	1743	8	US-10-128-558-48	Sequence 48, Appl
25	2604.5	91.8	1929	8	US-10-128-558-49	Sequence 49, Appl
26	2601	91.6	2730	9	US-10-450-763-22868	Sequence 22868, A
27	2129.5	75.0	1695	9	US-10-450-763-22867	Sequence 22867, A
28	2011	70.9	1185	6	US-10-029-386-20369	Sequence 20369, A
29	1972	69.5	1612	6	US-10-169-051-1	Sequence 1, Appl
30	1968	69.3	1612	6	US-10-169-051-3	Sequence 3, Appl
31	1952	68.8	1575	6	US-10-463-190-117	Sequence 117, App
32	1952	68.8	1575	9	US-10-868-497-86	Sequence 86, Appl
33	1952	68.8	2032	5	US-10-044-716-13	GENERAL INFORMATI
34	1952	68.8	2032	6	US-10-286-152A-39	Sequence 39, Appl
35	1952	68.8	2032	6	US-10-139-814-13	Sequence 13, Appl
36	1952	68.8	2032	6	US-10-172-118-570	Sequence 570, App
37	1952	68.8	2032	6	US-10-295-027-67	Sequence 67, Appl
38	1952	68.8	2032	6	US-10-295-027-788	Sequence 788, App
39	1952	68.8	2032	6	US-10-295-027-836	Sequence 836, App
40	1952	68.8	2032	6	US-10-295-027-880	Sequence 880, App
41	1952	68.8	2032	6	US-10-173-999-63	Sequence 63, Appl
42	1952	68.8	2032	6	US-10-463-190-118	Sequence 118, App
43	1952	68.8	2032	7	US-10-058-270A-5	Sequence 5, Appl
44	1952	68.8	2032	7	US-10-342-887-570	Sequence 570, App
45	1952	68.8	2032	7	US-10-692-824-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-874-628-1
; Sequence 1, Application US/09874628
; Patent No. US20020137133A1
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, John
; CELESTE, Anthony J.
; THIES, R. Scott
; YAMAJI, No. US20020137133A1oru
; TITLE OF INVENTION: RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genetics Institute Inc.- Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/874,628
; FILING DATE: 05-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/123,934
; FILING DATE: 17-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, Steven R

```

; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 876 1170
; TELEFAX: 617 876 5951
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1813 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: CFK1-23a
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 61..1656
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-874-628-1

Alignment Scores:
Pred. No.: 0 Length: 1813
Score: 2838.00 Matches: 532
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Dbs: 3 Gaps: 0

US-10-600-645-2 (1-532) x US-09-874-628-1 (1-1813)

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QY 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
Db 121 GTTCAAGGGCAGCAATCTAGATAGTAGTCTCCATGCTACTGGTATGAAATCAGACGTGGAC 180

QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
Db 181 CAGAAAGAACCGGAAATGGAGTACGCTTAGCACCAGAGGACACCTTACCTTTCTTAAAA 240

QY 61 CysTyrCysSerGlyHisCysProaspAspAlaileAsnAsnThrCysyleThrAsnGly 80
Db 241 TGCTATTGCTCAGGACACTGCCACATGACGCTATTATAACACATGATCAATCAATGGC 300

QY 81 HisCysPheAlaileileGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 301 CATTCGTTTGCCATTATAGAAGAGATGATCAGGGAGAAACACACGTTAACTTCTGGGTGT 360

QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db 361 ATGAAGATATGAAGGCTCTGATTTTCAATGCAAGGATTCAACAAAAGCCAGCTAGCCAGG 420

QY 121 ThrileGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
Db 421 ACAATAGAAATGTGTGCGACCAATTTGCAACCAATATTTGCAACGCTTACACTGCCCCCT 480

QY 141 ValValileGlyProPhePheAspGlySerValArgTrpLeuAlaValleuileSerMet 160
Db 481 GTCGTTATAGGCCCATTTCTTGATGCGAGCGTCCGATGGCTGGCTGCTCATCTCTATG 540

QY 161 AlaValCysileValAlaMetileValPheSerSerCysPheCysTyrLysHisTyrCys 180
Db 541 GCTGTCTGTATTGTGCCATGATGCTTCTCCAGCTGCTTCTCCAGCTGCTTCTGTTACAAACATTTACTGT 600

QY 181 LysSerileSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspAlaPheile 200
Db 601 AAGATATCTCAAGCAGAGGTCGTTTACAAACCGTGACTTGGAAACAGGATGAAGCATTTATT 660

QY 201 ProValGlyGlusSerLeuLysAspLeuileAspGlnSerGlnSerSerGlySerGlySer 220
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QY 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluLysThrGlnThr 280
Db 841 AAAGTATTTTACCACCTGAAGAAGCTAGCTGGTTTACAGAAACAGAAATCTTACCAGACG 900

QY 281 ValLeuMetArgHisGluAsnileLeuGlyPheileAlaAlaAspLysGlyThrGly 300
Db 901 GTGTTAATGCGTCATGAAAAATATATCTTGGTTTTATAGCTGCAGACATTTAAAGGCCACCGT 960

QY 301 SerTrpThrGlnLeuTyrLeuileThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db 961 TCCTGGACTCAGCTGATTTGATTACTGATTTACCATGAGAAATGGGTCTCTCTATGACTTC 1020

QY 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db 1021 CTGAAATGTGCCACCTGGACACAGAGCCCTACTCAAGTTAGCTTATTTCTGCTGCCGTGT 1080

QY 341 GlyLeuCysHisLeuHisThrGluileThrGlyThrGlnGlyLysProAlaileAlaHis 360
Db 1081 GGTCTGTGCCACCTCCACACAGAAATTTATGGCAGCAAGGCAAGCCCTGCAATTCCTCAT 1140

QY 361 ArgAspLeuLysSerLysAsnileLeuileLysLysAsnGlySerCysCysileAlaAsp 380
Db 1141 CGAGACCTGAAGACGCAAAAACATCTTTATTAAGAAAAAATGGTAGTTGCTGTTACTGCTGAC 1200

QY 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspPheProLeuAsnThr 400
Db 1201 CTGGCCCTAGCTGTTAAATTCACAGTGACACAAATGAAGTTTGACATACCTTTGAACACC 1260

QY 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLysSerLysAsn 420
Db 1261 AGSGTGGGCACACAGCGGTACATGGCTCCAGAAGTGTCTGAGAGAGCTTGAGTAAAAAC 1320

QY 421 HisPheGlnProTyrileMetAlaAspTyrSerPheGlyLeuileileTrpGluMet 440
Db 1321 CATTTCCAGCCCTACATCATGCTGACATCTACAGCTTTGGTTTGATCATTTGGAGATG 1380

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Db 1381 GCCCGTCGCTGTTTACAGGAGGAATCGTGAGGAATATCAATTACCATATTTACAACATG 1440

QY 461 ValProSerAppProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db 1441 GTGCTTAGTGACCCATCTTATGAAGACATGCTGAGGTGCTGTGTGTGAAACGCTTGGCG 1500

QY 481 ProileValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
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QY 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgileLysLysThr 520
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QY 521 LeuAlaLysMetValGluSerGlnAspVallylle 532
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RESULT 2

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US-10-600-645-1
; Sequence 1, Application US/10600645
; Publication No. US20040142417A1
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, John
; CELESTE, Anthony J.
; THIES, R. Scott
;

```

YAMAJI, Noboru
TITLE OF INVENTION: RECEPTOR PROTEINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute Inc.- Legal Affairs
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/600,645
FILING DATE: 23-Jun-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/123,934A
FILING DATE: 17-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5203
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 876 1170
TELEFAX: 617 876 5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1813 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: CPK1-23a
FEATURE:
NAME/KEY: CDS
LOCATION: 61..1656
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-600-645-1

Alignment Scores:
Pred. No.: 0 Length: 1813
Score: 2838.00 Matches: 532
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-600-645-2 (1-532) x US-10-600-645-1 (1-1813)

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QY	21	ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetIysSerAspValAsp	40
DB	121	GTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGGTACTGGTATGAAATCAGACGTGGAC	180
QY	41	GlnIysLysProGluAsnGlyValThrLeuAlaProGluAspThrIleuProPheIleIys	60
DB	181	CAGAAGAACCGGAAATGGAGTGAGGTAGCACCAGAGGACACCTTACTCTTTCTTAAAA	240
QY	61	CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly	80
DB	241	TGCTATTGCTCAGGACACTGCCAGATGACGCTATTAAACACATGCTAATACTAATGSC	300
QY	81	HisCysPheAlaIleIleGluAspAspGlnGlyThrThrIleuThrSerGlyCys	100
DB	301	CATTGCTTGGCATTATAGAAGAAGATGATCAGGGAGAAACACACGTTAACTTCTGGGTGT	360

QY	101	MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuAsgAtc	120
DB	361	ATGAAGTATCAAGGCTCTGATTTTCAATCAAGAGATTACCAAAAGCCAGCTACGAGG	420
QY	121	ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro	140
DB	421	ACAATAGAATGTTGTCGGACCAATTTGTGCAACCAATATTTGCAGCTACACCTGCCCT	480
QY	141	ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet	160
DB	481	GTCGTTATAGGCCCATTTCTTTGATGGCAGCGTCCGATGGCTGGCTCATCTCTCTATG	540
QY	161	AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrIysHisTyrCys	180
DB	541	GCTGCTGTATTGTCGCCCATGATCGTCTCTCCAGCTGCTTCTGTTACAAACATTACTGT	600
QY	181	LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle	200
DB	601	AAGAGTATCTCAAGCAGAGGTCGTTACAAACCGTGACTTGGAAACAGGATGAAGCATTTAT	660
QY	201	ProValGlyGluSerLeuIysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer	220
DB	661	CCAGTAGGAGAATCACTGAAAGACCTGATTGACCAAGCTCTGGTAGTGATCT	720
QY	221	GlyLeuProLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal	240
DB	721	GGATTACCTTTATTTGGTTCAGCGAATATTGGCNAACAGATTACAGATGGTTCCGCGAGTT	780
QY	241	GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTyrTrpArgGlyGluLysValAlaVal	260
DB	781	GGTAAGGGCCGCTATGGAGAGTATGGATGGGTAAATGGCGTGGTGAAGATGGCGTGC	840
QY	261	LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr	280
DB	841	AAAGTATTTTACCACCTGAAGAGCTAGCTGGTTTAGAGAAACAGAAATCTACCCAGAGC	900
QY	281	ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly	300
DB	901	GTGTTAATGGCTCATGAAATATATCTTGGTTTTATAGCTGCAGACATTAAGGCCCGGT	960
QY	301	SerTrpThrGlnLeuTyrIleuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe	320
DB	961	TCCTGGACTCAGCTGTATTTGATTACTGATTACCATGAGATGGGTCTCTCTATGACTTC	1020
QY	321	LeuLysCysAlaThrIleuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys	340
DB	1021	CTGAAATGTGCCACCCCTGGACACCCAGAGCCCTACTCAAGTTAGCTTATTTCTGCTGCTGT	1080
QY	341	GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis	360
DB	1081	GGTCTGTGCCACCTCCACACAGAAATTTATGGCAGCAAGGCAAGCTGCAATTTGCTCAT	1140
QY	361	ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp	380
DB	1141	CGAGACCTGAACAGACAAACCATCTCTATTAAAGAAAAATGGTAGTTGCTGTATTGCTGAC	1200
QY	381	LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr	400
DB	1201	CTGGGCCCTAGCTGTTAAATTTCAACAGTGACACAAATGAAGTTGACATACCCCTTGAAACACC	1260
QY	401	ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn	420
DB	1261	AGGGTGGGCACCCAGCGGTACATGGCTCCAGAAATGCTGGACGAGGCTGTAGTAAAAAC	1320
QY	421	HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet	440
DB	1321	CATTTCCAGCCCTACATCATGCTGCATCTACAGCTTTGGTTTGTATCATCTTTGGGAGATG	1380
QY	441	AlaArgArgCysIleIleThrGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet	460
DB	1381	GCCCGTCGCTGTATTACAGGAGGAATCGTGGAGGAATATCAATTACCATATTACAACATG	1440

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QY 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysVallysArgLeuArg 480
Db 1441 GTGCCCTAGGACCCATCTTAAAGACATGCGGTGAGGTGCTGTGTGTAACCGCTTGGCG 1500
QY 481 ProfileValSerAsnArgTyrAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1501 CCAATCGTCTCTAACCGCTGGACAGTGAATGCTCTCGAGCGGTTTGAAGCTGATG 1560
QY 501 SerGluCysTyrAlaHisAsnProLaserArgLeuThrAlaLeuArgIleLysThr 520
Db 1561 TCAGATGCTGGGCCCATTAATCCAGCATCCAGACTCACAGCTTTCAGAAATCAAGAAGCG 1620
QY 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db 1621 CTCGCAAGATGGTTGAATCCAGGATGTAAGATT 1656

RESULT 3
US-10-463-190-121
; Sequence 121, Application US/10463190
; Publication No. US2004000935A1
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary E.
; APPLICANT: Galas, David J.
; APPLICANT: Kovacevich, Brian
; APPLICANT: Mulligan, John T.
; APPLICANT: Paepel, Bryan W.
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Winkler, David G.
; TITLE OF INVENTION: COMPOSITIONS AND MEHTODS FOR
; TITLE OF INVENTION: INCREASING BONE MINERALIZATION
; FILE REFERENCE: 240083.508C2
; CURRENT APPLICATION NUMBER: US/10/463,190
; CURRENT FILING DATE: 2003-06-16
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 121
; LENGTH: 3003
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-463-190-121

Alignment Scores:
Pred. No.: 0 Length: 3003
Score: 2838.00 Matches: 532
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-600-645-2 (1-532) x US-10-463-190-121 (1-3003)
QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
Db 83 ATGACTCAGCTATACATTCATCAGATTACTTGGGAGCGTGTCTGTTCATCATTTCTCAT 142
QY 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
Db 143 GTTCAAGGGCAGAATCTAGATAGTATGCTCCATGTTACTGTTATGAAATCAGACGTTGAC 202
QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
Db 203 CAGAGAAGCCGGAATAATGGAGTGGCTTAGCAGGAGGACACCTTACCTTTCTTAAAA 262
QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
Db 263 TGCTATTGCTCAGGACACTGCCAGATGACGCTATTATAACACATGATCACTAATGGC 322
QY 81 HisCysPheAlaIleGluGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 323 CATTCGTTTGCATATAGAGAAGATGATCAGGGAGAAACACCGTTTAACCTTCTGGGTGT 382
QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db 1463 GTGCTAGTACCCTCTTTATGAAGACATGCGTGGGTGCTGTGTGTGTAACCGCTTGGCG 1522
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Db 383 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCCACCAAAAGCCCGCTACGCAGG 442
QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
Db 443 ACAATAGAAATGTTGCGGACCAATTTGTGTCAACCAATATTTGCGAGCCTACACTGCCCCCT 502
QY 141 ValValIleGlyProPhePheAspGlySerValArgTyrLeuAlaValLeuIleSerMet 160
Db 503 GTCGTATTAGGCCCATTTCTTTGATGGCAGCGTCGATGGCTGGCTGTCTCATCTCTATG 562
QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
Db 563 GCTGCTGTATTGTGCCCATGATCGTCTTCCAGCTGCTTCTGTTCACAAACATTACTGT 622
QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
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QY 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
Db 683 CCAGTAGAGAAATCACTGAAAGACCTGATTGACCAAGTCCACAAAGCTCTGGTAGTGATCT 742
QY 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 743 GGATTACCTTTTATGGTTCAGCGAACTATTGCCAAACAGATTTCAGATGGTTCGGCAGGT 802
QY 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTyrPArgGlyGluLysValAlaVal 260
Db 803 GGTAAAGCCCGGTATGGAGAAAGTAGTGGTAAATGGCGTGTGTAAGAAAGTGGCTGTC 862
QY 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
Db 863 AAAGTATTTTATCCACTGAAAGAGCTAGCTGCTTTAGAGAAACAGAAATCTTACCAGACG 922
QY 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db 923 GTGTTAATGCGTCAATGAAATATATCTGTGTTTATAGCTGCAGACATTAAAGGCGCCGT 982
QY 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db 983 TCCTGGACTCAGCTGTATTTGATTACTCATGATTACCATGAGATGGGTCTCTCTATGACTTC 1042
QY 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db 1043 CTGAAATGTGCCACCCCTGGACACCAGAGCCCTACTCAAGTTAGCTTATTTCTGCTGCCGT 1102
QY 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1103 GGTCTGTGCCACCTCCACACAGAAATTTATGGCAGCAAGGCAAGCCTGCAATTTGCTCAT 1162
QY 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
Db 1163 CGAGACCTGGAAGAGCAAAACATCCTTATTAGAAAAATGGTAGTTGCTGTTATGCTGCTGAC 1222
QY 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db 1223 CTGGCCCTAGCTGTATAATTCACAGTGACACAAATGAAGTTGACATACCCCTTGAACACC 1282
QY 401 ArgValGlyThrArgTyrMetAlaProGluValLeuAspGluSerLysLysAsn 420
Db 1283 AGGTGGCACACAGCGGTATACATGGCTCCAGAGTGTCTGGACGAGAGCTGAGTAAAAAC 1342
QY 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
Db 1343 CATTTCCAGCCCTACATCATGGCTGACATCTACAGCTTTGGTTTGCATCATTTGGGAGATG 1402
QY 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db 1403 GCGCGTCGCTGTATTACAGGAGGAATCGTGAGGAATATCAATTTACCATATTTACAAACATG 1462
QY 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db 1463 GTGCTAGTACCCTCTTTATGAAGACATGCGTGGGTGCTGTGTGTGTAACCGCTTGGCG 1522
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Db 1583 TCAGATGCTGGGCCCATTAATCCAGATCCAGACTCCAGCTTTTGAGAATCAAGAAGACG 1642

Qy 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532

Db 1643 CTCGCAAGATGGTTGAATCCAGGATGTAAGATT 1678

RESULT 5

US-10-463-190-119

Sequence 119, Application US/10463190

Publication No. US20040009535A1

GENERAL INFORMATION:

APPLICANT: Brunkow, Mary E.

APPLICANT: Galas, David J.

APPLICANT: Kovacevich, Brian

APPLICANT: Mulligan, John T.

APPLICANT: Paepker, Bryan W.

APPLICANT: Van Ness, Jeffrey

APPLICANT: Winkler, David G.

TITLE OF INVENTION: COMPOSITIONS AND MEHTODS FOR

TITLE OF INVENTION: INCREASING BONE MINERALIZATION

FILE REFERENCE: 240083.508C2

CURRENT APPLICATION NUMBER: US/10/463,190

CURRENT FILING DATE: 2003-06-16

NUMBER OF SEQ ID NOS: 143

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 119

LENGTH: 3167

TYPE: DNA

ORGANISM: Rattus sp.

US-10-463-190-119

Alignment Scores:

Pred. No.: 0 Length: 3167

Score: 2838.00 Matches: 532

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-600-645-2 (1-532) x US-10-463-190-119 (1-3167)

Qy 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20

Db 226 ATGACTCAGCTATACCTTACATCATGATTACTGGAGCGCTGCTGTTTCATCATTTCTCAT 285

Qy 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40

Db 286 GTTCAAGGCGACAATCTAGATAGTATGCTCCATGGTACTGGTATCGAAATCAGACGTGGAC 345

Qy 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60

Db 346 CAGAAAGACCGGAAATGGAGTGACGTTAGCACCAGAGGACACCTTACCTTTCTTAAAA 405

Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80

Db 406 TGCTATGCTCAGGACACTGCCACATGACGCTATTATTAACACATGATCACTAATGGC 465

Qy 81 HisCysPheAlaIleIleGluAspAspGlnGlyThrThrLeuThrSerGlyCys 100

Db 466 CATTGCTTTGCCATTATAGAAGATGATCAGGAGAAACCACTTTCCTGGGTGT 525

Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120

Db 526 ATGAAGATGATGAAGGCTCTGATTTTCAATGCAAGGATTACACAAAAGCCAGCTACGCAGG 585

Qy 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140

Db 586 ACAATAGAAATGTGTGGGACCAATTTGTCAACCAATATTTTCGACGCTACACTGCCCTT 645

Qy 141 ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160

Db 646 GTCGTTATAGGCCCATCTCTTTTCATGGCAGCGTCCGATGGCTGGCTGCTCATCTCTATG 705

Qy 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180

Db 706 GCTGCTGTATGTGCGCATGATCGTCTTCCAGCTGCTTCTGTTTCAAAACATTACTGT 765

Qy 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200

Db 766 AAGAGTATCTCAAGCAGAGGTGCTTACAAACGCTGACTTGGAACAGGATGAAGCAITTTATT 825

Qy 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220

Db 826 CCAGTAGGAGAATCACTGAAAGACCTGATTGACCAGTCACAAAGCTCTGTGATGATGATCT 885

Qy 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240

Db 886 GGATTACCTTTATTGGTTTCAGCGAACTATTGCCAAACAGATTACAGATGTTTCGGCAGGTT 945

Qy 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260

Db 946 GGTAAGGCGGTATGGAGAAGTATGGATGGTAAATGGCGTGGTGAAGAAAGTGGCTGTC 1005

Qy 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280

Db 1006 AAAGTATTTTATACCACTGAAAGACCTAGCTGCTGTTTAGAGAAACAGAAATCTTACCAGCG 1065

Qy 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300

Db 1066 GTGTTAATGCGTCATGAAATATATCTTGGTTTATAGCTGCAGACATTAAGGACCCCGT 1125

Qy 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320

Db 1126 TCCTGGACTCAGCTGTTATTTGATTACTGATTACCATGAGATGGGTCTCTCTATGACTTC 1185

Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340

Db 1186 CTGAAATGTGCGACCTGGACACCAAGCCCTACTCAAGTTAGCTTATTTCTGCTGCCCTGT 1245

Qy 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360

Db 1246 GGTCTGTGCCACCTCCACACAGAAATTTATGGCAGCGAAGGCAAGCCCTGCAATTTGCTCAT 1305

Qy 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380

Db 1306 CGAGACCTGAAGACGCAAAAACATCTTATTAAGAAAAATGGTAGTTGCTGTTACTCTGAC 1365

Qy 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400

Db 1366 CTGGGCTTAGCTGTTAAATTCACAGTGACACAAATGAAGTTGACATACCTTGAACACC 1425

Qy 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420

Db 1426 AGGTTGGGCACCGCGGTACATGGCTCCAGAAAGTGTGGACGAGAGCTCAGTAAAAAC 1485

Qy 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440

Db 1486 CATTTCCAGCCCTACATCATCGCTGACATCTACAGCTTTGGTTGATCATTTGGAGATG 1545

Qy 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460

Db 1546 GCGCGTCTGCTATTACAGGAGGAATCGTGAGGAATATCAATTAACCATATTTTACAACATG 1605

Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480

Db 1606 GTGCTTAGTGACCATCTTATGAAGACATGCGTGAGGTGCTGTGTGTAAGCGCTTGGCG 1665

Qy 481 ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500

Db 1666 CCAATGCTCTTAACCGCTGGAAACAGTGATGAATGCTTCGAGCGCTTTTGAAGCTGATG 1725

Qy 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520

Db 1726 TCAGAAATGCTGGGCCCAATAATCCAGATCCAGACTCCAGCTTTTGAAGATCAAGAAGACG 1785

Qy 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532

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Db 1786 CTCGCAAGATGGTTGAATCCAGGATGTAAAGATT 1821
RESULT 6
US-10-463-190-120
; Sequence 120, Application US/10463190
; Publication No. US20040009535A1
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary E.
; APPLICANT: Galas, David J.
; APPLICANT: Kovacevich, Brian
; APPLICANT: Mulligan, John T.
; APPLICANT: Paepel, Bryan W.
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Winkler, David G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; INCREASING BONE MINERALIZATION
; FILE REFERENCE: 240083.508C2
; CURRENT APPLICATION NUMBER: US/10/463,190
; CURRENT FILING DATE: 2003-06-16
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 120
; LENGTH: 3167
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-463-190-120
Alignment Scores:
Pred. No.: 0 Length: 3167
Score: 2838.00 Matches: 532
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-600-645-2 (1-532) x US-10-463-190-120 (1-3167)
QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuGluValAlaCysLeuPheIleIleSerHis 20
Db 226 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCCCTGCTGTTTCATCATTTCTCAT 285
QY 21 ValGlnGlnAenLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
Db 286 GTTCAAGGGCAGAACTTAGATAGTATGCTCCATGGTACTGGTATGAATCAGACGGTGGAC 345
QY 41 GlnLysAspProGluAenGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
Db 346 CAGAAGAAGCCGGAAATGGAGTGACGTTAGCACACAGAGGACACCTTACCTTTCTTAAAA 405
QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAenAenThrCysIleThrAsnGly 80
Db 406 TGCATTGCTCAGACACCTGCCAGATGACGCTATTAAATACACATGCATAACTAATGGC 465
QY 81 HisCysPheAlaIleIleGluGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 466 CATTGCTTTGCCATTATAGAAGATGATCAGGAGAAACACACGTTAACTTCTGGGTGT 525
QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db 526 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCAAAAGCCAGCTACGCAGG 585
QY 121 ThrIleGluCysCysArgThrAenLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
Db 586 ACAATAGAATGTTGTGGACCAATTTGTGCAACCAATATTTGACGCTACACTGCCCTCT 645
QY 141 ValValIleGlyProPheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
Db 646 GTCGTTATAGGCCCATCTTTGATGGCAGGCTCCGATGGCTGGCTGCTCATCTCTATG 705
QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
Db 706 GCTGTCTGTATTGTCGCCCATGATCGTCTTCTCCAGCTGCTTCTGTTTACAAACATTACTGT 765
QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
Db 766 AAGAGTATCTCAAGCAGAGAGGTGCTTACACCCGTGACTTGGAAACAGGATGAAGCATTTATT 825
QY 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
Db 826 CCAGTAGGAGAAATCACTGAAAGACCTGATTGACCAAGTACAAAGCTCTGCTAGTGGATCT 885
QY 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 886 GGATTACCTTTTATTTGGTTACAGCAACTATTGCGCAACAGATTGAGTGGTTCGCGCAGGT 945
QY 241 GlyLysGlyArgTyrGlyGluValTyrMetGlyLysTyrArgGlyGluLysValAlaVal 260
Db 946 GGTAAAGGCCGTATCGAGAGATGATGGATGGGTAAATGGCTGGTGAANAAGTGGCTGTC 1005
QY 261 LysValPhePheThrThrGluGluAlaSerTyrPheArgGluThrGluIleTyrGlnThr 280
Db 1006 AAGTATTTTACCACCTGAAGAAGCTAGCTGGTTTAGAGAAAACAGAAATCTACACAGCG 1065
QY 281 ValLeuMetArgHisGluAenIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db 1066 GTGTTAATGCGTCATGAAATATATCTTGGTTTATAGCTGCAGACATTAAGAAGCACCGGT 1125
QY 301 SerTyrThrGlnLeuTyrLeuIleThrAspTyrHisGluAenGlySerLeuTyrAspPhe 320
Db 1126 TCCTGGACTCAGCTGTTTGTATTGATTACTGATTACCATGAGNATGGGTCTCTCTATGACTTC 1185
QY 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db 1186 CTGAATGTGCCACCTGGACACACAGAGCCCTACTCAAGTTAGCTTTATTCTGCTGCTGT 1245
QY 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1246 GGTCTGTGCCACCTCCACACAGAAATTTATGGCACCAAGGACGCTGCAATTTGCTCAT 1305
QY 361 ArgAspLeuLysSerLysAenIleLeuIleLysLysAenGlySerCysCysIleAlaAsp 380
Db 1306 CGAGACCTCGAGAGCNAANAACATCTCTATTAGAAAAAATGGTAGTTGCTGTATTGCTGAC 1365
QY 381 LeuGlyLeuAlaValLysPheAenSerAspThrAsnGluValAspIleProLeuAenThr 400
Db 1366 CTGGGCTTAGCTGTTAAATTTCAACAGTGCACACAAATGAAGTTGACATACCTTTGAACACC 1425
QY 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAen 420
Db 1426 AGGGTGGGCACCCAGGCGGTACATGGCTCCAGAAGTCTCGACGAGAGCCTGAGTAAAAAC 1485
QY 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTyrGluMet 440
Db 1486 CATTTCCAGCCCTACATCATGCTGACATCTACAGCTTTGGTTTGTATCATTTGGGAGATG 1545
QY 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db 1546 GCCCGTCGCTGTTATTACAGAGAGAAATCGTGGAGGAATATCAATTACCATATTACAACATG 1605
QY 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db 1606 GTGCTCTAGTGACCATCTTTATGAAGACATCGCTGAGGTGCTGTGTGTGAAACCTTTGCCG 1665
QY 481 ProIleValSerAsnArgTrpAenSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1666 CCAATCGTCTTAACCGCTGGAAACAGTGAATGCTTCGAGCCCTTTTGAAGCTGATG 1725
QY 501 SerGluCysTrpAlaHisAenProAlaSerArgLeuThrAlaLeuArgIleLysThr 520
Db 1726 TCAGAAATGCTGGGCCCAATAATCCAGACTCCAGACTCCAGCTTTTGAGATCAAGAAGACG 1785
QY 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db 1786 CTCGCAAGATGGTTGAATCCAGGATGTAAAGATT 1821
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RESULT 7

US-10-868-497-88
 ; Sequence 88, Application US/10868497
 ; Publication No. US20050106683A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Winkler, David G.
 ; APPLICANT: Shi, Jiye
 ; APPLICANT: Latham, John
 ; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR SCLEROSTIN AND
 ; TITLE OF INVENTION: METHODS FOR INCREASING BONE MINERALIZATION
 ; FILE REFERENCE: 60117-128
 ; CURRENT APPLICATION NUMBER: US/10/868,497
 ; CURRENT FILING DATE: 2004-06-15
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 88
 ; LENGTH: 3167
 ; TYPE: DNA
 ; ORGANISM: Rattus sp.
 US-10-868-497-88

Alignment Scores:

Pred. No.: 0 Length: 3167
 Score: 2838.00 Matches: 532
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-10-600-645-2 (1-532) x US-10-868-497-88 (1-3167)

QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
 DB 226 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCGCTGTCTGTTCATCTCTCAT 285
 QY 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
 DB 286 GTTCAAGGCGAGATCTAGATAGTATGCTCCATGGTACTGGTATGAAATCAGACGTGGAC 345
 QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
 DB 346 CAGAGAAGCCGGAATGGAGTGAGCTTTAGCACAGAGGACACCTTTACTTTCTTAAAA 405
 QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
 DB 406 TGCATTTGCTCAGGACACTGCCAGATGACGCTATTAAATACACATGCTAATACTAATGGC 465
 QY 81 HisCysPheAlaIleIleGluGluAspAspGlnGlyThrThrLeuThrSerGlyCys 100
 DB 466 CATTTGCTTTGCCATTTATAGAGAGATGATCAGGGAGAAACCCAGTTAACTTCTGGGTGT 525
 QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
 DB 526 ATGAAGTATGAAGCTCTCATTTTCAATCAAGAGATTACCAAAAGCCAGCTACGCAGG 585
 QY 121 ThrIleGluCysAspArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
 DB 586 ACAATAGAATGTTGTCGACCAATTTGTGCAACCAATATTTCAGCTTACACTGCCCCCT 645
 QY 141 ValValIleGlyProPhePheAspGlySerValArgTyrLeuAlaValLeuIleSerMet 160
 DB 646 GTCTGTATAGGCCCATCTTTTGTATGTCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 705
 QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
 DB 706 GCTGTCTGTATTGTCGCCATGATCGTCTTCTCAGCTGCTTCTGTTTACAAACATTACTGT 765
 QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGlnAlaPheIle 200
 DB 766 AAGAGTATCTCAAGCAGAGAGTGTGTTACAAACCGCTGACTTGGAAACAGGATGAAGCATTTAT 825
 QY 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220

RESULT 8

US-10-868-497-89
 ; Sequence 89, Application US/10868497
 ; Publication No. US20050106683A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Winkler, David G.
 ; APPLICANT: Shi, Jiye

DB 826 CCAGTAGGAGAACTCACTGAAAGACCTGATTGACCAGTCAACAAGCTCTGGTAGTGGATCT 885
 QY 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
 DB 886 GGAATTACCTTTATTGGTTTCAAGCAACTATTGCCAAACAGATTTCAGATGGTTCCGGCAGGTT 945
 QY 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
 DB 946 GGTAAAGGCCGGTATGGAGAAAGTATGGATGGGTAATGGCGTGGTGAAGAAAGTGGCTGTC 1005
 QY 261 LysValPhePheThrThrGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
 DB 1006 AAGTATTTTACCACCTGAAGAGCTAGCTGGTTTAGAGAAACAGAAATCTACCAGACG 1065
 QY 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
 DB 1066 GTGTTAATGCGTCATGAAATATATACTTGGTTTATAGCTGCAGACATTAAGGCCACCGGT 1125
 QY 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
 DB 1126 TCCTGGACTCAGCTGTATTGATTACTTACCATTAGAAATGGGTCTCTCTATGACTTTC 1185
 QY 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
 DB 1186 CTGAATGTGCCACCTCGACACACAGAGCCCTACTCAAGTTAGCTTATTCTGCTGCTGT 1245
 QY 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
 DB 1246 GGTCTGTGCCACCTCCACACAGAAATTTATGGCAGCAAGGCAAGCCTGCAATTTGCTCAT 1305
 QY 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
 DB 1306 CGAGACCTGGAAGAGCAAAACATCTCTTATTAAGAAAAATGGTAGTTGCTGTATTGCTGAC 1365
 QY 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
 DB 1366 CTGGGCTTAGCTGTTAAATTCACACAGTCACACAAATGAAGTTGACATACCTTTGAACACC 1425
 QY 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
 DB 1426 AGGTGGGCAACAGCGGTACATGCTCCAGAAAGTCTGGACGAGAGCCTGAGTAAAAAC 1485
 QY 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTrpGluMet 440
 DB 1486 CATTTCCAGCCCTACATCATGCTGCATCTACAGCTTACAGCTTTGGTTTGTATTTGGGAGATG 1545
 QY 441 AlaArgArgCysIleThrGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
 DB 1546 GCCCGTCTGTATTACAGGAGGAATCGTGGAGGAATATCAATTACCATATTACAACATG 1605
 QY 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
 DB 1606 GTGCCCTAGTACCCCATCTTATGAAGACATGCGTGAAGTCTGTGTGTGTAACCGTTGCGG 1665
 QY 481 ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
 DB 1666 CCAATCGTCTCTAACCCCTGGAACAGTGAATGATGCTCTTCGAGCGCTTTTGAAGCTGATG 1725
 QY 501 SerGluCysTyrAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
 DB 1726 TCAGAAATGCTGGGCCCATTAATCCACCATCCAGACTCCAGACTTTTCAGAAATCAAGAAGACG 1785
 QY 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
 DB 1786 CTCGCAAGAGTGGTTGAATCCAGGATGTAAGATT 1821

APPLICANT: Latham, John
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR SCLEROSTIN AND
FILE OF INVENTION: METHODS FOR INCREASING BONE MINERALIZATION
FILE REFERENCE: 60117-128
CURRENT APPLICATION NUMBER: US/10/868,497
CURRENT FILING DATE: 2004-06-15
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 89
LENGTH: 3167
TYPE: DNA
ORGANISM: Rattus norvegicus
US-10-868-497-89

Alignment Scores:

Pred. No.: 0 Length: 3167
Score: 2838.00 Matches: 532
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-600-645-2 (1-532) x US-10-868-497-89 (1-3167)

Qy 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
Db 226 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCGTCTGTTTCATCTTCAT 285
Qy 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
Db 286 GTTCAAGGCGAGAACTTAGATAGTATGCTCCATGCTACTGCTATGAAATCAGACGTGGAC 345
Qy 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
Db 346 CAGAGAAAGCGGAAATGAGTAGTACGTTAGCACAGGACACCTTACCTTCTTTAAAA 405
Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
Db 406 TGCTATTGCTCAGGACACTGCCAGATGACGCTATTATTAATACATGCACTAATATGGC 465
Qy 81 HisCysPheAlaIleIleGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 466 CATTGCTTTGCCATTATAGAAAGAGATGATCAGGAGAAACACCGTTAACTTCTGGGTGT 525
Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db 526 ATGAAGTATGAAGCTCTGATTTTCAATGCAAGATTCACAAAGCCCAAGCTACGCAGG 585
Qy 121 ThrIleGluCysCysArgThrAsnLeuLeuAsnGlnTyrLeuGlnProThrLeuProPro 140
Db 586 ACAATAGAAATGTTGCGACCAATTTGTGCAACCAATATTTGCGAGCTACACTGCCCCCT 645
Qy 141 ValValIleGlyProPheAspGlySerValArgThrLeuAlaValLeuIleSerMet 160
Db 646 GTGGTTATAGGCCCATCTTTTGTATGGCAGCGTCCGATGGCTGCTGCTCTCTATG 705
Qy 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
Db 706 GCTGTCTGATTTGTCGCATGATCGCTCTTCAGCTGCTTCTGTACAAACATTTACTGT 765
Qy 181 LysSerIleSerArgGlyArgTyrAsnArgAspLeuGlnAspGluAlaPheIle 200
Db 766 AAGAGTATCTCAAGCAGAGGTCTGTACAAACCGTGACTTGGAAACAGATGAGATTTAT 825
Qy 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerLysSerGlySerGlySer 220
Db 826 CCAGTAGGAGAACTCACTGAAAGACCTGATGACAGTCACAAAGCTCTGGTAGTGATCT 885
Qy 221 GlyLeuProLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 886 GGATTACCTTTATTTGGTTACGCAACTATTGCAAAACAGATTCAGATGGTTCCGCGAGTT 945
Qy 241 GlyLysGlyArgTyrGlyGluValTyrMetGlyLysTyrArgGlyGluLysValAlaVal 260

Db 946 GGTAAAGCGCGGTATGAGAAGTATGATGGTAAATGGCGTGTGCTGCTGCTGCTGCTC 1005
Qy 261 LysValPhePheThrThrGluGluAlaSerTyrPheArgGluThrGluIleTyrGlnThr 280
Db 1006 AAAAGTATTTTATACCACTGAAGAAGCTAGCTGGTGTAGAGAAACAGAAATCTACACAGC 1065
Qy 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaPheIleLysGlyThrGly 300
Db 1066 GTGTTAATGCTCATGAAATATATCTTGGTTTATAGCTCGAGACATTAAGGACCGGT 1125
Qy 301 SerTyrThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db 1126 TCCTGGACTCAGCTGATTTGATTACTGATTACCATGAGAATGGTCTCTCTATGACTTC 1185
Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db 1186 CTGAAATGTGCCACCTCGGACACAGAGCCCTACTCAAGTTAGCTTATCTGCTGCTGT 1245
Qy 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1246 GGTCTGTGCCACCTCCACAGAAATTTATGGCAGCGCAAGCGCTGCAATTCCTCAT 1305
Qy 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
Db 1306 CGAGACTGTAAGAGCAAAACATCTTATTAGAAATAATGTTAGTGTCTGTTGCTGCTGAC 1365
Qy 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db 1366 CTGGGCTAGCTGTTAAATTTCAACAGTGACACAAATGAAGTTGACATACCTTTGAACACC 1425
Qy 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
Db 1426 AGGTGGGACACAGGCGGTACATGGCTCCAGAAAGTCTGGACGAGACCTTGAGTAAANAC 1485
Qy 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTyrGluMet 440
Db 1486 CATTTCCAGCCCTACATCATGCTGCTGACATCTACAGCTTTGGTTTGTATCATCTTGGAGATG 1545
Qy 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db 1546 GCCCGTGTGTATTACAGAGGAATCGTGGAGAAATATCAATTACCATATTACAAACATG 1605
Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db 1606 GTGCTTAGTGACCCATCTTATGAAGACATCGGTGAGGTCTGTGTGAAACCTTGCCTG 1665
Qy 481 ProIleValSerAsnArgTyrAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1666 CCAATGCTCTTAACCGCTGGAACAGTGATGAATGCTTTCGAGCCGTTTGAAGCTGATG 1725
Qy 501 SerGluCysTyrAlaHisAsnProLysSerArgLeuThrAlaLeuArgIleLysThr 520
Db 1726 TCAGATGTGGGCCCATTAATCCAGCATCCAGACTCACAGCTTTGAGAATCAAGAAGACG 1785
Qy 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db 1786 CTCGCAAGATGTTGTAATCCAGGATGTAAGATT 1821

RESULT 9

US-09-903-068-13
Sequence 13, Application US/09903068
Patent No. US20020123139A1
GENERAL INFORMATION:
APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESS: Felice & Lynch
STREET: 805 Third Avenue
CITY: New York City

STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/903,068
FILING DATE: 11-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/679,187
FILING DATE: <Unknown>
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. US20020123139A1ember-1993
APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. US20020123139A1ember-1992
APPLICATION NUMBER: 9304677.9
FILING DATE: 8-March-1993
APPLICATION NUMBER: 9304680.3
FILING DATE: 8-March-1993
APPLICATION NUMBER: 9311047.6
FILING DATE: 28-May-1993
APPLICATION NUMBER: 9313763.6
FILING DATE: 2-July-1993
APPLICATION NUMBER: 9316099.2
FILING DATE: 3-August-1993
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-October-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kohlei, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD 5298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 698-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2070 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Mouse
FEATURE:
NAME/KEY: CDS
LOCATION: 217..1812
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-903-068-13

Alignment Scores:
Pred. No.: 0 Length: 2070
Score: 2823.00 Matches: 526
Percent Similarity: 99.81% Conservative: 5
Best Local Similarity: 98.87% Mismatches: 1
Query Match: 99.47% Indels: 0
DB: 3 Gaps: 0

US-10-600-645-2 (1-532) x US-09-903-068-13 (1-2070)

QY 1 MetThrGlnLeuThrThrValArgLeuLeuGlyAlaCysLeuPheIleSerHis 20
DB 217 ATGACTCAGCTATACACTTACATCAGATTACTGGGAGCCTGTCTGTTCATCTCTCAT 276
QY 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
DB 277 GTTCAAGGGCAGAACTAGATAGTATGCTCCATGGCAGCTGGTATGAAATCAGACTTGGAC 336
QY 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60

Db 337 CAGAAAGCCAGAAAATGGAGTGACTTTAGCACCAGAGATACCTTGTCTTTCTTAAAG 396
QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
Db 397 TGCTATTGCTCAGGACACTGCCAGATGATGCTATTATAACACATGCATATACTAATGCC 456
QY 81 HisCysPheAlaIleGluGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 457 CATTCGCTTTGCCAATTATAGAAAGATGATCAGGGAGAAACACACATTAACTTCTGGGTGT 516
QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuAAsp 120
Db 517 ATGAAGATATGAAGGCTCTGATTTTCAATGCAAGGATTCACCGAAAGCCAGCTACGCAGG 576
QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
Db 577 ACAATAGAATGTTGTCGGACCAATTTGTGCAACCATGATTTTGCAGCCTACACTGCCCCCT 636
QY 141 ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
Db 637 GTTGTATTAGGTCCTGTTTTCATGGCAGCATCCGATGGCTGGTGTGCTCATTTCCATG 696
QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
Db 697 GCTGTCTGTATAGTTGCTATGATCATCTTCTCAGCTGCTTTTGTCTATGAAGCATTTATGT 756
QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
Db 757 AAGACTATCTCAAGCAGGGGTCGTTACAACCGTGATTTGGAACAGGATCAAGCAITTTAT 816
QY 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
Db 817 CCAGTAGGAGAAATCATTTGAAAGACCTGATGACCATGCCAGTCCCAAGCTCTGGAGTGCATCT 876
QY 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 877 GGATTTGCCCTTTATTTGGTTCAGCGAACTATTTGCCAAACAGATTCAGATGGTTTCGGCAGGTT 936
QY 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgTyrGlyGluLysValAlaVal 260
Db 937 GGTAAAGGCCGCTATGGAGAGTATGGATGGTAAATGGCGTGGTGAAGAGTGGCTGTC 996
QY 261 LysValPhePheThrThrGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
Db 997 AAAGTGTTTTTACCACCTGAGAGAGCTAGCTGGTGTAGAGAAACAGAAATCTACCAGACG 1056
QY 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db 1057 GTGTTAATGCGTCATGAAATAATATCTTGTTTTATAGCTGCAGACATTAAGGCATCTGTT 1116
QY 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db 1117 TCCTGGACTCAGCTGATTTGATTTACTGATTACCATGAAATGGATCTCTCTATGACTTC 1176
QY 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db 1177 CTGAAATGTGCCACACTAGACACAGAGCCCTACTCAAGTATAGCTTTATTCGCTGCTTGT 1236
QY 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1237 GGTCTGTGCCACCTCCACACAGAAATTTATGTTATCCCAAGGGAAGCCTGCAATTTGCTCAT 1296
QY 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
Db 1297 CGAGACCTGAAGAGCAAAACATCCTTATTAGAAAAATGGAAGTTGCTGTATTCGTGAC 1356
QY 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db 1357 CTGGGCCCTAGCTGTTAAATTTCAACAGTGTATACAAATGAAGTTGACATACCTTGAATACC 1416
QY 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420

Db 1417 AGGTGGGACCAACGGGTACATGGCTCCAGAAAGTGTGGATGAAACGCTGAATAAAAAAC 1476
Qy 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTyrGluMet 440
Db 1477 CATTTCCAGGCCCTACATCATGGCTGACATCTATAGCTTTGGTTTGATCAATTTGGGAAATG 1536
Qy 441 AlaArgArgCysIleThrGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db 1537 GCTCGTGTGTATTACAGGAGGANTCGTGAGAGAAATATCAATACCATATTACAAATG 1596
Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValIleAspArgLeuArg 480
Db 1597 GTGCCAGTGAACCATCTATAGGACATGCGTGAGGTGTGTGTGTGTAACGCTTCCGG 1656
Qy 481 ProfileValSerAsnArgTyrAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1657 CCAATCGTGTCTAACCCCTGGAACAGCGATGAATGTCTTCGAGCAGTTTTTGAAGCTAATG 1716
Qy 501 SerGluCysTyrAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
Db 1717 TCAGAAATGTTGGGCCCATATCCAGCTCCAGACTCACAGCTTTGAGAAATCAAGAGACA 1776

RESULT 10

US-10-739-413-13
; Sequence 13, Application US/10739413
; Publication No. US20050048607A1
; GENERAL INFORMATION:
; APPLICANT: MIYAZONO, Kohei
; APPLICANT: INAMURA, Takeshe
; APPLICANT: DEN DIJKE, Peter
; TITLE OF INVENTION: PROTEINS HAVING SERINE/THREONINE KINASE DOMAINS, CORRESPONDING
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND THEIR USE
; FILE REFERENCE: LUD 5539.1 CIP
; CURRENT APPLICATION NUMBER: US/10/739,413
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US/09/267,963
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/GB93/02367
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: US 09/039,177
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-739-413-13

Alignment Scores:
Pred. No.: 0 Length: 2070
Score: 2823.00 Matches: 526
Percent Similarity: 99.81% Conservative: 5
Best Local Similarity: 98.87% Mismatches: 1
Query Match: 99.47% Indels: 0
DB: 9 Gaps: 0

US-10-600-645-2 (1-532) x US-10-739-413-13 (1-2070)

Qy 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
Db 217 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCTGTCTGTTCATCAATTTCTCAT 276
Qy 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
Db 277 GTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGGCAGCTGGTATGAATCAGACTTGGAC 336
Qy 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60

Db 337 CAGAAGAAGCCAGAAATGGAGTGACTTTTAGCACCAGAGGATACCTTTGCTCTTTCTTAAG 396
Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleIleThrAsnGly 80
Db 397 TGTCTATTGTCTCAGACACTGCCCCAGATGATGCTATTAAATAACACATGCATCAATAATG 456
Qy 81 HisCysPheAlaIleIleGluGluAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 457 CATTTGCTTTGCCATTATAGAAAGAGATGATCAGGGAGAAACCAATTAATCTTCTGGGTGT 516
Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db 517 ATCAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCACCGAAAGCCAGCTACGCAGG 576
Qy 121 ThrIleGluCysCysArgThrAsnLeuLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
Db 577 ACAATAGAATGTTGTTCGGACCAATTTTGTGCAACAGCATATTTCGAGCCCTACACTGCC 636
Qy 141 ValValIleGlyProPhePheAspGlySerValArgTyrLeuAlaValLeuIleSerMet 160
Db 637 GTTGTATTAGTCCGTTCTTTGTATGGCAGCATCCGATGGTGGTGTGTGCTCATTTCCATG 696
Qy 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
Db 697 GCTGTCTGTATAGTTCGTATGATCATCTTCTCAGCTGCTTTTGTCTATAAGCATTTATGT 756
Qy 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGlnAspGluGlnAspGluAlaPheIle 200
Db 757 AAGAGTATCTCAAGCAGGGGTCTGTACACCGTGTATTGGAAACAGGATGAAGCATTTATT 816
Qy 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
Db 817 CCAGTAGGAGAAATCATTTGAAAGACCTGATTGACCATGCCAAGACTCTGGAGTGATCT 876
Qy 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 877 GGATTGCCTTTATTGGTTTCAGCGAACTATTTCGCAACACAGATTTCAGATGGTTCCG 936
Qy 241 GlyLysGlyArgTyrGlyGluValTyrMetGlyLysTyrPargGlyGluLysValAlaVal 260
Db 937 GGTAAAGGCCGTATCGAGAAGTATGGATGGGTAAATGGCGTGTGAAAAAGTGGCTGTC 996
Qy 261 LysValPhePheThrThrGluGluAlaSerTyrPheArgGluThrGluIleTyrGlnThr 280
Db 997 AAGTGTGTTTTTACCACCTGAAGAGCTAGCTGTTTTAGAGAAACAGAAATCTACCAGAC 1056
Qy 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db 1057 GTGTTAATGCGTCATGAAATATATCTTGGTTTTTATAGCTGCAGACATTAAGGCACCTGT 1116
Qy 301 SerTyrThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db 1117 TCCTGGACTCAGCTGTATTGTTGATTACTGATTACCATGAAATGGATCTCTCTATGACTTC 1176
Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db 1177 CTGAAATGTGCCACACTAGACAGGCCCTACTCAAGTTAGCTTATTCTGCTGCTGTGT 1236
Qy 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1237 GGTCTGTGCCACCTCCACACAGAAATTTATGGTACCAAGGAAAGCTGCAATTTGCTCAT 1296
Qy 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
Db 1297 CGAGACTCTGAAGAGCAAAACATCTCTTATTAAAGAAAAATGGAAGTTGCTGTATTGTGTC 1356
Qy 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db 1357 CTGGGCTAGCTGTGTTAAATTTCAACAGTGATACAAATGAAGTTGACATACCTTTGAATACC 1416
Qy 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
Db 1417 AGGGTGGCACCACCAAGGGTACATGGCTCCAGAAAGTCTCGATCAAGACCTGGAATAAAAC 1476


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QY 421 HisPheGlnProTyrIleMetAlaSerPheTyrSerPheGlyLeuIleIleTrpGluMet 440
DB 1477 CATTTCCAGCCCTACATCATGCTGACATCTATAGCTTTGGTTGGTTCATCATTTGGGAAATG 1536
QY 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
DB 1537 GTCGTCGTGTATTACAGAGAGAAATCGTGGAGGAATATCAATTACCATATTACAAATG 1596
QY 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValIysArgLeuArg 480
DB 1597 GTGCCAGTGACCCATCTATCAGGACATGCGTGAGGTTGTGTGTGAACGCTTGGCG 1656
QY 481 ProIleValSerAsnArgTrpAsnSerAspGluCysLeuArgAlaValLeuIysLeuMet 500
DB 1657 CCAATCGTGTCTAACCGCTGGAAACAGCGATGAATGTCTTCGAGCAGTTTTTGAAGCTAATG 1716
QY 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleIysIysThr 520
DB 1717 TCAGAAATGTGGCCCATTAATCCAGCCTCCAGACTCACAGCTTTGAGAAATCAAGAAGACA 1776
QY 521 LeuAlaLysMetValGluSerGlnAspValIysIle 532
DB 1777 CTTGCAAAAAATGGTTGAATCCCGAGGATGTAAGATT 1812

RESULT 11
US-09-742-153-11
; Sequence 11, Application US/09742153
; Publication No. US20030096296A1
; GENERAL INFORMATION:
; APPLICANT: Rosenbaum, Jan S
; TITLE OF INVENTION: The Use of a BMP Protein Receptor
; Complex for Screening Bone Metabolism Actives and Cells
; Co-Transfected With a Type II BMP Receptor and a Type I
; BMP Receptor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Procter & Gamble Company
; STREET: 11810 East Miami River Road
; CITY: Ross
; STATE: OH
; COUNTRY: USA
; ZIP: 45061
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/742,153
; FILING DATE: 20-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,467
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hersko, Bart S.
; REGISTRATION NUMBER: 32,572
; REFERENCE/DOCKET NUMBER: 5474R
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (513) 627-0633
; TELEFAX: (513) 627-0260
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2402 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-742-153-11
Alignment Scores:
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Pred. No.: 0 Length: 2402
Score: 2823.00 Matches: 526
Percent Similarity: 99.81% Conservative: 5
Best Local Similarity: 98.87% Mismatches: 1
Query Match: 99.47% Indels: 0
DB: 3 Gaps: 0

US-10-600-645-2 (1-532) x US-09-742-153-11 (1-2402)

QY 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
DB 11 ATGACTCAGCTATACACTTACATCAGATTACTGGAGCGCTGCTGTTTCATCATTTCTCAT 70
QY 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetCysSerAspValAsp 40
DB 71 GTTCAAGGGCAGAAATCTAGATAGTATGCTCCATGGCACTGGGTATGAAATCAGACTTGGAC 130
QY 41 GlnIysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
DB 131 CAGAAGAAAGCCAGAAAAATGGAGTGACTTTAGCACCAGAGGATACCTTGCTTTCTTTAAAG 190
QY 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
DB 191 TGCTATTGCTCAGGACACTGCCAGATGATGCTATTATACACATGATCAATAATGGC 250
QY 81 HisCysPheAlaIleIleGluGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
DB 251 CATTTGCTTTGCCATTATAGAAGAAATGATCAGGGAGAAACACATTAACATTTCTGGGTGT 310
QY 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
DB 311 ATGAAGTATGAAGGCTCTGATTTTCAATGCAAGGATTCAACGAAAGCCAGCTACGAGG 370
QY 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
DB 371 ACAATAGAAATGTTGTCGACCAATTTGTGCAACAGTATTTGCAGCCTCACTGCCCCCT 430
QY 141 ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
DB 431 GTTGTATAGGTCCGTTCTTTGATGGCAGCATCCGATGGCTGGTTGTGCTCATTTCCATG 490
QY 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrIysHisTyrCys 180
DB 491 GCTGTCTGTATAGTTGCTATGATCATCTCTCCAGCTGCTTTTGTCTATAAGCATTAATTGT 550
QY 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
DB 551 AAGAGTATCTCAAGCAGGGGTCTGTACAACTGATTTTGGAAACAGGATGAAGCATTTATT 610
QY 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
DB 611 CCAGTAGGAGAAATCATTTGAAAGACCTGATTGACAGTCCCAAAGCTTTTGGTAGTATAT 670
QY 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
DB 671 GGATTGCTTTTATTGGTTTCAGGAACTATTGCCAAACAGATTTCAGATGGTTTCGGCAGGT 730
QY 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
DB 731 GGTAAGGCCCGCTATGGAGAAAGTATGGATGGTAAATGGCGTGGTGAAGAAAGTGGCTGTC 790
QY 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
DB 791 AAAGTGTTTTTTACCACCTGAAGAAAGCTAGCTGGTTTGTAGAGAAACAGAAATCTACAGAG 850
QY 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleIysGlyThrGly 300
DB 851 GTGTTAATGCGCTCATGAAAAATATATCTTGTTTATAGCTGCAGACATTAAAGGCACTGTGT 910
QY 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
DB 911 TCCTGGACTCAGCTGATTTTCATTACTGATTACCATGAAATGGATGATCTCTCTATGACTTC 970
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Db 1371 CGAGACCTGAAGCAAAACATCTTATTAGAAAAATGGAGTTGCTGTATTCTGAC 1430
Qy 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspLeuProLeuAsnThr 400
Db 1431 CTGGCCCTAGCTGTTAAATTTCAACAGTGATACAAATGAAGTTGACATACCTTGAATACC 1490
Qy 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
Db 1491 AGGGTGGGCACCAAGCGGTACATGGCTCCAGAAGTGCTGGATGAAGACCTGAATAAAAAAC 1550
Qy 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTyrGluMet 440
Db 1551 CATTTCCAGCCCTACATCATGCTGACATCTATAGCTTTGGTTTGTATCATTTGGGAATG 1610
Qy 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db 1611 GCTCGTCGTGTATTACAGGAGGAATCGTGGAGGAATATCAATTACCATATTACAACATG 1670
Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db 1671 GTGCCAGTGACCCATCTTATGAGGACATGCGTGAGGTTGTGTGTGAAACGCTTGCGG 1730
Qy 481 ProfileValSerAsnArgTyrAsnSerAspGlu----- 491
Db 1731 CCAATCGTCTTAACCGCTGGAAACAGCGATGAAGTAAAGTTCCTGCTAAAG 1790
Qy 491 ----- 491
Db 1791 TGATGAGTGAGTGGCCGAGTTACTCTGTGCTCACCACACTCTGTTGTCATTTATTTCTCTT 1850
Qy 492 ---CysLeuArgAlaValLeuLysLeuMetSerGluCysTyrAlaHisAsnProLysSer 510
Db 1851 TAGTGTCTTCGAGCAGTTTGAAGCTAATGTCAGAAATGTTGGGCCCAATAATCCAGCCTCC 1910
Qy 511 ArgLeuThrAlaLeuArgIleLysLysThrLeuAlaLysMetValGluSerGlnAspVal 530
Db 1911 AGACTCAGAGCTTTGAGAAATCAAGAAACACATTTGCAGAAATGGTTGAATCCCGAGATGTA 1970
Qy 531 LysIle 532
Db 1971 AAGATT 1976
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RESULT 13

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US-10-745-237-307
; Sequence 307, Application US/10745237
; Publication No. US20050227301A1
; GENERAL INFORMATION:
; APPLICANT: Cyclacel Limited
; APPLICANT: Glover, David
; APPLICANT: Bell, Graham
; APPLICANT: Frenz, Lisa
; APPLICANT: Midgley, Carol
; TITLE OF INVENTION: Cell Cycle Progression Proteins
; FILE REFERENCE: P015819W0 CYK
; CURRENT APPLICATION NUMBER: US/10/745,237
; PENDING FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: US 60/439,123
; PRIOR FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 60/468,402
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 307
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Z22535
US-10-745-237-307
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Alignment Scores:

Pred. No.: 0 Length: 1599

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Score: 2769.00 Matches: 517
Percent Similarity: 98.50% Conservative: 7
Best Local Similarity: 97.18% Mismatches: 8
Query Match: 97.57% Indels: 0
DB: 9 Gaps: 0
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US-10-600-645-2 (1-532) x US-10-745-237-307 (1-1599)

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Qy 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
Db 1 ATGACTAGCTATACATTTTACATCAGATTATTGGAGGCTATTGTTTCATCATTTCTCGT 60
Qy 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
Db 61 GTTCAAGGACAGAAATCTGGATAGTATGCTTCATGGCACTGGGATGAAATCAGACTCCGAC 120
Qy 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
Db 121 CAGAAAAAGTCAGAAAAATGGAGTAACCTTAGCACCAGAGGATACCTTGCCCTTTTAAAG 180
Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
Db 181 TGCTATTGCTCAGGGCACTGTCCAGATGATGCTATTATAACACATGATCAATAATGA 240
Qy 81 HisCysPheAlaIleIleGluGluAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 241 CATTGCTTTGGCATCATAGAAAGATGACCAGGGAGAAACCCACATTAGCTTTCAGGGTGT 300
Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db 301 ATGAAAAATAGAGGATCTGATTTTCAGTGCAGAAAGATCTCCAAAAAGCCAGCTAGCCGG 360
Qy 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
Db 361 ACAATAGAAATGTTGCGGACCAATTTATGTAAACAGTATTTGCAACCCACACTGCCCCCT 420
Qy 141 ValValIleGlyProPhePheAspGlySerValArgTyrLeuAlaValLeuIleSerMet 160
Db 421 GTTGTGATAGTCGCTTTTGTGATGGCAGCAATTCGATGGCTGGTTCCTCATTTCTATG 480
Qy 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
Db 481 GCTGTCTGCATAATTGCTATGATCATCTTCTCCAGCTGCTTTTGTTCACAAACATTATTGC 540
Qy 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
Db 541 AAGAGCATCTCAAGCAGACGTCGTTTACAATCGTGATTTGGAACAGGATGAAGCAATTATT 600
Qy 201 ProValGlyGluSerLeuLysAspIleAspGlnSerGlnSerSerGlySerGlySer 220
Db 601 CCAGTTGGAGAAATCACTAAAAAGACCTTATTGACCAGTCACAAAGTTCTGGTAGTGGGTCT 660
Qy 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 661 GGACTACCTTTATTGGTTTCAGCAACTATTGCCAAACAGATTTCAGATGTCGCGCAAGTT 720
Qy 241 GlyLysGlyArgTyrGlyGluValTyrMetGlyLysTyrArgGlyGlyLysValAlaVal 260
Db 721 GGTAAGGCCGATATGAGAAAGTATGGATGGCAAAATGCGCTGGCGAAAAAGTGGCGGTG 780
Qy 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
Db 781 AAAGTATTCTTTTACCACCTGAAAGACCCAGCTGGTTTCGAGAGAAACAGAAATCTACCAAACT 840
Qy 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAspIleLysGlyThrGly 300
Db 841 GTGCTAATGCCCCATGAAACATATCTTGGTTTCATAGCGGCAGACATTAAAGGTACAGGT 900
Qy 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db 901 TCCTGGACTCAGCTCTATTGATTGATTACCATGAAATGGATCTCTCTATGACTTC 960
Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
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Db 961 CTGAAATGTGCTACACTGGACACAGAGCCCTGCTTAAATGGCTTATTTCAGCTGCCTGT 1020
Qy GlyLeuCyHisLeuHisThrGluLeuThrGlnGlyLysProAlaIleAlaHis 360
Db 1021 GGTCTGTGCCACCTGCCACAGAAATTTATGGACCCAGAAAGCCCGCAATGTCTCAT 1080
Qy 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
Db 1081 CGAGACCTTAAGAGCAAAACATCTCATCAAGAAAAATGGAGTTGCTGCATTGCTGAC 1140
Qy 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db 1141 CTGGGCTTGTGTTAAATTAACAGATGACACAAATGAAGTTGATGTGCCCTTGAATACC 1200
Qy 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLysAsn 420
Db 1201 AGGGTGGGACCAACCTACATGGCTCCCGAGTGTGGACGAAGCCCTGAACAAAAAC 1260
Qy 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTyrGluMet 440
Db 1261 CACTTCCAGCCCTACATCATGGCTGACATCTACAGCTTGGCCTTAATCATTGGGAGATG 1320
Qy 441 AlaArgGlyCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db 1321 GCTCGTGTGTATCACAGAGGATCGTGGAAAGAAATACCAATTGGCATAATTACAACATG 1380
Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db 1381 GTACCGAGTATCGTCATACGAAGATATCGTGAGGTGTGTGTGTGCAACGTTTGGCG 1440
Qy 481 ProIleValSerAsnArgTyrAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1441 CCAATTGTGCTAATCGGTGGAACAGTGAATGTCTACAGCAGTTTGAAGCTAATG 1500
Qy 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
Db 1501 TCAGAATGCTGGGCCCAACATCCAGCTCCAGACTCCAGACTCAGACATTTAGAAGACG 1560
Qy 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db 1561 CTTGCCAAGATGTTGAATCCCAAGATGTAAAAATC 1596

RESULT 14

US-10-153-217-1
; Sequence 1, Application US/10153217
; Publication No. US20030072758A1
; GENERAL INFORMATION:
; APPLICANT: HOWE, JAMES R.
; TITLE OF INVENTION: BMPRIA INVOLVEMENT IN JUVENILE POLYPOSIS
; FILE REFERENCE: IOWA:037US
; CURRENT APPLICATION NUMBER: US/10/153,217
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: 60/292,691
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1596)
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-153-217-1
Alignment Scores:
Pred. No.: 0 Length: 2623
Score: 2769.00 Matches: 517
Percent Similarity: 98.50% Conservative: 7
Best Local Similarity: 97.18% Mismatches: 8

Query Match: 97.57% Indels: 0
DB: 5 Gaps: 0
US-10-600-645-2 (1-532) x US-10-153-217-1 (1-2623)
Qy 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
Db 1 ATGACTCAGCTATACATTTACATTCAGATTATTGGGAGCCTATTGTTCATCATTTCTCGT 60
Qy 21 ValGlnGlyGluAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
Db 61 GTTCAAGAGCAGACATCTGGATAGTATGCTTCATGGCAGCTGGGATGAAATCAGACTCCGAC 120
Qy 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
Db 121 CAGAAAAAGTCAGAAAAATCGAGTAACCTTAGCACCAGAGGATACCTTGGCTTTTAAAG 180
Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
Db 181 TGTATTGCTCAGGGCACTGTCAGATGATGCTATTATAACACATGCATTAATAATGGA 240
Qy 81 HisCysPheAlaIleIleGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 241 CATTTGCTTTGCCATCATAGAAGATGACAGGGAGAAAAACACATTTAGCTTCAGGGTGT 300
Qy 101 MetLysTyrGluGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db 301 ATGAAATATGAAGATCTGATTTTCAGTGCAGAAAGATTCCTCAAAAGCCAGCTACGCCG 360
Qy 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
Db 361 ACAATAGAATGTTGTCGACCAATTTATGTAACCAAGTATTTGCAACCCACACTGCCCCCT 420
Qy 141 ValValIleGlyProPhePheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
Db 421 GTTGTATAGATGTCGCTTTTTCATGGCAGCATTCGATGGCTGCTTTTGTCTATTCTATG 480
Qy 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTyrLysHisTyrCys 180
Db 481 GCTGTCTGCATTAATTTGCTATGATCTTCACAGCTGCTTTTGTTCACAAACATTATTC 540
Qy 181 LysSerIleSerSerArgGlyArgTyrAsnArgAspLeuGluGlnAspGluAlaPheIle 200
Db 541 AAGAGCATCTCAAGCAGACGCTCGTTACAATCGTATTTGGAACAGGATCAAGCATTTATT 600
Qy 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySerGlySer 220
Db 601 CCAGTTGGAGAAATCACTAAAGACCTTATTGACCAAGTTCACAAAGTTCTGGTAGTGGTCT 660
Qy 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 661 GGACTACCTTTATTGTTTCAGCGAACTATTGCCAAACAGATTTCAGATGTCGCGCAAGTT 720
Qy 241 GlyLysGlyArgTyrGlyGluValTrpMetGlyLysTrpArgGlyGlyLysValAlaVal 260
Db 721 GGTAAAGCCCGATATGGAGAAAGTATGGATGGCAAAATGGCGTGGCGAAAAAGTGGCGTG 780
Qy 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTyrGlnThr 280
Db 781 AAAGTATTCTTTTACCACCTGAAGAACCCAGCTGGTTTCGAGAAACAGAAATCTACCAACT 840
Qy 281 ValLeuMetArgHisGluAsnIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db 841 GTGCTAATGCCCATGAAACATACCTTGGTTTCATAGCGGCAGACATTTAAAGGTACAGGT 900
Qy 301 SerTrpThrGlnLeuTyrLeuIleThrAspTyrHisGluAsnGlySerLeuTyrAspPhe 320
Db 901 TCCTGGACTCAGCTCTATTGATTACTGATTACCATGAAATGGATCTCTCTATGACTTC 960
Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaAlaCys 340
Db 961 CTGAAATGTGCTACACTGGACACAGAGCCCTGCTTAAATTTGGCTTATTTCAGCTGCCTGT 1020

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Qy 341 GlyLeuCysHisLeuHisThrGluIleTyrGlyThrGlnGlyProAlaIleAlaHis 360
Db 1021 GGTCTGTGCACCTGCACACAGAAATTTATGGACCCCAAGGAAGCCCAATGTCAT 1080
Qy 361 ArgAspLeuLysSerLysAsnIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
Db 1081 CGAGACCTAAGACGACAAACATCCTCATCAAGAAAATGGGAGTTGCTGCATTGCTGAC 1140
Qy 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db 1141 CTGGGCTTGTCTGTTAAATTCACAGTGCACACAAATGAAGTTGATGTCCTTGAATACC 1200
Qy 401 ArgValGlyThrArgArgTyrMetAlaProGluValLeuAspGluSerLysAsn 420
Db 1201 AGGTGGGACCAACAGCTACATGGCTCCGAAGTGTGGAGCAAGCCCTGAACAAAAAC 1260
Qy 421 HisPheGlnProTyrIleMetAlaAspIleTyrSerPheGlyLeuIleIleTyrGluMet 440
Db 1261 CACTCCAGCCCTACATCATGCTGCATCTACAGCTTCGGCTTAATCATTTGGAGATG 1320
Qy 441 AlaArgArgCysIleThrGlyGlyIleValGluGluTyrGlnLeuProTyrTyrAsnMet 460
Db 1321 GCTCGTGTGTATCACAGGAGGATCGTGAAGAATACCAATTCCTATATTACAACATG 1380
Qy 461 ValProSerAspProSerTyrGluAspMetArgGluValValCysValLysArgLeuArg 480
Db 1381 GTACCGAGTGATCCGCTACCAAGATATGCGTGAGTTGTGTGTCAACGTTTGGCG 1440
Qy 481 ProIleValSerAsnArgTyrAsnSerAspGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1441 CCAATTGTCTAATCGTGGAAACAGTGTATGATCTACGAGCAGTTTGAAGCTAATG 1500
Qy 501 SerGluCysTyrAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520
Db 1501 TCAGATGCTGGGCGCCACAAATCCAGCCTCCAGACTCACAGCATTCAGAAATTAAGAAGACG 1560
Qy 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db 1561 CITGCCAAGATGGTTGAATCCCAAGATGTAAAAATC 1596

RESULT 15
US-09-903-068-5
; Sequence 5, Application US/09903068
; Patent No. US20020123139A1
; GENERAL INFORMATION:
; APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
; Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik
; TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/903,068
; FILING DATE: 11-Jul-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/679,187
; FILING DATE: <Unknown>
; APPLICATION NUMBER: PCT/GB93/02367
; FILING DATE: 17-No. US20020123139A1ember-1993
; APPLICATION NUMBER: 9224057.1
; FILING DATE: 17-No. US20020123139A1ember-1992
; APPLICATION NUMBER: 9304677.9
; FILING DATE: 8-March-1993
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; APPLICATION NUMBER: 9304680.3
; FILING DATE: 8-March-1993
; APPLICATION NUMBER: 9311047.6
; FILING DATE: 28-May-1993
; APPLICATION NUMBER: 9313763.6
; FILING DATE: 2-July-1993
; APPLICATION NUMBER: 9136099.2
; FILING DATE: 3-August-1993
; APPLICATION NUMBER: 9321344.5
; FILING DATE: 15-October-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohlei, Vinset
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: LUD 5298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2932 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 310..1905
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-903-068-5

Alignment Scores:
Pred. No.: 0 Length: 2932
Score: 2769.00 Matches: 517
Percent Similarity: 98.50% Conservative: 7
Best Local Similarity: 97.18% Mismatches: 8
Query Match: 97.57% Indels: 0
DB: 3 Gaps: 0

US-10-600-645-2 (1-532) x US-09-903-068-5 (1-2932)
Qy 1 MetThrGlnLeuTyrThrTyrIleArgLeuLeuGlyAlaCysLeuPheIleIleSerHis 20
Db 310 ATGACTCAGCTATACATTTACATCAGATTATTGGAGGCTATTGTTTCATCATTTCTCGT 369
Qy 21 ValGlnGlyGlnAsnLeuAspSerMetLeuHisGlyThrGlyMetLysSerAspValAsp 40
Db 370 GTTCAAGGACAGAATCTGGATAGTAGTCTTCATGGCACTGGGATGAAATCAGACTCCGAC 429
Qy 41 GlnLysLysProGluAsnGlyValThrLeuAlaProGluAspThrLeuProPheLeuLys 60
Db 430 CAGAAAAAGTCAGAAAAATGGAGTAGACCTTAGCACCAGAGGATACCTTGCTTTTAAAG 489
Qy 61 CysTyrCysSerGlyHisCysProAspAspAlaIleAsnAsnThrCysIleThrAsnGly 80
Db 490 TGCTATTGCTCAGGGCACTGTCCAGATGATGCTATTATAACACATGCAATAATGGA 549
Qy 81 HisCysPheAlaIleIleGluGluAspAspGlnGlyGluThrThrLeuThrSerGlyCys 100
Db 550 CATTGCTTTGCCATCATAGAAGAGATGACCAGGGAGAAACCCACATTAGCTTCAGGGTGT 609
Qy 101 MetLysTyrGlyGlySerAspPheGlnCysLysAspSerProLysAlaGlnLeuArgArg 120
Db 610 ATGAAATATGAAGGATCTGATTTTCAGTGCAGAAAGATCTCCAAAAAGCCAGCTAGCCGG 669
Qy 121 ThrIleGluCysCysArgThrAsnLeuCysAsnGlnTyrLeuGlnProThrLeuProPro 140
Db 670 ACAATAGATGTTGTCGGACCAATTTATGTAACACAGTATTGTAACACCCACACTGCCCCCT 729
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Qy 141 ValValIleGlyPropPheAspGlySerValArgTrpLeuAlaValLeuIleSerMet 160
Db 730 GTTGTCAATGCTCGTGTGTTTGTATGGCAGCATTCGATGGCTGGTGTTCCTCAATTCCTATG 789
Qy 161 AlaValCysIleValAlaMetIleValPheSerSerCysPheCysTrpLysHisTrpCys 180
Db 790 GCTGTCGCAATAATGCTATGATCATCTTCTCAGCTGCTTTGTACAAACATATTGC 849
Qy 181 LysSerIleSerArgGlyArgTrpAsnArgAspLeuGluGlnAspGluAlaPheIle 200
Db 850 AAGAGCATCTCAAGCAGACGCTGTTACATCGTGATTTGGAAACAGGATGAAGCATTTATT 909
Qy 201 ProValGlyGluSerLeuLysAspLeuIleAspGlnSerGlnSerSerGlySer 220
Db 910 CCAGTTCGAGAAATCACTAAAGACCTTATTGACCAGTCACAAAGTTCTGCTAGTGGTCT 969
Qy 221 GlyLeuProLeuLeuValGlnArgThrIleAlaLysGlnIleGlnMetValArgGlnVal 240
Db 970 GGACTACCTTTATTGGTTTCAGCGCAACTATTGCCAAACAGATTGATGGTCCGGCAAGTT 1029
Qy 241 GlyLysGlyArgTrpGlyGluValTrpMetGlyLysTrpArgGlyGluLysValAlaVal 260
Db 1030 GGTAAAGCCGATATGGAAGATGATGGATGGGCAATGGCGTGGCAAAAGTGGCGTG 1089
Qy 261 LysValPhePheThrThrGluGluAlaSerTrpPheArgGluThrGluIleTrpGlnThr 280
Db 1090 AAAGTATTCTTTACCACCTGAAGAAGCCAGCTGGTTTCGAGAAACAGAAATCTACCAACT 1149
Qy 281 ValLeuMetArgHisGluAenIleLeuGlyPheIleAlaAlaAspIleLysGlyThrGly 300
Db 1150 GTGCTAATGGCCATGAAACATACCTTGGTTTCATAGCGGCAGACATTTAAGGTACAGGT 1209
Qy 301 SerTrpThrGlnLeuTrpLeuIleThrAspTrpHisGluAsnGlySerLeuTrpAspPhe 320
Db 1210 TCTGTGACTCAGCTCTATTGATTACTGATTACATGAAATGGATCTCTATGACTTC 1269
Qy 321 LeuLysCysAlaThrLeuAspThrArgAlaLeuLeuLysLeuAlaTyrSerAlaLys 340
Db 1270 CTGAAATGTCTACACTGGACACCAGAGCCCTGCTTAAATTGGCTTATTTCAGCTGCTGT 1329
Qy 341 GlyLeuCysHisLeuHisThrGluIleTrpGlyThrGlnGlyLysProAlaIleAlaHis 360
Db 1330 GGTCTGTGGCCACTGCACACAGAAATTTATGGCACCCCAAGAAAGCCGCAATTGCTCAT 1389
Qy 361 ArgAspLeuLysSerLysAenIleLeuIleLysLysAsnGlySerCysCysIleAlaAsp 380
Db 1390 CGAGACCTTAAGAGCAAAACATCCTCATCAAGAAATAAGGAGTTGCTGCAATGCTGAC 1449
Qy 381 LeuGlyLeuAlaValLysPheAsnSerAspThrAsnGluValAspIleProLeuAsnThr 400
Db 1450 CTGGGCTTGTCTGTTAAATTCACAGTGACACAAATGAAGTTGATGCTGCCCTTGAATACC 1509
Qy 401 ArgValGlyThrArgTrpMetAlaProGluValLeuAspGluSerLeuSerLysAsn 420
Db 1510 AGGGTGGGCACCAACGCTACATGGCTCCCGAAGTGTGGACGAAAGCCTGAACAAAAAC 1569
Qy 421 HisPheGlnProTrpIleMetAlaAspIleTrpSerPheGlyLeuIleIleTrpGluMet 440
Db 1570 CACTTCAGCCCTTACATCATGGCTGACATCTACAGCTTCGGCTTAATCATTTGGGAGATG 1629
Qy 441 AlaArgAlaCysIleThrGlyGlyIleValGluGluTrpGlnLeuProTrpTrpAsnMet 460
Db 1630 GCTCGTGTGTATACAGGAGGGATCGTGGAGAATACCAATTCGCATATTACAACATG 1689
Qy 461 ValProSerAspProSerTrpGluAspMetArgGluValValCysValLysArgLeuArg 480
Db 1690 GTACCGAGTGATCCGTCATACGAAGATATGCGTGAGGTTGTGTGTCAAAACGTTTGGCG 1749
Qy 481 ProIleValSerAenArgTrpAenSerAsnGluCysLeuArgAlaValLeuLysLeuMet 500
Db 1750 CCAATTGTGTCTAATCGGTGGAACAGTGATGAATGTCTACGAGCAGTTTTTGAAGCTAATG 1809
Qy 501 SerGluCysTrpAlaHisAsnProAlaSerArgLeuThrAlaLeuArgIleLysLysThr 520

Db 1810 TCAGAATGCTGGGCCCAACAATCCAGACTCCAGACTCACAGCAATTGAGAATTAAGAAGACG 1869
Qy 521 LeuAlaLysMetValGluSerGlnAspValLysIle 532
Db 1870 CTTGCCAAGATGGTTGAATCCCAAGATGTAAAAATC 1905

Search completed: December 10, 2005, 00:09:40
Job time : 852 secs

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